

Score: 547.00 Matches: 99
 Percent Similarity: 96.36% Conservative: 7
 Best Local Similarity: 90.00% Mismatches: 4
 Query Match: 92.71% Indels: 0
 Gaps: 0
 DB: 22

US-10-019-455A-24 (1-110) x AAF59080 (1-330)

QY 1 HisGlyIlePheMetAspArgLeuAlaSerIleLysLeuCyseAlaAspAspGluCysVal 20
 DB 1 CATGGTGTATTATGATGAATTAACCTTTCTTAAGAGCTGTGTGGGATGAGAGAGTGTCT 60
 QY 21 TyrThrIleSerLeuAlaSerAlaGlnGluAspIleProAspCysArgPheIle 40
 DB 61 TATACTATTCTCTGGCAGAGCACAGAAATTACATGCCCCAGACTGTAGTTTCATC 120
 QY 41 AsnValIleLysGlnGlnGlnIleTyrValTyrSerIleValIleValAsnGlyAla 60
 DB 121 GATGTCAGAAAGGCGACAGATCTATGTTACTCCAGCTGTAAACAGAAACGAGAGCT 180
 QY 61 GlyGluPheTTPAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValGly 80
 DB 181 GGAGAGTTTGGGCTGGCAGCTGTTATGTGACACCGAGATGAGATGGGAATTGTAGCT 240
 QY 81 TyrPheProArgAsnLeuValIleGlnGlnArgValTyrGlnGlnAlaThrLysGluVal 100
 DB 241 TATTTCCCGACCACTGTGTGAGAGGAGCGGTGTATACCGAGAGGCCACCAAGAGATC 300
 QY 101 ProThrThrAspIleAspPheCysGlu 110
 DB 301 CCAACCAAGATTTGACTTCTTCTGTGA 330
 QY 101 ProThrThrAspIleAspPheCysGlu 110
 DB 301 CCAACCAAGATTTGACTTCTTCTGTGA 330
 RESULT 13
 AAF59068
 ID AAF59068 standard; DNA; 384 BP.
 XX AAF59068;
 AC
 XX 23-APR-2001 (first entry)
 DT
 XX Mouse MLP nucleotide sequence SEQ ID NO:10.
 DE
 XX MLP, MIA; melanoma inhibitory activity; cancer; bone disease;
 KM joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
 KM cardiant; gene therapy; secretory cell function regulator; promoter;
 KM inhibitor; ds.
 XX
 OS Mus musculus.
 XX
 PN WO200102564-A1.
 XX
 PD 11-JAN-2001.
 XX
 PF 29-JUN-2000; 2000WO-JP04278.
 XX
 PR 30-JUN-1999; 99JP-0186718.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Itoh Y, Nishi K, Ogi K, Okubo S, Mogi S, Noguchi Y, Yoshimura K;
 PI Tanaka H;
 XX
 DR MPI; 2001-159271/16.
 XX
 DR P-PSDB; AAB69125.
 XX
 PT Safe, low-toxicity secretory cell function-regulatory protein and
 PT encoded DNA, applicable as drugs, in diagnosis and development of
 PT promoters and inhibitors for preventing or treating e.g. bone and joint
 PT diseases -
 XX
 PS Claim 11; Page 93; 11pp; Japanese.
 XX
 CC The present invention describes novel MLP proteins and their encoding

CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
 CC activities, and can be used in gene therapy and as secretory cell
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in
 CC the diagnosis and development of promoters and inhibitors for preventing
 CC or treating bone and joint diseases as well as pathologic angiogenesis.
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
 CC in the exemplification of the present invention.
 CC
 XX

Sequence 384 BP; 98 A; 68 C; 111 G; 107 T; 0 other;

Alignment Scores:

Pred. No.: 3,68e-69 Length: 384
 Score: 547.00 Matches: 99
 Percent Similarity: 96.36% Conservative: 7
 Best Local Similarity: 90.00% Mismatches: 4
 Query Match: 92.71% Indels: 0
 DB: 22 Gaps: 0

US-10-019-455A-24 (1-110) x AAF59068 (1-384)

QY 1 HisGlyIlePheMetAspArgLeuAlaSerIleLysLeuCyseAlaAspAspGluCysVal 20
 DB 55 CATGGTGTATTATGATGAATTAACCTTTCTTAAGAGCTGTGTGGGATGAGAGAGTGTCT 114
 QY 21 TyrThrIleSerLeuAlaSerAlaGlnGluAspIleProAspCysArgPheIle 40
 DB 115 TATACTATTCTCTGGCAGAGCACAGAAATTACATGCCCCAGACTGTAGTTTCATC 174
 QY 41 AsnValIleLysGlnGlnGlnIleTyrValTyrSerIleValIleValAsnGlyAla 60
 DB 175 GATGTCAGAAAGGCGACAGATCTATGTTACTCCAGCTGTAAACAGAAACGAGAGCT 234
 QY 61 GlyGluPheTTPAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValGly 80
 DB 235 GGAGAGTTTGGGCTGGCAGCTGTTATGTGACACAGAGATGAGATGGGAATTGTAGCT 294
 QY 81 TyrPheProArgAsnLeuValIleGlnGlnArgValTyrGlnGlnAlaThrLysGluVal 100
 DB 295 TATTTCCCGACCACTGTGTGAGAGGAGCGGTGTATACCGAGAGGCCACCAAGAGATC 354
 QY 101 ProThrThrAspIleAspPheCysGlu 110
 DB 355 CCAACCAAGATTTGACTTCTTCTGTGA 384
 QY 101 ProThrThrAspIleAspPheCysGlu 110
 DB 355 CCAACCAAGATTTGACTTCTTCTGTGA 384
 RESULT 14
 AAF59084
 ID AAF59084 standard; DNA; 947 BP.
 XX AAF59084;
 AC
 XX AAF59084;
 AC
 XX 23-APR-2001 (first entry)
 DT
 XX Mouse MLP nucleotide sequence SEQ ID NO:30.
 DE
 XX MLP, MIA; melanoma inhibitory activity; cancer; bone disease;
 KM joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
 KM cardiant; gene therapy; secretory cell function regulator; promoter;
 KM inhibitor; ds.
 XX
 OS Mus musculus.
 XX
 PN WO200102564-A1.
 XX
 PD 11-JAN-2001.
 XX
 PF 29-JUN-2000; 2000WO-JP04278.
 XX
 PR 30-JUN-1999; 99JP-0186718.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Itoh Y, Nishi K, Ogi K, Okubo S, Mogi S, Noguchi Y, Yoshimura K;
 PI Tanaka H;

XX DR WPI; 2001-159271/16.
XX PT Safe, low-toxicity secretory cell function-regulatory protein and
XX encoded DNA, applicable as drugs, in diagnosis and development of
XX PT promoters and inhibitors for preventing or treating e.g. bone and joint
XX PT diseases -
XX PS Example 2; Page 100-101, 111pp; Japanese.
XX CC The present invention describes novel MLP proteins and their encoding
XX CC DNAs. The MLP proteins and DNAs have anti-inflammatory and cardiant
XX CC activities, and can be used in gene therapy and as secretory cell
XX CC function regulators. The MLP proteins and DNAs can be used in drugs, in
XX CC the diagnosis and development of promoters and inhibitors for preventing
XX CC or treating bone and joint diseases as well as pathologic angiogenesis.
XX CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
XX CC in the exemplification of the present invention.
SQ Sequence 947 BP; 279 A; 158 C; 221 G; 289 T; 0 other;
Alignment Scores:
Pred. No.: 1,32e-68 Length: 947
Score: 547.00 Matches: 99
Percent Similarity: 96.36% Conservative: 7
Best Local Similarity: 90.00% Mismatches: 4
Query Match: 92.71% Indels: 0
DB: Gaps: 0
US-10-019-455A-24 (1-110) x AAF59084 (1-947)
QY 1 HisGlyIlePheMetAspArgLeuAlaSerLysLysLeuCyAlaAspAspGluCysVal 20
DB 65 CATGGTGTATTATGATGATTAACCTTCTCTAAGAGTTGTGTGGATGAGAGTGTGTC 124
QY 21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
DB 125 TATACTATTCTCTGGCAGACGACAGAGATTACAAATGCCAGACTGTAGTTTCATC 184
QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 60
DB 185 GATGTCAGAAAGGCGACAGATCTATGTTACTCCAAAGTGATGACGAAACGAGACT 244
QY 61 GlyGluPheTyrAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80
DB 245 GGAGAGTTTGGCTGGCAGAGTGTATTATGGTACCAACGATGAGATGGGAAATTGTAGT 304
QY 81 TyrPheProArgAsnLeuValLysGlnGlnArgValTyrGlnGlnAlaThrLysGluVal 100
DB 305 TATTTCCCGACCACTTGTGTAAGAGCAGCGCTGTATACAGAGAGCCACCAAGAGATC 364
QY 101 ProThrThrAspIleAspPhePheCysGlu 110
DB 365 CCAACCAAGATATTGACTTCTTGTGAA 394
RESULT 15
AAF59099 standard; DNA; 330 BP.
XX AAF59099;
XX AC
XX XX 23-APR-2001 (first entry)
XX DE Rat MLP nucleotide sequence SEQ ID NO:48.
XX KM MLP; MTA; melanoma inhibitory activity; cancer; bone disease;
XX KM joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
XX KM cardiant; gene therapy; secretory cell function regulator; promoter;
XX KM inhibitor; ds.
XX OS Ratus sp.
XX PN W0200102564-A1.

XX PD 11-JAN-2001.
XX PF 29-JUN-2000; 2000WC-JP04278.
XX PR 30-JUN-1999; 99JP-0186718.
XX PA (TAKE) TAKEDA CHEM IND LTD.
XX PI Itoh Y, Nishi K, Ogi K, Okubo S, Mogi S, Noguchi Y, Yoshimura K,
XX PI Tanaka H.
XX DR WPI; 2001-159271/16.
XX DR P-PSDB; AAB69131.
XX PT Safe, low-toxicity secretory cell function-regulatory protein and
XX PT encoded DNA, applicable as drugs, in diagnosis and development of
XX PT promoters and inhibitors for preventing or treating e.g. bone and joint
XX PT diseases -
XX PS Claim 12; Page 107, 111pp; Japanese.
XX CC The present invention describes novel MLP proteins and their encoding
XX CC DNAs. The MLP proteins and DNAs have anti-inflammatory and cardiant
XX CC activities, and can be used in gene therapy and as secretory cell
XX CC function regulators. The MLP proteins and DNAs can be used in drugs, in
XX CC the diagnosis and development of promoters and inhibitors for preventing
XX CC or treating bone and joint diseases as well as pathologic angiogenesis.
XX CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
XX CC in the exemplification of the present invention.
SQ Sequence 330 BP; 91 A; 62 C; 91 G; 86 T; 0 other;
Alignment Scores:
Pred. No.: 2.17e-68 Length: 330
Score: 541.00 Matches: 98
Percent Similarity: 95.45% Conservative: 7
Best Local Similarity: 89.09% Mismatches: 5
Query Match: 91.69% Indels: 0
DB: Gaps: 0
US-10-019-455A-24 (1-110) x AAF59099 (1-330)
QY 1 HisGlyIlePheMetAspArgLeuAlaSerLysLysLeuCyAlaAspAspGluCysVal 20
DB 1 CATGGCATGTTATGATTAACCTTCTCTAAGAGTTGTGTGGATGAGAGTGTGTC 60
QY 21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
DB 61 TATACCATTTCTTGGCAGACGACAGCAAGACTACAAATGCCAGACTGTAGTTTCATC 120
QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 60
DB 121 AATGTCAGAAAGGCGACAGATCTATGTTATTCACACTGTTACAGAAATGAGACT 180
QY 61 GlyGluPheTyrAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80
DB 181 GGCGCATTTCTGGCTGGCAGAGTGTATTATGGTACCAACAGATGATGGGAAATTGTGGCT 240
QY 81 TyrPheProArgAsnLeuValLysGlnGlnArgValTyrGlnGlnAlaThrLysGluVal 100
DB 241 TATTTCCCGACCACTTGTGTAAGAGCAGAGTGTACAGAGGCCACCAAGAGATT 300
QY 101 ProThrThrAspIleAspPhePheCysGlu 110
DB 301 CCAACCAAGATATTGACTTCTTGTGAA 330
Search completed: December 29, 2003, 16:41:10
Job time : 136.647 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: December 29, 2003, 19:57:30 ; Search time 246.807 Seconds
(without alignments)
1527.048 Million cell updates/sec

Title: US-10-019-455a-24

Perfect score: 590
Sequence: 1 HGFMDRLASKKLCADDECV.....RYQEAETKEVPTIDPFCE 110

Scoring table:
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Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2244575 seqs, 1713117285 residues

Total number of hits satisfying chosen parameters: 4489150

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=num40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Published Applications NA:*

1: /cgnt2_6/prodata/2/pubpna/US07_PUBCOMB.seq:*
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6: /cgnt2_6/prodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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8: /cgnt2_6/prodata/2/pubpna/US08_PUBCOMB.seq:*
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13: /cgnt2_6/prodata/2/pubpna/US09_NEW_PUB.seq:*
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15: /cgnt2_6/prodata/2/pubpna/US10_PUBCOMB.seq:*
16: /cgnt2_6/prodata/2/pubpna/US10_NEW_PUB.seq:*
17: /cgnt2_6/prodata/2/pubpna/US60_NEW_PUB.seq:*
18: /cgnt2_6/prodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No. Score Match Length DB ID Description

SUMMARIES

| Result No. | Score | Match Length | DB ID | Description |
|------------|-------|--------------|-------|-------------------|
| 1 | 590 | 100.0 | 426 | US-10-216-038-1 |
| 2 | 590 | 100.0 | 521 | US-10-216-163-71 |
| 3 | 590 | 100.0 | 521 | US-10-216-765-71 |
| 4 | 590 | 100.0 | 521 | US-10-219-063-71 |
| 5 | 590 | 100.0 | 521 | US-10-219-066-71 |
| 6 | 590 | 100.0 | 521 | US-10-219-067-71 |
| 7 | 590 | 100.0 | 521 | US-10-219-068-71 |
| 8 | 590 | 100.0 | 521 | US-10-219-069-71 |
| 9 | 590 | 100.0 | 521 | US-10-219-073-71 |
| 10 | 590 | 100.0 | 521 | US-10-219-475-71 |
| 11 | 590 | 100.0 | 521 | US-10-219-480-71 |
| 12 | 590 | 100.0 | 521 | US-10-219-483-71 |
| 13 | 590 | 100.0 | 521 | US-10-219-525-71 |
| 14 | 590 | 100.0 | 521 | US-10-219-526-71 |
| 15 | 590 | 100.0 | 521 | US-10-219-530-71 |
| 16 | 590 | 100.0 | 521 | US-10-219-531-71 |
| 17 | 590 | 100.0 | 521 | US-10-219-532-71 |
| 18 | 590 | 100.0 | 521 | US-10-219-533-71 |
| 19 | 590 | 100.0 | 521 | US-10-223-081-359 |
| 20 | 590 | 100.0 | 521 | US-10-230-437-71 |
| 21 | 590 | 100.0 | 521 | US-10-232-228-71 |
| 22 | 590 | 100.0 | 521 | US-10-223-082-359 |
| 23 | 590 | 100.0 | 521 | US-10-227-884-71 |
| 24 | 590 | 100.0 | 521 | US-10-230-163-71 |
| 25 | 590 | 100.0 | 521 | US-10-230-163-71 |
| 26 | 590 | 100.0 | 521 | US-10-230-163-71 |
| 27 | 590 | 100.0 | 521 | US-10-230-163-71 |
| 28 | 590 | 100.0 | 521 | US-10-230-163-71 |
| 29 | 590 | 100.0 | 521 | US-10-218-849-71 |
| 30 | 590 | 100.0 | 521 | US-10-227-883-71 |
| 31 | 590 | 100.0 | 521 | US-10-227-883-71 |
| 32 | 590 | 100.0 | 521 | US-10-219-076-71 |
| 33 | 590 | 100.0 | 521 | US-10-230-434-71 |
| 34 | 590 | 100.0 | 521 | US-10-219-003-71 |
| 35 | 590 | 100.0 | 521 | US-10-219-003-71 |
| 36 | 590 | 100.0 | 521 | US-10-219-075-71 |
| 37 | 590 | 100.0 | 521 | US-10-219-464-71 |
| 38 | 590 | 100.0 | 521 | US-10-219-466-71 |
| 39 | 590 | 100.0 | 521 | US-10-219-469-71 |
| 40 | 590 | 100.0 | 521 | US-10-219-481-71 |
| 41 | 590 | 100.0 | 521 | US-10-230-260-71 |
| 42 | 590 | 100.0 | 521 | US-10-232-231-71 |
| 43 | 590 | 100.0 | 521 | US-10-232-233-71 |
| 44 | 590 | 100.0 | 521 | US-10-216-165-71 |
| 45 | 590 | 100.0 | 521 | US-10-218-956-71 |
| | | | 15 | US-10-219-468-71 |

ALIGNMENTS

RESULT 1
US-10-216-038-1
Sequence 1, Application US/10216038
Publication No. US20030124573A1
GENERAL INFORMATION:
APPLICANT: Nize, Nancy K
APPLICANT: Boyle, Bryan J
APPLICANT: Ford, John E
APPLICANT: Arterburn, Matthew C
APPLICANT: Tang, Y Tom
APPLICANT: Liu, Chenghua
APPLICANT: Drmanac, Radoje T
APPLICANT: Sjastad, Michael
TITLE OF INVENTION: Methods and Materials Relating to No. US20030124573A1 Growth R
FILE REFERENCE: Hys-7c1p
CURRENT FILING DATE: 2002-08-08
PRIOR APPLICATION NUMBER: US 09/563,786
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR FILING DATE: 2000-01-25
NUMBER OF SEQ ID NOS: 8

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SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 1
/ LENGTH: 426
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ NAME/KEY: misc_feature
/ LOCATION: (426)..(426)
/ OTHER INFORMATION: n = A, T, G, or C
US-10-216-038-1

Alignment Scores:
Pred. No.: 1.17e-81 Length: 426
Score: 590.00 Matches: 110
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-10-019-455A-24 (1-110) x US-10-216-038-1 (1-426)

QY 1 HisGlyIlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysVal 20
Db 73 CATGGAATATTATGAGCCGCTTAGCTTCCAGAAAGCTCTGTGCAGATGATGATGCTC 132
QY 21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
Db 133 TATACCTATTCTCTGGCTAGTGTCTCAAGAAATTATTAAGCCCGGAGCTGTAGATTCAAT 192
QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 60
Db 193 AAGCTTAAAAAGGCGACGAGATCTATGTGTAAGCTGTAAGAAAGAAATGAGAGCT 252
QY 61 GlyGluPheTyrPalaGlySerValTyrGlyAsnGlyGlnAspGluMetGlyValValGly 80
Db 253 GGAGAAATTTGGGCTGCGAGTGTATGATGAGCGCAGACGAGATGGAGTCTGGCT 312
QY 81 TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100
Db 313 TATTTCCCGAGGAACCTTGGTCMAAGAAAGACCGGTGTACAGGAAGCTACCAAGAAAGTT 372
QY 101 ProThrThrAspIleAspPheCysGlu 110
Db 373 CCCACACCGGATATTGACTTCTTCTGCGAG 402

RESULT 2
US-10-216-163-71
/ Sequence 71, Application US/10216163
/ Publication No. US20030149239A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Gerritsen, Mary
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Philippe F.
/ APPLICANT: Watanabe, Colin L.
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3530PIC3
/ CURRENT APPLICATION NUMBER: US/10/216,163
/ PRIOR FILING DATE: 2002-08-09
/ PRIOR APPLICATION NUMBER: 10/119,480
/ PRIOR FILING DATE: 2002-04-09
/ PRIOR APPLICATION NUMBER: 60/059113
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/062287
/ PRIOR FILING DATE: 1997-10-17
/ PRIOR APPLICATION NUMBER: 60/063549
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/ PRIOR FILING DATE: 1997-10-28
/ PRIOR APPLICATION NUMBER: 60/064103
/ PRIOR FILING DATE: 1997-10-31
/ PRIOR APPLICATION NUMBER: 60/069873
/ PRIOR FILING DATE: 1997-12-17
/ PRIOR APPLICATION NUMBER: 60/078910
/ PRIOR FILING DATE: 1998-03-20
/ PRIOR APPLICATION NUMBER: 60/079294
/ PRIOR FILING DATE: 1998-03-25
/ PRIOR APPLICATION NUMBER: 60/079656
/ PRIOR FILING DATE: 1998-03-26
/ PRIOR APPLICATION NUMBER: 60/079728
/ PRIOR FILING DATE: 1998-03-27
/ Remaining Prior Application data removed - See file wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 246
/ SEQ ID NO 71
/ LENGTH: 521
/ TYPE: DNA
/ ORGANISM: Homo Sapien
US-10-216-163-71

Alignment Scores:
Pred. No.: 1.56e-81 Length: 521
Score: 590.00 Matches: 110
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-019-455A-24 (1-110) x US-10-216-163-71 (1-521)

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Db 92 CATGGAATATTATGAGCCGCTTAGCTTCCAGAAAGCTCTGTGCAGATGATGATGCTC 151
QY 21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
Db 152 TATACCTATTCTCTGGCTAGTGTCTCAAGAAATTATTAAGCCCGGAGCTGTAGATTCAAT 211
QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 60
Db 212 AACCTTAAAAAGGCGACGAGATCTATGTGTAAGCTGTAAGAAAGAAATGAGAGCT 271
QY 61 GlyGluPheTyrPalaGlySerValTyrGlyAsnGlyGlnAspGluMetGlyValValGly 80
Db 272 GGAGAAATTTGGGCTGCGAGTGTATGATGAGCGCAGACGAGATGGAGTCTGGCT 331
QY 81 TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100
Db 332 TATTTCCCGAGGAACCTTGGTCMAAGAAAGACCGGTGTACAGGAAGCTACCAAGAAAGTT 391
QY 101 ProThrThrAspIleAspPheCysGlu 110
Db 392 CCCACACCGGATATTGACTTCTTCTGCGAG 421

RESULT 3
US-10-218-765-71
/ Sequence 71, Application US/10218765
/ Publication No. US20030187201A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Gerritsen, Mary
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Philippe F.
/ APPLICANT: Watanabe, Colin L.
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3530PIC3
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FILE REFERENCE: P3530P1C19
CURRENT APPLICATION NUMBER: US/10/218,765
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/086392
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089905
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090691
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/095302
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/095318
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/095916
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/096146
PRIOR FILING DATE: 1998-08-11
PRIOR APPLICATION NUMBER: 60/096791
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 60/097986
PRIOR FILING DATE: 1998-08-26
PRIOR APPLICATION NUMBER: 60/098544
PRIOR FILING DATE: 1998-08-31
PRIOR APPLICATION NUMBER: 60/099596
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099598
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099803
PRIOR FILING DATE: 1998-09-10

PRIOR APPLICATION NUMBER: 60/099811
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099812
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099816
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/100038
PRIOR FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: 60/100385
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100390
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100627
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100848
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/100919
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/101477
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101738
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101741
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101786
PRIOR FILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: 60/101916
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101922
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/106178
PRIOR FILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: 60/106248
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 60/106464
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 60/106905
PRIOR FILING DATE: 1998-11-03
PRIOR APPLICATION NUMBER: 60/108787
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/108801
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/108849
PRIOR FILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: 60/112422
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/113296
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/113605
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113621
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/115558
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115565
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115733
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/119549
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/123618
PRIOR FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: 60/125259
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 60/125775
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 60/126773
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: 60/127887
PRIOR FILING DATE: 1999-04-05
PRIOR APPLICATION NUMBER: 60/130232
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/131022

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PRIOR FILING DATE: 1999-04-26
PRIOR APPLICATION NUMBER: 60/131270
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131291
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131445
PRIOR FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 60/134287
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/140650
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/140723
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/141037
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 60/144758
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/145698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: 60/146222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: 60/146963
PRIOR FILING DATE: 1999-08-03
PRIOR APPLICATION NUMBER: 60/149330
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/149638
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/151733
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/164418
PRIOR FILING DATE: 1999-11-09
PRIOR APPLICATION NUMBER: 60/166361
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: 60/169445
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169495
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169835

```

```

Alignment Scores:
Pred. No.: 1,56e-81 Length: 521
Score: 590.00 Matches: 110
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

```

US-10-019-455a-24 (1-110) x US-10-219-765-71 (1-521)

```

QY 1 HIGSLYIlePheMetAspArgLeuAlaSerLysLysLeuCyAlaAspAspGluCysVal 20
DB 92 CATGGAATTTTATGACCGCTAGCTTCAAGAACTCTGGCAGATGATGATGCTC 151
QY 21 TYRThrIleSerLeuAlaSerLagInguAspTYRAsnAlaProAspCysArgPheIle 40
DB 152 TATACATTTCTGCTGCTAGCTCTCAAGAGATTATTAATGCCCGGACTGTAATTCATT 211
QY 41 AsnValLysLysGlyGlnGlnIleTYRValTYRSerLysLeuValLysGluAsnGlyAla 60
DB 212 AACGTTAAAAAGGCGACAGATCTATGTAAGCTGTAAGAAAGAAATGAGACT 271
QY 61 GlyGluPheThrAlaGlySerValTYRGIYAspGlyGlnAspGluMetGlyValValIly 80
DB 272 GGAGAAATTTGGCTGGCGAGTGTATGATGAGCCAGAGAGATGGAGTCTGGGT 331
QY 81 TYRPhenProArgAsnLeuValLysGluGlnArgValTYRGIYAlaIleThrLysGluVal 100
DB 332 TATTTCCCGAGGAACCTTGCTCAAGAACGCTGTACAGAAAGCTAACCAAGAGATT 391
QY 101 ProThrTrpAspIleAspPheCysGlu 110
DB 392 CCCACGAGATATGACTTTCTTGGCAG 421

```

RESULT 4

US-10-219-063-71

Sequence 71, Application US/10219063
Publication No. US20030187202A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Geritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Macanade, Colin L.

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C24

CURRENT APPLICATION NUMBER: US/10/219,063

PRIOR FILING DATE: 2002-08-13

PRIOR APPLICATION NUMBER: 10/119,480

PRIOR FILING DATE: 2002-04-09

PRIOR APPLICATION NUMBER: 60/059113

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/062287

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/063549

PRIOR FILING DATE: 1997-10-28

PRIOR APPLICATION NUMBER: 60/064103

PRIOR FILING DATE: 1997-10-31

PRIOR APPLICATION NUMBER: 60/069873

PRIOR FILING DATE: 1997-12-17

PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/079294

PRIOR FILING DATE: 1998-03-25

PRIOR APPLICATION NUMBER: 60/079656

PRIOR FILING DATE: 1998-03-26

PRIOR APPLICATION NUMBER: 60/079728

PRIOR FILING DATE: 1998-03-27

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 246

SEQ ID NO 71

LENGTH: 521

TYPE: DNA

ORGANISM: Homo Sapien

US-10-219-063-71

Alignment Scores:

```

Pred. No.: 1,56e-81 Length: 521
Score: 590.00 Matches: 110
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

```

US-10-019-455a-24 (1-110) x US-10-219-063-71 (1-521)

```

QY 1 HIGSLYIlePheMetAspArgLeuAlaSerLysLysLeuCyAlaAspAspGluCysVal 20
DB 92 CATGGAATTTTATGACCGCTAGCTTCAAGAACTCTGGCAGATGATGATGCTC 151
QY 21 TYRThrIleSerLeuAlaSerLagInguAspTYRAsnAlaProAspCysArgPheIle 40
DB 152 TATACATTTCTGCTGCTAGCTCTCAAGAGATTATTAATGCCCGGACTGTAATTCATT 211
QY 41 AsnValLysLysGlyGlnGlnIleTYRValTYRSerLysLeuValLysGluAsnGlyAla 60
DB 212 AACGTTAAAAAGGCGACAGATCTATGTAAGCTGTAAGAAAGAAATGAGACT 271
QY 61 GlyGluPheThrAlaGlySerValTYRGIYAspGlyGlnAspGluMetGlyValValIly 80

```

DB 272 GGAGATTITGGGCTGGCAGTGTATGTATGTCGCGACGACAGATGGAGTCTGGCT 331
QY 81 TyrPheProArgAsnLeuValIysGluArgValIYrGlnGluAlaThrIysGluVal 100
DB 332 TATTTCCCGAGACTGTGTCAGAACAGCGCTGTGTCAGAGAGCTACCAAGAAATT 391
QY 101 ProThrThrAspIleAspPheCysGlu 110
DB 392 CCCACCGAGATATTGACTTCTTCTGCGAG 421

RESULT 5
US-10-219-066-71
; Sequence 71, Application US/10219066
; Publication No. US20030187203A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerltsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Macanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C37
; CURRENT FILING DATE: 2002-08-13
; PRIOR FILING DATE: 2002-04-09
; PRIOR FILING DATE: 2002-04-09
; PRIOR FILING DATE: 1997-09-17
; PRIOR FILING DATE: 1997-09-17
; PRIOR FILING DATE: 1997-10-17
; PRIOR FILING DATE: 1997-10-17
; PRIOR FILING DATE: 1997-10-28
; PRIOR FILING DATE: 1997-10-28
; PRIOR FILING DATE: 1997-10-31
; PRIOR FILING DATE: 1997-10-31
; PRIOR FILING DATE: 1997-12-17
; PRIOR FILING DATE: 1997-12-17
; PRIOR FILING DATE: 1998-03-20
; PRIOR FILING DATE: 1998-03-20
; PRIOR FILING DATE: 1998-03-25
; PRIOR FILING DATE: 1998-03-25
; PRIOR FILING DATE: 1998-03-26
; PRIOR FILING DATE: 1998-03-26
; PRIOR FILING DATE: 1998-03-27
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-066-71

Alignment Scores:
Pred. No.: 1,566-81 Length: 521
Score: 590.00 Matches: 110
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-019-455a-24 (1-110) x US-10-219-066-71 (1-521)

QY 1 HisGlyIlePheMetSerPargLeuAlaSerIyIysLeuCysAlaAspAspGluCysVal 20
DB 92 CATGGATATATTATGACCGCTTACCTTCCAAAGAGCTCTGTGACAGATGATGATGTGTGC 151

QY 21 TyrThrIleSerIleuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
DB 152 TATCTATTCTCTCGGTAGTGTGCAAGAGATTATATATCCCGGACTGTATTCATT 211
QY 41 AsnValIysIysGlnGlnIleTyrValIYrSerIysLeuValIysGluAsnGlyAla 60
DB 212 AACCTTAAAAAGGCGCAGCATCTATGTGTACTCAAGCTGTAAAAAGAAATGGAGCT 271
QY 61 GlyIlePheTrpAlaGlySerValIYrGlyAspGlyGlnAspGluMetGlyValIYrGly 80
DB 272 GGAGATTITGGGCTGGCAGTGTATGTATGTCGCGACGACAGATGGAGATCTGGCT 331
QY 81 TyrPheProArgAsnLeuValIysGluArgValIYrGlnGluAlaThrIysGluVal 100
DB 332 TATTTCCCGAGACTGTGTCAGAACAGCGCTGTGTCAGAGAGCTACCAAGAAATT 391
QY 101 ProThrThrAspIleAspPheCysGlu 110
DB 392 CCCACCGAGATATTGACTTCTTCTGCGAG 421

RESULT 6
US-10-219-067-71
; Sequence 71, Application US/10219067
; Publication No. US20030187204A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerltsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Macanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C51
; CURRENT FILING DATE: 2002-08-14
; PRIOR FILING DATE: 2002-08-14
; PRIOR FILING DATE: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR FILING DATE: 1997-09-17
; PRIOR FILING DATE: 1997-09-17
; PRIOR FILING DATE: 1997-10-17
; PRIOR FILING DATE: 1997-10-17
; PRIOR FILING DATE: 1997-10-28
; PRIOR FILING DATE: 1997-10-28
; PRIOR FILING DATE: 1997-10-31
; PRIOR FILING DATE: 1997-10-31
; PRIOR FILING DATE: 1997-12-17
; PRIOR FILING DATE: 1997-12-17
; PRIOR FILING DATE: 1998-03-20
; PRIOR FILING DATE: 1998-03-20
; PRIOR FILING DATE: 1998-03-25
; PRIOR FILING DATE: 1998-03-25
; PRIOR FILING DATE: 1998-03-26
; PRIOR FILING DATE: 1998-03-26
; PRIOR FILING DATE: 1998-03-27
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-067-71

Alignment Scores:
Pred. No.: 1,566-81 Length: 521
Score: 590.00 Matches: 110
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 13 Gaps: 0

US-10-019-455a-24 (1-110) x US-10-219-067-71 (1-521)

QY 1 HisGlyIlePheMetAspArgLeuAlaSerIleValysLeuCyAlaAspAspGluCyVal 20
 DB 92 CATGGAATATTATGACCGCTCTAGCTCCAGAGAGCTGTGCGAGTATGATGCTGTC 151
 QY 21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCyAspPheIle 40
 DB 152 TATACTATTCTCTGGCTGAGTGTCAAGAGATTATATGCCCGGAGCTGATTCATT 211
 QY 41 AsnValIleValysGlyGlnGlnIleTyrValTyrSerIleValysGluAsnGlyAla 60
 DB 212 AACGTTAAAAAGGCGACGACATCTATGTACTCAAGCTGGTAAAAAGAAATGGAGCT 271
 QY 61 GlyIlePheTPrAlaGlySerValTyrGlyAspGlyAspGluMetGlyValValGly 80
 DB 272 GGAGAAATTTGGCTGGCGAGTGTATGCGATGCCAGAGACGAGATGGAGTCTGGCT 331
 QY 81 TyrPheProArgAsnLeuValysGlyGlnArgValTyrGlnGluAlaThrIysGluVal 100
 DB 332 TATTTCCCGAGAACTGTGTCAAGAAACAGGTGTGTACCGAGAACTCAAGAAATT 391
 QY 101 ProThrThrAspIleAspPhePheCyAsGlu 110
 DB 392 CCCACACGAGATTGACTTCTTCTGCGAG 421

RESULT 7

US-10-219-068-71 Application US/10219068
 Sequence 71, Application US/10219068
 Publication No. US20030187205A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Desnoyers, Luc
 APPLICANT: Gerritsen, Mary
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Smith, Victoria
 APPLICANT: Stephan, Jean-Philippe F.
 APPLICANT: Watanabe, Colin L.
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P3530P1C31
 CURRENT APPLICATION NUMBER: US/10/219,068
 CURRENT FILING DATE: 2002-08-13
 PRIOR APPLICATION NUMBER: 10/119,480
 PRIOR FILING DATE: 2002-04-09
 PRIOR APPLICATION NUMBER: 60/059113
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/062287
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/063549
 PRIOR FILING DATE: 1997-10-28
 PRIOR APPLICATION NUMBER: 60/064103
 PRIOR FILING DATE: 1997-10-31
 PRIOR APPLICATION NUMBER: 60/069873
 PRIOR FILING DATE: 1997-12-17
 PRIOR APPLICATION NUMBER: 60/078910
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/079294
 PRIOR FILING DATE: 1998-03-25
 PRIOR APPLICATION NUMBER: 60/079566
 PRIOR FILING DATE: 1998-03-26
 PRIOR APPLICATION NUMBER: 60/079728
 PRIOR FILING DATE: 1998-03-27
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 246

SEQ ID NO 71
 LENGTH: 521
 TYPE: DNA
 ORGANISM: Homo Sapien
 US-10-219-068-71

Alignment Scores:

| Pred. No.: | 156e-81 | Length: | 521 |
|------------------------|---------|---------------|-----|
| Score: | 590.00 | Matches: | 110 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 13 | Gaps: | 0 |

US-10-019-455a-24 (1-110) x US-10-219-068-71 (1-521)

QY 1 HisGlyIlePheMetAspArgLeuAlaSerIleValysLeuCyAlaAspAspGluCyVal 20
 DB 92 CATGGAATATTATGACCGCTCTAGCTCCAGAGAGCTGTGCGAGTATGATGCTGTC 151
 QY 21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCyAspPheIle 40
 DB 152 TATACTATTCTCTGGCTGAGTGTCAAGAGATTATATGCCCGGAGCTGATTCATT 211
 QY 41 AsnValIleValysGlyGlnGlnIleTyrValTyrSerIleValysGluAsnGlyAla 60
 DB 212 AACGTTAAAAAGGCGACGACATCTATGTACTCAAGCTGGTAAAAAGAAATGGAGCT 271
 QY 61 GlyIlePheTPrAlaGlySerValTyrGlyAspGlyAspGluMetGlyValValGly 80
 DB 272 GGAGAAATTTGGCTGGCGAGTGTATGCGATGCCAGAGACGAGATGGAGTCTGGCT 331
 QY 81 TyrPheProArgAsnLeuValysGlyGlnArgValTyrGlnGluAlaThrIysGluVal 100
 DB 332 TATTTCCCGAGAACTGTGTCAAGAAACAGGTGTGTACCGAGAACTCAAGAAATT 391
 QY 101 ProThrThrAspIleAspPhePheCyAsGlu 110
 DB 392 CCCACACGAGATTGACTTCTTCTGCGAG 421

RF ULT 8

US-10-219-069-71
 Sequence 71, Application US/10219069
 Publication No. US20030187206A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Desnoyers, Luc
 APPLICANT: Gerritsen, Mary
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Smith, Victoria
 APPLICANT: Stephan, Jean-Philippe F.
 APPLICANT: Watanabe, Colin L.
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P3530P1C40
 CURRENT APPLICATION NUMBER: US/10/219,069
 CURRENT FILING DATE: 2002-08-13
 PRIOR APPLICATION NUMBER: 10/119,480
 PRIOR FILING DATE: 2002-04-09
 PRIOR APPLICATION NUMBER: 60/059113
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/062287
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/063549
 PRIOR FILING DATE: 1997-10-28
 PRIOR APPLICATION NUMBER: 60/064103
 PRIOR FILING DATE: 1997-10-31
 PRIOR APPLICATION NUMBER: 60/069873
 PRIOR FILING DATE: 1997-12-17

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; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
;
US-10-219-069-71

Alignment Scores:
Pred. No.: 1,56e-81 Length: 521
Score: 590.00 Matches: 110
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-019-455a-24 (1-110) x US-10-219-069-71 (1-521)

QY 1 HisGlyIlePheMetAspArgLeuAlaSerIleValLeuCysAlaAspGluCysVal 20
Db 92 CATGGAATTTTATGAGACCGTCTGCTCCAGAGCTGTGCGAGATGATGAGTGTC 151
QY 21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
Db 152 TATACATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 211
QY 41 AsnValIleValGlyGlnGlnIleTyrValTyrSerIleValLeuValGlyAsnGlyVal 60
Db 212 AACGTTAAAAAGGCGACAGATCTATGCTACTCAAGCTGTTAAAGAAATGAGACT 271
QY 61 GlyGluPheTyrAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValAlaGly 80
Db 272 GGAGAAATTTGGCTGGCGAGTGTATGCTGATGGCCAGAGAGATGGAGTCTGCTGCT 331
QY 81 TyrPheProArgAsnLeuValIleGlnGluArgValTyrGlnGluAlaThrIleGluVal 100
Db 332 TATTTCCCGAGAACTTGCTCAAGAACGCTGTGCTACAGAGAACTTACCAAGAACTT 391
QY 101 ProThrThrAspIleAspPhePheCysGlu 110
Db 392 CCCACCAAGGATATTGACTTCTTCTGCGAG 421

RESULT 9
US-10-219-073-71
; Sequence 71, Application US/10219073
; Publication No. US20030187207A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin I.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P33301C52
; CURRENT APPLICATION NUMBER: US/10/219,073
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
```

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; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
;
US-10-219-073-71

Alignment Scores:
Pred. No.: 1,56e-81 Length: 521
Score: 590.00 Matches: 110
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-019-455a-24 (1-110) x US-10-219-073-71 (1-521)

QY 1 HisGlyIlePheMetAspArgLeuAlaSerIleValLeuCysAlaAspGluCysVal 20
Db 92 CATGGAATTTTATGAGACCGTCTGCTCCAGAGCTGTGCGAGATGATGAGTGTC 151
QY 21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
Db 152 TATACATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 211
QY 41 AsnValIleValGlyGlnGlnIleTyrValTyrSerIleValLeuValGlyAsnGlyVal 60
Db 212 AACGTTAAAAAGGCGACAGATCTATGCTACTCAAGCTGTTAAAGAAATGAGACT 271
QY 61 GlyGluPheTyrAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValAlaGly 80
Db 272 GGAGAAATTTGGCTGGCGAGTGTATGCTGATGGCCAGAGAGATGGAGTCTGCTGCT 331
QY 81 TyrPheProArgAsnLeuValIleGlnGluArgValTyrGlnGluAlaThrIleGluVal 100
Db 332 TATTTCCCGAGAACTTGCTCAAGAACGCTGTGCTACAGAGAACTTACCAAGAACTT 391
QY 101 ProThrThrAspIleAspPhePheCysGlu 110
Db 392 CCCACCAAGGATATTGACTTCTTCTGCGAG 421

RESULT 10
US-10-219-475-71
; Sequence 71, Application US/10219475
; Publication No. US20030187208A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
```

```

1  APPLICANT: Stephan, Jean-Philippe F.
2  APPLICANT: Matanabe, Colin L.
3  APPLICANT: Wood, William I.
4  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUC
5  TITLE OF INVENTION: ACIDS ENCODING THE SAME
6  FILE REFERENCE: P9350PLC49
7  CURRENT APPLICATION NUMBER: US/10/219,475
8  CURRENT FILING DATE: 2002-08-13
9  PRIOR APPLICATION NUMBER: 10/119,480
10 PRIOR FILING DATE: 2002-04-09
11 PRIOR APPLICATION NUMBER: 60/059113
12 PRIOR FILING DATE: 1997-09-17
13 PRIOR APPLICATION NUMBER: 60/062287
14 PRIOR FILING DATE: 1997-10-17
15 PRIOR APPLICATION NUMBER: 60/063549
16 PRIOR FILING DATE: 1997-10-28
17 PRIOR APPLICATION NUMBER: 60/064103
18 PRIOR FILING DATE: 1997-10-31
19 PRIOR APPLICATION NUMBER: 60/068673
20 PRIOR FILING DATE: 1997-12-17
21 PRIOR APPLICATION NUMBER: 60/078910
22 PRIOR FILING DATE: 1998-03-20
23 PRIOR APPLICATION NUMBER: 60/079294
24 PRIOR FILING DATE: 1998-03-25
25 PRIOR APPLICATION NUMBER: 60/079656
26 PRIOR FILING DATE: 1998-03-26
27 PRIOR APPLICATION NUMBER: 60/079728
28 PRIOR FILING DATE: 1998-03-27
29 Remaining Prior Application data removed - See File Wrapper or PALM
30 NUMBER OF SEQ ID NOS: 246
31 SEQ ID NO 71
32 LENGTH: 521
33 TYPE: DNA
34 ORGANISM: Homo Sapien
35 US-10-219-475-71

```

| Alignment Scores: | | | |
|--|---|---------------|-----|
| Score: | 1.56e-81 | Length: | 521 |
| Percent Similarity: | 100.00% | Matches: | 110 |
| Best Local Similarity: | 100.00% | Conservative: | 0 |
| Query Match: | 100.00% | Mismatches: | 0 |
| DB: | 13 | Indels: | 0 |
| | | Gaps: | 0 |
| US-10-019-455A-24 (1-110) x US-10-219-475-71 (1-521) | | | |
| QY | 1 HisGlyIlePheMetAspaGleuAlaSerLysLeuCysAlaAspAsnGluCysVal | 20 | |
| DB | 92 CAIGGAATATTATGACCGCTTACGTTCCAGAAAGCTTGCGAGATAGTGTGTC | 15 | |
| QY | 21 TyrThrIleSerLeuAlaSerAlaGlnLysAspTyrAsnAlaProAspCysArgPheIle | 40 | |
| DB | 152 TATACATTCTCTGGGTAGTGTCTCAAGAAATTATTAAGCCCCGAGCTGTGATTCTT | 21 | |
| QY | 41 AsnValLysLysGlnGlnIleIleTyrValTyrSerLysLeuValLysGlnAsnGlyAla | 60 | |
| DB | 212 AACGTTAAAAAAGGCGACGAGATCTGTGTCTCAAGCTGTAAAGAAATGAGACT | 27 | |
| QY | 61 GlyGluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly | 80 | |
| DB | 272 GGGAAATTTGGGCTGGCAGTGTATTATGTGTAGTGGCCAGGAAGATGGAGTCTGGGCT | 33 | |
| QY | 81 TyrPheProArgAsnLeuValLysGlnGlnAsnGlyAlaThrLysGlnVal | 100 | |
| DB | 332 TATTCCCCAGGAATTTGGTCAAGGAACGCTGTACCCAGGAAGCTTACCAAGGAATT | 39 | |
| QY | 101 ProThrThrAspIleAspPheCysGlu | 110 | |
| DB | 392 CCCACCACGATATTGACTTCTTCTGCG | 421 | |

```

: Publication No.: US20030187209A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Desnoyers, Luc
: APPLICANT: Gerritsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Smith, Victoria
: APPLICANT: Stephan, Jean-Philippe F.
: APPLICANT: Wabarrabe, Colin L.
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: TITLE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P3530P1C38
: CURRENT APPLICATION NUMBER: US/10/219,480
: CURRENT FILING DATE: 2002-08-13
: PRIOR APPLICATION NUMBER: 10/119,480
: PRIOR FILING DATE: 2002-04-09
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/062287
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/063549
: PRIOR FILING DATE: 1997-10-28
: PRIOR APPLICATION NUMBER: 60/064403
: PRIOR FILING DATE: 1997-10-31
: PRIOR APPLICATION NUMBER: 60/069873
: PRIOR FILING DATE: 1997-12-17
: PRIOR APPLICATION NUMBER: 60/078910
: PRIOR FILING DATE: 1998-03-20
: PRIOR APPLICATION NUMBER: 60/079294
: PRIOR FILING DATE: 1998-03-25
: PRIOR APPLICATION NUMBER: 60/079656
: PRIOR FILING DATE: 1998-03-26
: PRIOR APPLICATION NUMBER: 60/079728
: PRIOR FILING DATE: 1998-03-27
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 246
: SEQ ID NO 71
: LENGTH: 521
: TYPE: DNA
: ORGANISM: Homo Sapien
: IS-10-219-480-71

```

| Alignment Scores: | | Score: | Length: |
|------------------------|--|----------|-----------------|
| Pred. No.: | | 1.56e-81 | 521 |
| Score: | | 590.00 | Matches: 110 |
| Percent Similarity: | | 100.00% | Conservative: 0 |
| Best Local Similarity: | | 100.00% | Mismatches: 0 |
| Query Match: | | 100.00% | Indels: 0 |
| DB: | | 13 | Gaps: 0 |

| US-10-019-455A-24 (1-110) X US-10-219-480-71 (1-521) |
|---|
| QY 1 HISGLYILEPHEMELASPRGLEUALSERLYALYSLEUCYSAIASPSPGLUCYSVAL 20 |
| DB 92 CATGCAATTTATATGACCGCTTACTCTCCAGGAAGCTCTGTGCAGAGAGAGTGTCTC 15 |
| QY 21 TYRTHILSESLLEUALSEERLAGINGLUSPTYRANALAPROASPCEARPHETLE 40 |
| DB 152 TATACATTTCTCTGGCTAGTGTCAAGAAGTTTATATGCCCCGAGTGTAGTTATT 21 |
| QY 41 AENVALVLSLYEGLYGLINGINILETYRVALTYRSERLYSEUVALVLEGLIASNGLYALA 60 |
| DB 212 AACGTTAAAAAGGCGACAGATCTATGTGTGACTCAAGCGTGGTAAAAAGAAATAGGAGCT 27 |
| QY 61 GLYGLUPHETRALGLYSERVALTYRGLYASPGLYGNASPGIUMETGLYVALVALGLY 80 |
| DB 272 GGAAGATTTTGGAGCTGGCAGTGTTTATGTATATGGCCAGGCGAGATGGAGTGTGGGT 33 |
| QY 81 TYRPHETPROARGASNLLEUVALVLEGLINGLNAIGVALTYRGLINGLUALATHRLYGLUVAL 100 |

DB 332 TATTTCCCGAGAACTGTGTCAGAGACGCGTGTGTCAGAGAGCTTACCAAGAGATT 391
QY 101 ProThrinAspIleAspPheCysGlu 110
DB 392 CCCACCGAGATATTGACTTCTTCTGCGAG 421

RESULT 12
US-10-219-483-71
Sequence 71, Application US/10219483
Publication No. US20030187210A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C43
CURRENT APPLICATION NUMBER: US/10/219,483
PRIOR FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 71
LENGTH: 521
TYPE: DNA
ORGANISM: Homo Sapien
US-10-219-483-71

Alignment Scores:
Pred. No.: 1,56e-81 Length: 521
Score: 590.00 Matches: 110
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-019-455a-24 (1-110) x US-10-219-483-71 (1-521)

QY 1 HisGlyIlePheMetAspArgLeuAlaSerIleuLysCysAlaIleAspGluCysVal 20
DB 92 CAGGGAATATTATGAGACCGCTTAGCTTCCAAAGAGCTGTGTCACAGATGATGAGTGTGTC 151

QY 21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysAspPheIle 40
DB 152 TATACATTTTCTCTGCTAGTGTGCTCAAGAGATTATATATCCCCGAGCTGTAGATTCA 211

QY 41 AsnValIleuLysGlyGlnGlnIleTyrValIleTyrSerIleuValIleuGlnGlnVal 60
DB 212 AACCTTAAAAAAGGCGACGATCTATGTACTCAAGCTGTAAAGAAAATGAGACT 271

QY 61 GlyIleuPheIlePheIleValIleuLysGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
DB 272 GGAAGATTTTGGCTGGCAGTGTATTATGATGCGCAGGACGAGATGGAGATCGTGGCT 331

QY 81 TyrPheProArgAsnLeuValIleuLysGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 100
DB 332 TATTTCCCGAGAACTGTGTCAGAGACGCGTGTGTCAGAGAGCTTACCAAGAGATT 391

QY 101 ProThrinAspIleAspPheCysGlu 110
DB 392 CCCACCGAGATATTGACTTCTTCTGCGAG 421

RESULT 13
US-10-219-525-71
Sequence 71, Application US/10219525
Publication No. US20030187211A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C29
CURRENT APPLICATION NUMBER: US/10/219,525
PRIOR FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 71
LENGTH: 521
TYPE: DNA
ORGANISM: Homo Sapien
US-10-219-525-71

Alignment Scores:
Pred. No.: 1,56e-81 Length: 521
Score: 590.00 Matches: 110
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-019-455a-24 (1-110) x US-10-219-525-71 (1-521)

```
QY 1 HisGlyIlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysVal 20
Db 92 CATGGAATATTATGACCGCTAGCTTCCAGAAAGCTGTGCGAGATGATGATGTC 151
QY 21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
Db 152 TATACATATTCTCTGCTAGTGTCTCAAGAAATTAATATGCCCCGAGCTGTGATTCATT 211
QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 60
Db 212 AACGTTAAAAAGGCGACAGATCTATGCTACTCAAGCTGTAAAGAAATGAGACT 271
QY 61 GlyIlePheTyrAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValAlaGly 80
Db 272 GGAGAAATTTGGCTGGCTGCTTTATGCTATGCGCCAGAGACGAGATGGAGTCTGGCT 331
QY 81 TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100
Db 332 TATTTCCCGAGAACTGTGTCAAGAAACGCGTGTGTACCAAGAAAGCTACCAAGAAAGTT 391
QY 101 ProThrThrAspIleAspPheCysGlu 110
Db 392 CCCACACGAGATATTGACTTCTTCTGCGAG 421
```

RESULT 14

```
US-10-219-526-71
Sequence 71, Application US/10219526
Publication No. US20030187212A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C41
CURRENT APPLICATION NUMBER: US/10/219,526
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 71
LENGTH: 521
TYPE: DNA
```

ORGANISM: Homo Sapien
US-10-219-526-71

Alignment Scores:

| | | | |
|------------------------|----------|---------------|-----|
| Pred. No.: | 1,566-81 | Length: | 521 |
| Score: | 590.00 | Matches: | 110 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 13 | Gaps: | 0 |

US-10-019-455a-24 (1-110) x US-10-219-526-71 (1-521)

```
QY 1 HisGlyIlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysVal 20
Db 92 CATGGAATATTATGACCGCTAGCTTCCAGAAAGCTGTGCGAGATGATGATGTC 151
QY 21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
Db 152 TATACATATTCTCTGCTAGTGTCTCAAGAAATTAATATGCCCCGAGCTGTGATTCATT 211
QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 60
Db 212 AACGTTAAAAAGGCGACAGATCTATGCTACTCAAGCTGTGTAAAGAAATGAGACT 271
QY 61 GlyIlePheTyrAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValAlaGly 80
Db 272 GGAGAAATTTGGCTGGCTGCTTTATGCTATGCGCCAGAGACGAGATGGAGTCTGGCT 331
QY 81 TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100
Db 332 TATTTCCCGAGAACTGTGTCAAGAAACGCGTGTGTACCAAGAAAGCTACCAAGAAAGTT 391
QY 101 ProThrThrAspIleAspPheCysGlu 110
Db 392 CCCACACGAGATATTGACTTCTTCTGCGAG 421
```

RESULT 15

```
US-10-219-530-71
Sequence 71, Application US/10219530
Publication No. US20030187213A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C44
CURRENT APPLICATION NUMBER: US/10/219,530
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
```

PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 71
LENGTH: 521
TYPE: DNA
ORGANISM: Homo Sapien
US-10-219-530-71

Alignment Scores:
Pred. No.: 1.56e-81 Length: 521
Score: 590.00 Matches: 110
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-019-455A-24 (1-110) X US-10-219-530-71 (1-521)

QY 1 HisGlyIlePheMetAspAlaGluValAspSerLysLysLeuCysAlaAspAspGluCysVal 20
DB 92 CATGGAATATTATGAGACCGCTCTAGCTTCAAGAACTGTGTGAGATGATGATGTC 151
QY 21 TyrThrIleSerLeuAlaSerAlaGluAspTyrAsnAlaProAspCysArgPheIle 40
DB 152 TATCTATTCTCTGGCTAGTGTCAAGAAATTATATGCCCCGACTGTAGATTCATT 211
QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 60
DB 212 AACGTTAAAAAGGCGACGACATCTATGTACTCAAAAGCTGTTAAAGAAATGGAGCT 271
QY 61 GlyGluPheTyrAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80
DB 272 GGAGAAATTTGGGCTGGCTGTTTATGTGATGGCCAGACGACATGGGAGTCTGGGT 331
QY 81 TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100
DB 332 TATTTCCCGAGAACTGTGCAAGAAACGCTGTGTACCAAGAACTACCAAGAAAGTT 391
QY 101 ProThrThrAspIleAspPheCysGlu 110
DB 392 CCCACCACGATATGACTTCTTCTGCGAG 421

Search completed: December 30, 2003, 02:01:04
Job time : 248.807 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 29, 2003, 16:24:24 ; Search time 34.972 Seconds

(without alignments)
1388.315 Million cell updates/sec

Title: US-10-019-455A-24

Perfect score: 590

Sequence: 1 HGFMRLAKSKLCADECV.....RVGEATKEVPTDIDFFCE 110

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Listing first 45 summaries

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-Fgapext=7 -Ygapop=10 -Ygapext=0.5 -Delop=6 -Delext=7

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 3 | 231.5 | 39.2 | 581 | 1 | US-08-578-649-4 |
| 4 | 210.5 | 35.7 | 305 | 1 | US-08-578-649-8 |
| 5 | 186 | 31.5 | 596 | 1 | US-08-578-649-24 |
| 6 | 160.5 | 27.2 | 3565 | 1 | US-08-578-649-3 |
| 7 | 86.5 | 14.7 | 2757 | 1 | US-08-306-691B-48 |
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| 9 | 86.5 | 14.7 | 4762 | 4 | US-09-300-958A-30 |
| 10 | 85.5 | 14.5 | 2793 | 4 | US-07-646-537B-1 |
| 11 | 79 | 13.4 | 467 | 4 | US-09-300-958A-28 |
| 12 | 78.5 | 13.3 | 5398 | 3 | US-09-356-952-11 |

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| 13 | 71.5 | 12.1 | 1664976 | 4 | US-08-916-421B-1 | Sequence 1, Appl |
| 14 | 70.5 | 11.9 | 1992 | 4 | US-09-134-078-57 | Sequence 57, Appl |
| 15 | 70.5 | 11.9 | 2043 | 4 | US-09-134-078-11 | Sequence 11, Appl |
| 16 | 69 | 11.7 | 1664976 | 4 | US-08-916-421B-1 | Sequence 1, Appl |
| 17 | 68 | 11.5 | 2873 | 4 | US-08-630-915A-193 | Sequence 193, Appl |
| 18 | 67 | 11.4 | 4403765 | 3 | US-09-103-840A-2 | Sequence 2, Appl |
| 19 | 67 | 11.4 | 4411529 | 3 | US-09-103-840A-1 | Sequence 39, Appl |
| 20 | 66 | 11.2 | 747 | 4 | US-08-630-915A-39 | Sequence 7, Appl |
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| 22 | 66 | 11.2 | 840 | 1 | US-08-459-967-7 | Sequence 7, Appl |
| 23 | 66 | 11.2 | 840 | 1 | US-08-460-327-7 | Sequence 7, Appl |
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| 25 | 66 | 11.2 | 840 | 3 | US-09-024-532A-1 | Sequence 1, Appl |
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| 27 | 66 | 11.2 | 840 | 4 | US-09-019-532-1 | Sequence 1, Appl |
| 28 | 66 | 11.2 | 840 | 4 | US-09-417-359A-1 | Sequence 1, Appl |
| 29 | 66 | 11.2 | 1110 | 1 | US-08-434-255-5 | Sequence 5, Appl |
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| 33 | 66 | 11.2 | 1191 | 1 | US-08-434-255-3 | Sequence 3, Appl |
| 34 | 66 | 11.2 | 1191 | 1 | US-08-459-967-3 | Sequence 3, Appl |
| 35 | 66 | 11.2 | 1191 | 1 | US-08-460-327-3 | Sequence 3, Appl |
| 36 | 66 | 11.2 | 1191 | 1 | US-08-459-871-3 | Sequence 3, Appl |
| 37 | 66 | 11.2 | 1191 | 4 | US-09-252-991A-6755 | Sequence 6755, Ap |
| 38 | 66 | 11.2 | 1236 | 4 | US-09-252-991A-6804 | Sequence 6804, Ap |
| 39 | 66 | 11.2 | 2017 | 1 | US-08-434-255-27 | Sequence 27, Appl |
| 40 | 66 | 11.2 | 2017 | 1 | US-08-459-967-27 | Sequence 27, Appl |
| 41 | 66 | 11.2 | 2017 | 1 | US-08-460-327-27 | Sequence 27, Appl |
| 42 | 66 | 11.2 | 2017 | 1 | US-08-459-871-27 | Sequence 27, Appl |
| 43 | 66 | 11.2 | 2511 | 4 | US-09-252-991A-6942 | Sequence 6942, Ap |
| 44 | 66 | 11.2 | 2702 | 1 | US-08-434-255-1 | Sequence 1, Appl |
| 45 | 66 | 11.2 | 2702 | 1 | US-08-459-967-1 | Sequence 1, Appl |

ALIGNMENTS

RESULT 1
US-08-578-649-18
; Sequence 18, Application US/08578649
; Patent No. 5770366
; GENERAL INFORMATION:
; APPLICANT: Ulrich Bogdan
; APPLICANT: Reinhard Butner
; APPLICANT: Brigitte Kaluza
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felte & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44 MB storage diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/578, 649
; FILING DATE: 29-July-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 24 247.2
; FILING DATE: 20-July-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Andrew L. Tiajoleff
; REGISTRATION NUMBER: 31,575
; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 638-3884

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; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 330 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 7..327
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: 4..6
; OTHER INFORMATION: /function="startcodon Met"
US-08-578-649-18

Alignment Scores:
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Score: 253.50 Matches: 49
Percent Similarity: 64.81% Conservative: 21
Best Local Similarity: 45.37% Mismatches: 33
Query Match: 42.97% Indels: 5
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QY 25 LeuAlaSerAlaGlnGlnAspTyrAsnAlaProAspCysArgPheIleAsnValLys 44
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QY 45 GlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyIu---Phe 63
Db 133 GGCACAGTGTATGATCTTCTCCAAAGCTG-----AAGGCGCGTGGCGGCTCTTC 183
QY 64 TPAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyVal---ValGlyTyrPhe 82
Db 184 TGGGAGGAGCGGCTTCAGAGATACATGAGATCTGCGCTGCGCTGCGCTATTC 243
QY 83 ProArgAsnLeuValLysGlnGlnArgValTyrGlnGlnAlaThrLysGluValProThr 102
Db 244 CCCAGTAGCATGTTCGAGAGCAGACCCCTGAACCTGCGAAAGTCGATGTGAAGCA 303
QY 103 ThrAspIleAspPhePheCysGlu 110
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RESULT 2
US-08-578-649-1
; Sequence 1, Application US/08578649
; Patent No. 5770366
; GENERAL INFORMATION:
; APPLICANT: Ulrich Bogdan
; APPLICANT: Reinhard Buttner
; APPLICANT: Brigitte Kaluza
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felte & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/578,649
; FILING DATE: 29-July-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 24 247.2
; FILING DATE: 20-July-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Andrew L. TiaJoleff
; REGISTRATION NUMBER: 31,575
; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 459 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 40..432
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 40..111
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 112..432
US-08-578-649-1

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Pred. No.: 2.5e-28 Length: 459
Score: 253.50 Matches: 49
Percent Similarity: 64.81% Conservative: 21
Best Local Similarity: 45.37% Mismatches: 33
Query Match: 42.97% Indels: 5
DB: Gaps: 3

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Db 178 ATGGCTGTGGCCCTTCAGAGCTACATGCCCCGCTGCGCTGCGCTGACCATTCACCG 237
QY 45 GlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyIu---Phe 63
Db 238 GGCAGAGTGTATGATCTTCTCCAAAGCTG-----AAGGCGCGTGGCGGCTCTTC 288
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Db 349 CCCAGTAGCATGTTCGAGAGCAGACCCCTGAACCTGCGAAAGTCGATGTGAAGCA 408
QY 103 ThrAspIleAspPhePheCysGlu 110
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RESULT 3
US-08-578-649-4
; Sequence 4, Application US/08578649
; Patent No. 5770366
; GENERAL INFORMATION:
; APPLICANT: Ulrich Bogdan
; APPLICANT: Reinhard Buttner
; APPLICANT: Brigitte Kaluza
```

TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felife & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-July-1993
ATTORNEY/AGENT INFORMATION:
NAME: Andrew L. TiaJoloff
REGISTRATION NUMBER: 31,575
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 581 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 110..499
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 110..178
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LOCATION: 179..499
US-08-578-649-4
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Score: 231.50 Matches: 47
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Best Local Similarity: 43.52% Mismatches: 35
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DB 245 ATGGCTGTGGCTCCGACGACTACGTGCGCTGATGCGGCTTCTGACTATATATAGG 304
QY 45 GlyGlnGlnIleIYrValIYrSerLysLeuValLysGlnGlnGlnGlnGlnGlnGln 63
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QY 103 ThrAspIleAspPhePheCysGlu 110
DB 476 GATCAATGAGATTCTACTGCGCAG 499
RESULT 4
US-08-578-649-8
Sequence 8, Application US/08578649
Patent No. 5770366
GENERAL INFORMATION:
APPLICANT: Ulrich Bogdan
APPLICANT: Reinhard Butner
APPLICANT: Brigitte Kaluza
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felife & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-July-1993
ATTORNEY/AGENT INFORMATION:
NAME: Andrew L. TiaJoloff
REGISTRATION NUMBER: 31,575
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 305 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: misc_RNA
LOCATION: join(1..29, 277..305)
OTHER INFORMATION: /function="Primer"
US-08-578-649-8
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Best Local Similarity: 44.44% Mismatches: 33
Query Match: 35.68% Indels: 5
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QY 52 SerLysLeuValLysGluAsnGlyAlaGlyGlu---PheTrpAlaGlySerValTyrGly 70
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 ; Sequence 24, Application US/08578649
 ; Patent No. 5770366
 ; GENERAL INFORMATION:
 ; APPLICANT: Ulrich Bogdan
 ; APPLICANT: Reinhard Butner
 ; APPLICANT: Brigitte Kaluza
 ; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Felfe & Lynch
 ; STREET: 805 Third Avenue
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10022
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
 ; COMPUTER: IBM PS/2
 ; OPERATING SYSTEM: PC-DOS
 ; SOFTWARE: Wordperfect
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/578,649
 ; FILING DATE: 29-July-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: DE P 43 24 247.2
 ; FILING DATE: 20-July-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Andrew L. Tiajolo
 ; REGISTRATION NUMBER: 31,575
 ; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 688-9200
 ; TELEFAX: (212) 838-3884
 ; INFORMATION FOR SEQ ID NO: 24:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 596 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: join(40..111, 40..166, 214..347, 393..503, 549
 ; LOCATION: ..569)
 ; FEATURE:
 ; NAME/KEY: sig peptide
 ; LOCATION: 40..111
 ; FEATURE:
 ; NAME/KEY: exon
 ; LOCATION: 40..166
 ; FEATURE:
 ; NAME/KEY: exon
 ; LOCATION: 214..347
 ; FEATURE:
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NAME/KEY: exon
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 NAME/KEY:
 LOCATION: one-of(194, 369, 527)
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 OTHER INFORMATION: and 527 denotes an indefinite number and sequence
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 Alignment Scores:
 Pred. No.: 3,31e-18
 Score: 186.00
 Percent Similarity: 45.81%
 Best Local Similarity: 32.26%
 Query Match: 31.53%
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 Gaps: 7
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 Db 177 GGAGGGTAGAATTGGGNCCTTCTATTCTCCCTAGACCCCTATTCATGGCTGTGGCC 236
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 QY 92 ValTyrGlnGluAlaThrLysGluValProThrThrAspIle----- 105
 Db 468 ACCCTGAACCTGGCAAGTCGATGG---AAGACAGAGCTGAGTGCATGCGGCTGG 524
 QY 106 -----AspPhePheCyGlu 110
 Db 525 CANTTCCCTTCTCTTTTTCAGAAATGGGATTTCTACTGCGAG 569
 RESULT 6
 ; Sequence 3, Application US/08578649
 ; Patent No. 5770366
 ; GENERAL INFORMATION:
 ; APPLICANT: Ulrich Bogdan
 ; APPLICANT: Reinhard Butner
 ; APPLICANT: Brigitte Kaluza
 ; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Felfe & Lynch
 ; STREET: 805 Third Avenue
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10022
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
 ; COMPUTER: IBM PS/2
 ; OPERATING SYSTEM: PC-DOS

SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-July-1993
ATTORNEY/AGENT INFORMATION:
NAME: Andrew J. TiaJoloff
REGISTRATION NUMBER: 31,575
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 638-3684
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3565 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 1378..1449
FEATURE:
NAME/KEY: exon
LOCATION: 1378..1504
FEATURE:
NAME/KEY: exon
LOCATION: 1586..1719
FEATURE:
NAME/KEY: exon
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NAME/KEY:
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OTHER INFORMATION: /note= "N in position 2216
OTHER INFORMATION: denotes an indefinite number ans sequence of
US-08-578-649-3
Alignment Scores:
Pred. No.: 2,578-13 Length: 3565
Score: 160.50 Matches: 36
Percent Similarity: 50.00% Conservative: 10
Best Local Similarity: 39.13% Mismatches: 15
Query Match: 27.20% Indels: 31
Gaps: 3
US-10-019-455a-24 (1-110) x US-08-578-649-3 (1-3565)
5 MetAspArgLeuAlaSerIleuLysLeuCysAlaAspArgGluCys----- 19
1456 ATGCCCAAGCTGGCTGACCGGAAAGCTGTGTGGGACCAAGAGTGCAGCCGTAAGATGGG 1515
19 ----- 19
1516 GAGGGTAGAATTTGGGCTGGGTGTAGCCTGTGATGCTGCTGATTCCTTCATT 1575
20 -----ValTyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCys 37
1576 CTTTCCCTAGACCCCTATCTTCATGCTGTGGCCCTTCAGACTACATGAGCCCGGACTGC 1635
38 ArgPheIleAsnValLysGlnGlnIleTyrValTyrSerLysLeuValLysGlu 57
1636 CGATTCCGACCATTCACCGGGCCAAAGTGTGATGCTTCTCCAAAGCTG----- 1686
58 AsnGlyAlaGlyGlu---PheTyrAlaGlySerVal 68

Db 1687 AAGGCGCGTGGCGGCTCTTCTGAGGAGGAGCGGTG 1722
RESULT 7
US-08-306-691B-48
Sequence 48, Application US/08306691B
Patent No. 5734039
GENERAL INFORMATION:
APPLICANT: Calabretta, Bruno
APPLICANT: Skorski, Tomasz
TITLE OF INVENTION: ANTISENSE
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seidel, Gonda, Lavoraga & Monaco, P.C.
STREET: Two Penn Center, Suite 1800
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,691B
FILING DATE: September 15, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8363
TELEFAX: (215) 568-5549
TELEX: No. 5734039E
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 2757 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-306-691B-48
Alignment Scores:
Pred. No.: 0,0146 Length: 2757
Score: 86.50 Matches: 23
Percent Similarity: 51.43% Conservative: 13
Best Local Similarity: 32.86% Mismatches: 21
Query Match: 14.66% Indels: 13
Gaps: 3
US-10-019-455a-24 (1-110) x US-08-306-691B-48 (1-2757)
26 AlAserIlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnValLysGly 45
2325 GCCAAAGCCCGCTATGACTTCTGCGCCGTCGACCGTTCAAGAGCTGCTCCAAAGAGGCT 2384
46 GlnGlnIleTyrValTyrSerLysLeuValLysGlnAsnGlyAlaGlyGluPheTyrPala 65
2385 GACATATC-----AGATCCTTAACAAAGAGGACAGCAAGAGGCTGTGGCA 2432
66 GlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPheProArgAsn 85
2433 GGGAGATCTATGGCGG-----GTTGGCTGTCTCCCTCCCAAC 2471
86 LeuValLysGlnGluArgValTyrGlnGlu 95
2472 TACGTGAGAGAGAT-----TATTCCTGA 2495

RESULT 8
PCT-US93-06251-79
Sequence 79, Application PC/TUS9306251
GENERAL INFORMATION:
APPLICANT: Mickelrom, Eric and Rife, Jason P.
TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
Stereospecific Alkylphosphonates and Arylphosphonates
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: NY
COUNTRY: USA
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06251
FILING DATE: 19930630
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Digilio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8586
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 2757 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US93-06251-79

Alignment Scores:
Pred. No.: 0.0146 Length: 2757
Score: 86.50 Matches: 23
Percent Similarity: 51.43% Conservative: 13
Best Local Similarity: 32.86% Mismatches: 21
Query Match: 14.66% Indels: 13
DB: 5 Gaps: 3

US-10-019-455A-24 (1-110) x PCT-US93-06251-79 (1-2757)

QY 26 AlaserlaagngluaptyrAsnAlaProAspCySarGpheIleaenValLysGly 45
Db 2225 GCCAAACCCCGCTAGCTTCGCGCCGACGCTCAAGAGCTGCTCAAGAGAGGT 2384

QY 46 GlnsinletyryValtyrSerlyLeuVallysgluasnGlyAlaGlyGluPheIleTPAla 65
Db 2385 GACATCATC-----AGATCTTAAACAAGAGGAGCAAGAGCTGAGCGCA 2432

QY 66 GlySerValtyrGlyAspGlyGlnAspGluMetGlyValAlaGlytyrPheProAspAan 85
Db 2433 GGGGAGATCTATGGCCG-----CTTGGCTGGTTCCCTGCCAAC 2471

QY 86 LeuVallysgluGlnAspGlytyrGlnGlu 95
Db 2472 TACGTGAGAGAGAT-----TATTTGAA 2495

RESULT 9
US-09-300-958A-30
Sequence 30, Application US/09300958A
GENERAL INFORMATION:
PATENT NO. 6495319
APPLICANT: McClelland, Michael

APPLICANT: Welsh, John
APPLICANT: Trenkle, Thomas
TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
TITLE OF INVENTION: Using Same
FILE REFERENCE: P-PH 3457
CURRENT APPLICATION NUMBER: US/09/300,958A
CURRENT FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/083,331
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/098,070
PRIOR FILING DATE: 1998-08-27
PRIOR APPLICATION NUMBER: 60/118,624
PRIOR FILING DATE: 1999-02-04
NUMBER OF SEQ ID NOS: 85
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 30
LENGTH: 4762
TYPE: DNA
ORGANISM: Homo sapiens
US-09-300-958A-30

Alignment Scores:
Pred. No.: 0.0323 Length: 4762
Score: 86.50 Matches: 21
Percent Similarity: 52.24% Conservative: 14
Best Local Similarity: 31.34% Mismatches: 21
Query Match: 14.66% Indels: 11
DB: 4 Gaps: 2

US-10-019-455A-24 (1-110) x US-09-300-958A-30 (1-4762)

QY 23 lIeSerleuAlaserlaagngluaptyrAsnAlaProAspCySarGpheIleaenVal 42
Db 2405 CTGGGCAATGCCATCGCTGATGACTTCTGTGCAAGATATAGAGATTGCTCTTG 2464

QY 43 LysLysGlyGlnGlnletyryValtyrSerlyLeuVallysgluasnGlyAlaGlyGlu 62
Db 2465 TTGAAAGAGATGTGTGAGATTACACAAAGATG-----AGTCCAATGCGC 2512

QY 63 PheTPAlaGlySerValtyrGlyAspGlyGlnAspGluMetGlyValAlaGlytyrPhe 82
Db 2513 TGCTGAGAGGAGAACTAATATGCGCAG-----GTGGCTGGTTT 2551

QY 83 ProArgAsnLeuVallysglu 89
Db 2552 CCATCCACATATGTGGAGAG 2572

RESULT 10
US-07-646-537B-1
Sequence 1, Application US/07646537B
PATENT NO. 534864
GENERAL INFORMATION:
APPLICANT: Barbacid, Mariano
TITLE OF INVENTION: Vav Proto-Oncogene Protein
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company
STREET: P.O. Box 4000
CITY: Princeton
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 08543-4000
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/646,537B
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gaul, Timothy J.

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US-09-300-958A-28                                     ; LOCATION:(462)
Alignment Scores:
Pred. No.: 0.0142                                         Length: 467
Score: 79.00                                              Matches: 23
Percent Similarity: 50.00%                               Conservative: 16
Best Local Similarity: 29.49%                            Mismatches: 27
Query Match: 13.39%                                       Indels: 12
DB: 4                                                    Gaps: 3

US-10-019-455A-24 (1-110) x US-09-300-958A-28 (1-467)
QY      28 AlaGInguAspTYrAsnAlaProAspCYArgPheIleAsnVallyeISGIyGInGln 47
       |||:::|||||||:::|||||:::|||||:::|||||:::|||||
DB      152 GCTCGATAGACTTCTGTGCACAGATATAGAGAGAGTTCTCCTTTGGAAAGCATGTG 211
QY      48 ILeTyRyAlTySeerLySLeuVallySGluAenGlyAlaglyGluPheTrPAglYser 67
       :::::|||||:::|||||:::|||||:::|||||:::|||||
DB      212 GTGAAGATTTCACCAAGATG-----AGTCMAATGCCGTGGTGAGAGAGAA 255
QY      68 ValTyRGlyAspSgIGlnAspGluMetGlyValValGlyTyRPhPProArgAsnLeuVal 87
       ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      260 GTAATGCGCAGG-----GTGGGTGGTTTCCATCCACATATGTG 299
QY      88 LySGluInArGyAlTyrgInGuIuaThLrySGluValProTHrThaspIle 105
       :|||:::|||||:::|||||:::|||||:::|||||
DB      299 ----GGAGAGGAGATGAATTAATTCAAATCCGTTTGCAACCCTGCACCAAAATT 349

RESULT 12
US-09-356-952-11
; Sequence 11, Application US/09356952
; Patent No. 6117663
; GENERAL INFORMATION:
; APPLICANT: Bostack-Sjodin, Ann
; APPLICANT: Margalit, S. M.
; APPLICANT: Bor-Soggi, Dafna
; APPLICANT: Cole, Philip
; APPLICANT: Kuriyan, John
; TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE
; FILE REFERENCE: 600-1-228N
; CURRENT APPLICATION NUMBER: US/09/356,952
; EARLIER FILING DATE: 1999-07-19
; EARLIER APPLICATION NUMBER: 60/093,631
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 11
; LENGTH: 5398
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-356-952-11

Alignment Scores:
Pred. No.: 0.587                                           Length: 5398
Score: 78.50                                              Matches: 23
Percent Similarity: 49.44%                               Conservative: 21
Best Local Similarity: 25.84%                            Mismatches: 34
Query Match: 13.31%                                       Indels: 11
DB: 3                                                    Gaps: 4

US-10-019-455A-24 (1-110) x US-09-356-952-11 (1-5398)
QY      8 LeuAlaSerLySylSLeuCysAlaAspAspGluCyseValTyThrIlleSerLeuAlaser 27
       |||:::|||||:::|||||:::|||||:::|||||:::|||||
DB      445 TTTCCTTTCCCCCTCGACAGATGATGACACGATTCGCCAATGATACTATCT 504
QY      28 AlaGInguAspTYrAsnAlaPro-----AspCYArgPheIleAsnVal 42
       ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      505 GCTGCTATGACTTAAATATATCCCATTAATAAAAAAGACAGATTCTGCCAACCTTTGCTGTA 564

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Db 565 CAAACAAGGGGAACCATTTATCTTACAAA-----AACTCATCTGGG--- 609
Qy 63 PheTTPAlaGlySerValTYrGlyAspGlyGlnAspGlnMetGlyValValGlyTYrPhe 82
Db 610 TCGTGGCATGATGATTAATTATTTAGACGACGATGATGGGAAAGTTAAC--AGAGGCTGGTTT 666
Qy 83 ProArgAsnLeuValLysGluGlnArg 91
Db 667 CCTCAAACTCGGTAGACCTTTAGA 693
RESULT 13
US-08-916-421B-1
Sequence 1, Application US/08916421B
Patent No. 6503729
GENERAL INFORMATION:
APPLICANT: Buit et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanoco-
coccus jannaschii
PATENT NO. 6503729
FILE REFERENCE: PB275
CURRENT APPLICATION NUMBER: US/08/916,421B
CURRENT FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1664976
TYPE: DNA
ORGANISM: Methanococcus jannaschii
FEATURE:
NAME/KEY: misc_feature
LOCATION: (28222)..(28222)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (28257)..(28258)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (84773)..(84773)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (84808)..(84808)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (84812)..(84812)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (98120)..(98120)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (98159)..(98159)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (98239)..(98239)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (98256)..(98256)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (98343)..(98343)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (103998)..(103998)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (148948)..(148948)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (163385)..(163385)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (191989)..(191989)
OTHER INFORMATION: n equals a, t, c, or g

OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (191995)..(191995)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (231980)..(231980)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (234187)..(234187)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (234220)..(234220)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (234814)..(234814)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (309398)..(309398)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (309418)..(309418)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (312837)..(312837)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (312993)..(312993)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (319226)..(319226)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (559241)..(559241)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (600992)..(600992)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (622708)..(622708)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (657081)..(657081)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (657203)..(657203)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (674435)..(674435)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (682442)..(682442)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (713652)..(713652)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (741684)..(741684)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (779455)..(779455)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (779676)..(779676)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (855539)..(855539)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (871619)..(871619)
OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc feature
LOCATION: (1084830) .. (1084830)
OTHER INFORMATION: n equals a, c, c, or g
NAME/KEY: misc feature
LOCATION: (1096846) .. (1096846)
OTHER INFORMATION: n equals a, c, c, or g
NAME/KEY: misc feature
LOCATION: (1119881) .. (1119881)
OTHER INFORMATION: n equals a, c, c, or g
NAME/KEY: misc feature
LOCATION: (1130881) .. (1130881)
OTHER INFORMATION: n equals a, c, c, or g
NAME/KEY: misc feature
LOCATION: (1310988) .. (1310988)
OTHER INFORMATION: n equals a, c, c, or g
NAME/KEY: misc feature
LOCATION: (1313224) .. (1313224)
OTHER INFORMATION: n equals a, c, c, or g
NAME/KEY: misc feature
LOCATION: (1345473) .. (1345473)
OTHER INFORMATION: n equals a, c, c, or g
NAME/KEY: misc feature
LOCATION: (1349491) .. (1349491)
OTHER INFORMATION: n equals a, c, c, or g
NAME/KEY: misc feature
LOCATION: (1470091) .. (1470091)
OTHER INFORMATION: n equals a, c, c, or g
NAME/KEY: misc feature
LOCATION: (1569020) .. (1569020)
OTHER INFORMATION: n equals a, c, c, or g
NAME/KEY: misc feature
LOCATION: (1602912) .. (1602912)
OTHER INFORMATION: n equals a, c, c, or g
NAME/KEY: misc feature
LOCATION: (1603734) .. (1603734)
OTHER INFORMATION: n equals a, c, c, or g
NAME/KEY: misc feature
LOCATION: (1637998) .. (1637998)
OTHER INFORMATION: n equals a, c, c, or g
NAME/KEY: misc feature
LOCATION: (1664854) .. (1664854)
OTHER INFORMATION: n equals a, c, c, or g
US-08-916-421B-1

Alignment Scores:
Pred. No.: 2.58e+04
Score: 71.50
Percent Similarity: 46.67%
Best Local Similarity: 25.71%
Query Match: 12.12%
Matches: 27
Conservative: 22
Mismatches: 33
Indels: 23
Gaps: 6

US-10-019-455a-24 (1-110) x US-08-916-421B-1 (1-1664976)
QY 3 lIlePheNeaSpArlgIeuaIaSer-----LysIleuCySaIa 15
Db 414948 ATCTATGCTGAAGATTGGCTTAAGATTAAAGCTAAGCAAGAGATTATTTAA 415007
QY 16 AspaSpGlucys---ValTyrThrIleSerLeuaIaSerAlaGlnGluAspTyrAla 34
Db 415008 GAAGAGAGATGAGAGATGTTAAGGTAGCTAAGCAATGATGATGAT--- 415064
QY 35 ProAspCyArgPheIleAsnValLysLysGlnGlnIleTyrValTyrSerLysIeu 54
Db 415065 -----TTAATGAAGATTGAGTTGAATCCCTATCTATGATGCTTCAAGATG 415112
QY 55 ValLysGlnAsnGlyAlaGlyGlnPheTrpAlaGlySerValTyrGlyAspGlyGln 74
Db 415113 GCAAAATGAGATGATTAAGTTGTT-----CTATCTGGGCAAGAGCTGAT 415160
QY 75 GluMetGlyValValGlyTyrPheProArgAsnLeuValLysGlnGlnAlaGlyGln 94
Db 415161 GAGTTA---TTTGAGGCTAT-----GCAAGGCAAGAGATTTATAGG 415202

QY 95 GluAlaThrLysGln 99
Db 415203 GAGAGAGGAGAGAG 415217

RESULT 14
US-09-134-078-57
Sequence 57, Application US/09134078
Parent No. 6368844
GENERAL INFORMATION:
APPLICANT: Elyna, Edward J.
TITLE OF INVENTION: GLYCOSIDASE ENZYMES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gray Cary Ware & Freidenrich LLP
STREET: 4365 Executive Drive, Suite 1600
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/134,078
FILING DATE: 13-AUG-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/949,026
FILING DATE: 10-OCT-1997
APPLICATION NUMBER: 60/056,916
FILING DATE: 06-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09010/024002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858/677-1456
TELEFAX: 858/677-1465
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 1992 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...1989
US-09-134-078-57

Alignment Scores:
Pred. No.: 2.09
Score: 70.50
Percent Similarity: 37.93%
Best Local Similarity: 27.59%
Query Match: 11.95%
Matches: 32
Conservative: 12
Mismatches: 37
Indels: 35
Gaps: 6

US-10-019-455a-24 (1-110) x US-09-134-078-57 (1-1992)
QY 25 LeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnValLys 44
Db 1159 CTGTCACACACAGGTGAGACATAGAGACACACCTGCTTTCATCTTCAAAAAGAC 1218
QY 45 GlyGlnGlnIle-----TyrValTyrSerLys--- 53
Db 1219 GGCATGAGATCAAAAAAGACCGTGAAGTGAAGGCTGCTGTTTTCGACTACACACACG 1278
QY 54 -----LeuValLysGlnAsnGlyAlaGlyGlnPhe 63

Db 1279 TTGAAAGTGTCTGTCAAGTCGAGATCTGTTTGAATAAGATAGACATCTC 1338
QY 64 TTPAlaGlySerValIlyrGly-----AspGlyGlnAsp 74
Db 1339 GGATACGGA---ATTTCAGGCTTTGATCTGCACACACCCGGATCCGGATGAGAACAT 1395
QY 75 GluMetGlyValValAlaGlyTyrrPheProArgAsnLeuValIlysgLugln-----Arg 91
Db 1396 GAAATGTTCTTGAAGGCGACCTTCAGGAAAAACCGTGAAGACTCTATCAAGCGAAA 1455
QY 92 ValTyrgIngluAlaThrIlysgIuValProThrThraspIleAspPhe 107
Db 1456 GTGCTGAACGAAGCA---CGGTACGTCTCGCAGAGAAAGTTGATTTT 1500

RESULT 15
US-09-134-078-11
Sequence 11, Application US/09134078
Patent No. 6368844
GENERAL INFORMATION:
APPLICANT: Byline, Edward J.
TITLE OF INVENTION: GLYCOSIDASE ENZYMES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gray Cary Ware & Freidenrich LLP
STREET: 4365 Executive Drive, Suite 1600
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/134,078
FILING DATE: 13-AUG-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/949,026
FILING DATE: 10-OCT-1997
APPLICATION NUMBER: 60/056,916
FILING DATE: 06-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09010/024002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858/677-1456
TELEFAX: 858/677-1465
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 2043 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...2040
US-09-134-078-11

Alignment Scores:
Pred. No.: 2.17 Length: 2043
Score: 70.50 Matches: 32
Percent Similarity: 37.93% Conservative: 12
Best Local Similarity: 27.59% Mismatches: 37
Query Match: 11.95% Indels: 35
DB: 4 Gaps: 6

US-10-019-455a-24 (1-110) x US-09-134-078-11 (1-2043)

QY 25 LeuAlaSerAlaGlnGluAspTyrrAsnAlaProAspCysArgPheIleAsnValIlysLys 44

Db 1210 CTGTTCAACACAGGTGAAGACATTAAGAGAGACACCTGCTTTTCATCTTCAAAAAGAC 1269
QY 45 GlyGlnGlnIle-----TyrrValIlyrSerLys--- 53
Db 1270 GGCAATGGAGATCAAAAAGACCGTGAAGTAGGGCTGTGTTTTCGACTACAGCAACAGC 1329
QY 54 -----LeuValIlysgIuAsnGlyAlaGlyLuglnPhe 63
Db 1330 TTGAAAGTGTCTGTCAAGTCGAGATCTGTTTGAATAAGATAGACATCTC 1389
QY 64 TTPAlaGlySerValIlyrGly-----AspGlyGlnAsp 74
Db 1390 GGATACGGA---ATTTCAGGCTTTGATCTGCACACACCCGGATCCGGATGAGAACAT 1446
QY 75 GluMetGlyValValAlaGlyTyrrPheProArgAsnLeuValIlysgLugln-----Arg 91
Db 1447 GAAATGTTCTTGAAGGCGACCTTCAGGAAAAACCGTGAAGACTCTATCAAGCGAAA 1506
QY 92 ValTyrgIngluAlaThrIlysgIuValProThrThraspIleAspPhe 107
Db 1507 GTGCTGAACGAAGCA---CGGTACGTCTCGCAGAGAAAGTTGATTTT 1551

Search completed: December 29, 2003, 22:08:03
Job time : 213.972 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 22:08:26 ; Search time 1045 Seconds

(without alignments)
12918.830 Million cell updates/sec

Title: US-10-019-455A-25

Perfect score: 330

Sequence: 1 catgagctattcatgacataa.....atattgactctctctgtgaa 330

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2088711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database :

GeneB1:

1: gb_da:*
2: gb_hg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
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34: em_hg_pln:*
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39: em_higo_hum:*
40: em_higo_mus:*
41: em_higo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query % | Match | Length | DB | ID | Description |
|------------|-------|---------|-------|--------|-----------|----|---------------------|
| 1 | 330 | 100.0 | 330 | 6 | BD010817 | | BD010817 Novel pol |
| 2 | 330 | 100.0 | 330 | 6 | BD093118 | | BD093118 Novel pol |
| 3 | 330 | 100.0 | 384 | 6 | BD010805 | | BD010805 Novel pol |
| 4 | 330 | 100.0 | 384 | 6 | BD093106 | | BD093106 Novel pol |
| 5 | 330 | 100.0 | 929 | 10 | AF243504 | | AF243504 Mus muscu |
| 6 | 330 | 100.0 | 947 | 6 | BD010821 | | BD010821 Novel pol |
| 7 | 330 | 100.0 | 947 | 6 | BD093122 | | BD093122 Novel pol |
| 8 | 330 | 100.0 | 958 | 10 | MMU243939 | | MMU243939 Mus muscu |
| 9 | 330 | 100.0 | 1054 | 10 | AF233333 | | AF233333 Mus muscu |
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| 11 | 294.8 | 89.3 | 330 | 6 | BD093137 | | BD093137 Novel pol |
| 12 | 294.8 | 89.3 | 384 | 6 | BD010835 | | BD010835 Novel pol |
| 13 | 294.8 | 89.3 | 384 | 6 | BD093136 | | BD093136 Novel pol |
| 14 | 261.8 | 79.3 | 307 | 6 | BD010830 | | BD010830 Novel pol |
| 15 | 261.8 | 79.3 | 307 | 6 | BD093131 | | BD093131 Novel pol |
| 16 | 252.2 | 76.4 | 330 | 6 | BD010816 | | BD010816 Novel pol |
| 17 | 252.2 | 76.4 | 330 | 6 | BD093117 | | BD093117 Novel pol |
| 18 | 252.2 | 76.4 | 384 | 6 | BD010802 | | BD010802 Novel pol |
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| 20 | 252.2 | 76.4 | 521 | 6 | AX362311 | | AX362311 Sequence |
| 21 | 252.2 | 76.4 | 521 | 6 | AX454774 | | AX454774 Sequence |
| 22 | 252.2 | 76.4 | 521 | 6 | AX491252 | | AX491252 Sequence |
| 23 | 252.2 | 76.4 | 846 | 9 | AF243505 | | AF243505 Homo sapi |
| 24 | 252.2 | 76.4 | 846 | 9 | AF243505 | | AF243505 Homo sapi |
| 25 | 252.2 | 76.4 | 923 | 6 | BD010820 | | BD010820 Novel pol |
| 26 | 252.2 | 76.4 | 923 | 6 | BD093121 | | BD093121 Novel pol |
| 27 | 252.2 | 76.4 | 923 | 6 | BD010829 | | BD010829 Novel pol |
| 28 | 252.2 | 76.4 | 923 | 6 | BD093130 | | BD093130 Novel pol |
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| 30 | 252.2 | 76.4 | 923 | 6 | BD093130 | | BD093130 Novel pol |
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| 34 | 252.2 | 76.4 | 923 | 6 | BD093130 | | BD093130 Novel pol |
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ALIGNMENTS

RESULT 1
LOCUS BD010817 330 bp DNA linear PAT 31-JAN-2002
DEFINITION Novel polypeptide and DNA thereof.
ACCESSION BD010817
VERSION BD010817.1 GI:18639190
KEYWORDS UP 2001069994-A/18.
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
Yoshimura, K., and Tanaka, H.
TITLE Novel polypeptide and DNA thereof

PD 21-MAR-2001
 PF 29-JUN-2000 JP 2000195911
 PR YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI
 SHINICHI MOGI,
 PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
 PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC
 A61P19/08
 PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC
 G01N33/53//
 PC C12P21/08, C12N15/00, A61K37/02, C12N5/00
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 FH Key Location/Qualifiers
 FT source 1. .384
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 /mol_type="genomic DNA"
 /db_xref="taxon:10095"
 Location/Qualifiers
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 /organism="Mus sp."
 /mol_type="genomic DNA"
 /db_xref="taxon:10095"

BASE COUNT 98 a 68 c 111 g 107 t
 ORIGIN

Query Match 100.0%; Score 330; DB 6; Length 384;
 Best Local Similarity 100.0%; Pred. No. 2.7e-90;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATGCTGATTTATGATTAACCTTTCTTCTAGAGTTGTGTGCGGATGAGAGTGTCTC 60
 DB 55 CATGCTGATTTATGATTAACCTTTCTTCTAGAGTTGTGTGCGGATGAGAGTGTCTC 114
 QY 61 TATACATTTCTCTGCGAAGACACAGAAATTACAATGCCCGACAGTGTAGTTTCATC 120
 DB 115 TATACATTTCTCTGCGAAGACACAGAAATTACAATGCCCGACAGTGTAGTTTCATC 174
 QY 121 GATGTCAGAAAGGCGACAGATCTATGTTTACTCCAAAGCTGTATACAGAAACGAGCT 180
 DB 175 GATGTCAGAAAGGCGACAGATCTATGTTTACTCCAAAGCTGTATACAGAAACGAGCT 234
 QY 181 GGAGAGTTTGGGCTGGCAGTGTATGTTTATGTTTACCAACGAGATGATGGGATTTAGGT 240
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 QY 241 TATTTCCCAAGCACTGTGTGAAGAGAGAGCGGTATATACAGAGAGCGCCACCAAGAGATC 300
 DB 295 TATTTCCCAAGCACTGTGTGAAGAGAGCGGTATATACAGAGAGCGCCACCAAGAGATC 354
 QY 301 CCAACCAAGGATATTGACTTTCTGTGAA 330
 DB 355 CCAACCAAGGATATTGACTTTCTGTGAA 384

RESULT 4
 LOCUS BD093106 384 bp DNA linear PAT 27-AUG-2002
 DEFINITION Novel polypeptide and its DNA.
 ACCESSION BD093106
 VERSION BD093106.1 GI:22638694
 KEYWORDS WO 0102564-A/6.
 SOURCE Mus sp.
 ORGANISM Mus sp.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 384)
 Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
 Yoshimura, K. and Tanaka, H.
 Novel polypeptide and its DNA
 Patent: WO 0102564-A 6 11-JUN-2001.
 TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO
 OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,
 HIDEYUKI TANAKA
 OS Mus sp. (mouse)
 PN WO 0102564-A/6

PD 11-JAN-2001
 PF 29-JUN-2000 WO 2000JP004278
 PR 30-JUN-1999 JP 99P 186718
 PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI
 MOGI,
 PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
 PC C12N15/12, C12N5/10, C12P21/02, C07K14/47, C07K16/18, A61K45/00, PC
 A61K38/17,
 PC A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/7088//C12P21/
 02, C12R1:19
 CC
 FH Key Location/Qualifiers
 FT source 1. .384
 /organism="Mus sp."
 /mol_type="genomic DNA"
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BASE COUNT 98 a 68 c 111 g 107 t
 ORIGIN

Query Match 100.0%; Score 330; DB 6; Length 384;
 Best Local Similarity 100.0%; Pred. No. 2.7e-90;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATGCTGATTTATGATTAACCTTTCTTCTAGAGTTGTGTGCGGATGAGAGTGTCTC 60
 DB 55 CATGCTGATTTATGATTAACCTTTCTTCTAGAGTTGTGTGCGGATGAGAGTGTCTC 114
 QY 61 TATACATTTCTCTGCGAAGACACAGAAATTACAATGCCCGACAGTGTAGTTTCATC 120
 DB 115 TATACATTTCTCTGCGAAGACACAGAAATTACAATGCCCGACAGTGTAGTTTCATC 174
 QY 121 GATGTCAGAAAGGCGACAGATCTATGTTTACTCCAAAGCTGTATACAGAAACGAGCT 180
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 QY 241 TATTTCCCAAGCACTGTGTGAAGAGAGCGGTATATACAGAGAGCGCCACCAAGAGATC 300
 DB 295 TATTTCCCAAGCACTGTGTGAAGAGAGCGGTATATACAGAGAGCGCCACCAAGAGATC 354
 QY 301 CCAACCAAGGATATTGACTTTCTGTGAA 330
 DB 355 CCAACCAAGGATATTGACTTTCTGTGAA 384

RESULT 5
 LOCUS AF243504 929 bp mRNA linear ROD 26-DEC-2000
 DEFINITION Mus musculus fibrocyte-derived protein (Fdp) mRNA, complete cds.
 ACCESSION AF243504
 VERSION AF243504.1 GI:11991841
 KEYWORDS
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 929)
 Cohen-Salmon, M., Frenz, D., Liu, W., Verpy, E., Voegelings, S. and
 Petit, C.
 Fdp, a new fibrocyte-derived protein related to MIA/CD-RAP, has an
 in vitro effect on the early differentiation of the inner ear
 menenchyme
 J. Biol. Chem. 275 (51), 40036-40041 (2000)
 10598416
 J. Biol. Chem. 275 (51), 40036-40041 (2000)
 10598416
 2 (bases 1 to 929)
 Cohen-Salmon, M., Frenz, D., Verpy, E., Voegelings, S. and Petit, C.
 Direct Submission

JOURNAL Submitted (09-MAR-2000) Biotechnologies, Institut Pasteur, 25 rue

du Dr. Roux, Paris 75015, France

FEATURES Location/Qualifiers

source

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/mol_type="mRNA"
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CDS

BASE COUNT 260 a 156 c 220 g 293 t
ORIGIN

Query Match 100.0%; Score 330; DB 10; Length 929;
Best Local Similarity 100.0%; Pred. No. 2.9e-90;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATGTGTATTTATGATATAAATTCTTCTTAAGAAGTTGTCGGATGAGAGTGTGTC 60
Db 63 CATGTGTATTTATGATATAAATTCTTCTTAAGAAGTTGTCGGATGAGAGTGTGTC 122
QY 61 TATACTATTTCTTGGCAGAGCAGAGAAAGATTACATGCCCCAGACTGTAGTTCATC 120
Db 123 TATACTATTTCTTGGCAGAGCAGAGAAAGATTACATGCCCCAGACTGTAGTTCATC 182
QY 121 GATGTCAAGAAAGGAGCAGATCTATGTTTACTCCAGCTGTGTAAACAGAAACGAGCT 180
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QY 181 GGAGAGTTTGGGCTGGCAGTGTATTGNGACCAACGATGAGATGGGAATTGTAGT 240
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QY 241 TATTTCCCAAGCACTTGTGAAGAGCAGCGTGTATACAGAGAGCCCAAGAGAGATC 300
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QY 301 CCAACCAAGGATATTGACTTCTTCTGTGAA 330
Db 363 CCAACCAAGGATATTGACTTCTTCTGTGAA 392

RESULT 6
BD010821 947 bp DNA linear PAT 31-JAN-2002

LOCUS BD010821
DEFINITION Novel polypeptide and DNA thereof.

ACCESSION BD010821.1 GI:18639194

VERSION JP 2001069994-A/22.

KEYWORDS

SOURCE

ORGANISM

Mus sp.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

Yoshimura, K. and Tanaka, H.

Novel polypeptide and DNA thereof

Patent: JP 2001069994-A 22 21-MAR-2001;

TAKEDA CHEMICAL INDUSTRIES LTD

OS Mus sp. (mouse)

PN JP 2001069994-A/22

PD 21-MAR-2001

PF 29-JUN-2000 JP 2000195911

PR
PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI

SHINICHI MOGI.

PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA

PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC

A61P19/08,

PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC

G01N33/53//

PC C12P21/08, C12N15/00, A61K37/02, C12N5/00

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Query Match 100.0%; Score 330; DB 6; Length 947;

Best Local Similarity 100.0%; Pred. No. 2.9e-90;

Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATGTGTATTTATGATATAAATTCTTCTTAAGAAGTTGTCGGATGAGAGTGTGTC 60
Db 65 CATGTGTATTTATGATATAAATTCTTCTTAAGAAGTTGTCGGATGAGAGTGTGTC 124
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QY 241 TATTTCCCAAGCACTTGTGAAGAGCAGCGTGTATACAGAGAGCCCAAGAGAGATC 300
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QY 301 CCAACCAAGGATATTGACTTCTTCTGTGAA 330
Db 365 CCAACCAAGGATATTGACTTCTTCTGTGAA 394

RESULT 7
BD093122 947 bp DNA linear PAT 27-AUG-2002

LOCUS BD093122
DEFINITION Novel polypeptide and its DNA.

ACCESSION BD093122.1 GI:22638710

VERSION WO 0102564-A/22.

KEYWORDS

SOURCE

ORGANISM

Mus sp.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

Yoshimura, K. and Tanaka, H.

Novel polypeptide and its DNA

Patent: WO 0102564-A 22 11-JAN-2001;

TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO

OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,

HIDEYUKI TANAKA

OS Mus sp. (mouse)

PN WO 0102564-A/22

PD 11-JAN-2001

PF 29-JUN-2000 WO 2000JP004278

PR 30-JUN-1999 JP 99P 186718
 PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI
 MOGI,
 PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
 PC C12N15/12, C12N15/10, C12P21/02, C07K14/47, C07K16/18, A61K45/00, PC
 A61K38/17
 PC A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/7088// (C12P21/
 CC 02, C12R1:19)
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 Query Match 100.0%; Score 330; DB 6; Length 947;
 Best Local Similarity 100.0%; Pred. No. 2.9e-90;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CATGGTCTATTATGATTAACCTTCTTCTAAGAGTTGTGTGGATGAGAGTGTGTC 60
 DB 65 CATGGTCTATTATGATTAACCTTCTTCTAAGAGTTGTGTGGATGAGAGTGTGTC 124
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 DB 305 TATTTCCCGAGCACTGTGTGAAGAGCAGCTGTATACCAAGAGCCACCAAGAGATC 364
 QY 301 CCAACCAAGATATGACTTCTTCTGTGAA 330
 DB 365 CCAACCAAGATATGACTTCTTCTGTGAA 394
 RESULT 8
 MMU243939 958 bp mRNA linear ROD 29-JAN-2001
 LOCUS Mus musculus mRNA for melanoma inhibitory activity-like protein
 DEFINITION (Mial gene).
 ACCESSION AJ243939
 VERSION AJ243939.1 GI:12619174
 KEYWORDS melanoma inhibitory activity-like protein; Mial gene.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Buzaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1
 Rendtorff, N.D., Frodin, M., Attie-Bitach, T., Vekemans, M. and
 Tommerup, N.
 Identification and characterization of an inner ear-expressed human
 melanoma inhibitory activity (MIA)-like gene (MIAL) with a frequent
 polymorphism that abolishes translation
 Genomics 71 (1), 40-52 (2001)
 JOURNAL MEDLINE 21100875
 PUBMED 1161796
 REFERENCE 2 (bases 1 to 958)
 AUTHORS Rendtorff, N.D.
 TITLE Direct Submission
 JOURNAL Submitted (20-JUL-1999) Rendtorff N.D., Department of Medical

Genetics, Institute of Medical Biochemistry and Genetics,
 Blegdamsvej 3, 2200 Copenhagen N, DENMARK
 COMMENT Related sequence: AJ243552.
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 LOCUS Mus musculus otocypilin mRNA, complete cds.
 DEFINITION AF233333
 ACCESSION AF233333
 VERSION AF233333.1 GI:8927429
 KEYWORDS
 SOURCE Mus musculus (house mouse)
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 Buzaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 1
 Rendtorff, N.D., Frodin, M., Attie-Bitach, T., Vekemans, M. and
 Tommerup, N.
 Identification and characterization of an inner ear-expressed human
 melanoma inhibitory activity (MIA)-like gene (MIAL) with a frequent
 polymorphism that abolishes translation
 Genomics 71 (1), 40-52 (2001)
 JOURNAL MEDLINE 21100875
 PUBMED 1161796
 REFERENCE 2 (bases 1 to 1054)
 AUTHORS Rendtorff, N.D.
 TITLE Direct Submission
 JOURNAL Submitted (20-JUL-1999) Rendtorff N.D., Department of Medical

AUTHORS Robertson, N.G., Heller, S., Lin, J.S., Resendes, B.L., Meremowicz, S., Denis, C.S., Bell, A.M., Hudspeth, A.J., and Morton, C.C.
TITLE A novel conserved cochlear gene, OTOR: identification, expression analysis, and chromosomal mapping
JOURNAL Genomics 66 (3), 242-248 (2000)
GENOMICS 66 (3), 242-248 (2000)
REFERENCE 10873378
AUTHORS 2 (bases 1 to 1054)
TITLE Robertson, N.G., Heller, S., Lin, J.S., Resendes, B.L., Meremowicz, S., Denis, C.S., Bell, A.M., Hudspeth, A.J., and Morton, C.C.
JOURNAL Direct Submission
FEATURES Submitted (10-FEB-2000) Pathology, Brigham and Women's Hospital, 75 Francis Street, Boston, MA 02115, USA
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RESULT 10
LOCUS BD010836 330 bp DNA linear PAT 31-JAN-2002
DEFINITION Novel polypeptide and DNA thereof.
ACCESSION BD010836
VERSION BD010836.1 GI:18639209
KEYWORDS JP 2001069994-A/37.
SOURCE Rattus sp.
ORGANISM Rattus sp.
REFERENCE 1 (bases 1 to 330)
AUTHORS Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,

TITLE Yoshimura, K. and Tanaka, H.
JOURNAL Novel polypeptide and DNA thereof
COMMENT Patent: JP 2001069994-A 37 21-MAR-2001;
 TAKEDA CHEMICAL INDUSTRIES LTD
 OS Rattus sp. (rat)
 PN JP 2001069994-A/37
 PD 21-MAR-2001
 PE 29-JUN-2000 JP 2000195911
 PR
 PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI
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 PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
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RESULT 11
LOCUS BD093137 330 bp DNA linear PAT 27-AUG-2002
DEFINITION Novel polypeptide and its DNA.
ACCESSION BD093137
VERSION BD093137.1 GI:22638725
KEYWORDS WO 0102564-A/37.
SOURCE Rattus sp.
ORGANISM Rattus sp.
REFERENCE 1 (bases 1 to 330)
AUTHORS Yoshimura, K. and Tanaka, H.,

TITLE Novel polypeptide and its DNA
JOURNAL Patent: WO 0102564-A 37 11-JAN-2001;
TAKEDA CHEMICAL INDUSTRIES LTD, YASUOKI ITO, KAZUNORI NISHI, KAZUHIRO
OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,
HIDEYUKI TANAKA
COMMENT OS Rattus sp. (rat)
PN WO 0102564-A/37
PD 11-JAN-2001
PF 29-JUN-2000 WO 2000JP004278
PR 30-JUN-1999 JP 99P 186718
PI YASUOKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI
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YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/12, C12N5/10, C12P21/02, C07K14/47, C07K16/18, A61K45/00, PC
A61K38/17,
PC A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/7088// (C12P21/
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Best Local Similarity 93.3%; Pred. No. 1.8e-79;
Matches 308; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 1 CATGTGATTTATGATTAACCTTTCTTCTAAGAGTTGTGCGGATGAGAGTGTGC 60
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DEFINITION Novel polypeptide and DNA thereof.
ACCESSION BD010835
VERSION BD010835.1 GI:18639208
KEYWORDS JP 2001069994-A/36.
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 384)
AUTHORS Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
Yoshimura, K. and Tanaka, H.
TITLE Novel polypeptide and DNA thereof

JOURNAL Patent: JP 2001069994-A 36 21-MAR-2001;
TAKEDA CHEMICAL INDUSTRIES LTD
COMMENT OS Rattus sp. (rat)
PN JP 2001069994-A/36
PD 21-MAR-2001
PF 29-JUN-2000 JP 2000195911
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PI YASUOKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI
SHINICHI MOGI,
YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P19/00, A61P19/02, PC
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BD093136 384 bp DNA linear PAT 27-AUG-2002
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ACCESSION BD093136
VERSION BD093136.1 GI:22638724
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ORGANISM Rattus sp.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 384)
AUTHORS Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
Yoshimura, K. and Tanaka, H.
TITLE Novel polypeptide and its DNA
JOURNAL Patent: WO 0102564-A 36 11-JAN-2001;

COMMENT
TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHII, KAZUHIRO
OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,
HIDEYUKI TANAKA
OS Rattus sp. (rac)
PN WO 0102564-A/36
PD 11-JAN-2001
PF 29-JUN-2000 WO 2000JP004278
PR 30-JUN-1999 JP 99P 186718
PI YASUAKI ITO, KAZUNORI NISHII, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI
MOGI,
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
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A61K38/17,
PC A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/7088//C12P21/
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Best Local Similarity 93.3%; Pred. No. 1.8e-79;
Matches 308; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
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LOCUS
DEFINITION Novel polypeptide and DNA thereof.
ACCESSION BD010830
VERSION BD010830.1 GI:18639203
KEYWORDS JP 2001069994-A/31.
SOURCE
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Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 307)
Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
Yoshimura, K. and Tanaka, H.
Novel polypeptide and DNA thereof
Patent: JP 2001069994-A 31 21-MAR-2001;
TAKEDA CHEMICAL INDUSTRIES LTD

COMMENT
OS Rattus sp. (rac)
PN JP 2001069994-A/31
PD 21-MAR-2001
PF 29-JUN-2000 JP 2000195911
PR
PI YASUAKI ITO, KAZUNORI NISHII, KAZUHIRO OGI, SHOICHI OKUBO, PI
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PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
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A61P19/08,
PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC
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RESULT 15
BD093131 307 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION Novel polypeptide and its DNA.
ACCESSION BD093131
VERSION BD093131.1 GI:22638719
KEYWORDS WO 0102564-A/31.
SOURCE
Rattus sp.
Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 307)
Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
Yoshimura, K. and Tanaka, H.
Novel polypeptide and its DNA
Patent: WO 0102564-A 31 11-JAN-2001;
TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHII, KAZUHIRO
OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,

COMMENT

HIDEYUKI TANAKA
 OS Rattus sp. (rat)
 PN WO 0102564-A/31
 PD 11-JAN-2001
 PF 29-JUN-2000 WO 2000JP004278
 PR 30-JUN-1999 JP 99P 186718
 PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI

PI MOGI,
 PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
 PC C12N15/12, C12N5/10, C12P21/02, C07K14/47, C07K16/18, A61K45/00, PC
 A61K38/17,
 PC A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/7088// (C12P21/
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Query Match 79.3%; Score 261.8; DB 6; Length 307;
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 Matches 283; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

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GenCore version 5.1.6
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Title: US-10-019-455a-25

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16: em_estom.*
17: em_gss_hum.*
18: em_gss_inv.*
19: em_gss_pln.*
20: em_gss_vrt.*
21: em_gss_fun.*
22: em_gss_mam.*
23: em_gss_mus.*
24: em_gss_pro.*
25: em_gss_rtd.*
26: em_gss_phg.*
27: em_gss_vrt.*
28: gb_gss1.*
29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match Length | DB ID | Description |
|------------|-------|--------------|--------|---------------------|
| 1 | 330 | 100.0 | 398 13 | BQ570035 g1143b10. |
| 2 | 330 | 100.0 | 488 13 | BQ564607 BQ564607.Y |
| 3 | 330 | 100.0 | 514 13 | BQ568498 BQ568498.Y |
| 4 | 330 | 100.0 | 534 13 | BQ564134 BQ564134.Y |

| | | | | |
|----|-------|-------|---------|---------------------|
| 5 | 330 | 100.0 | 560 13 | BQ569741 BQ569741.Y |
| 6 | 330 | 100.0 | 608 13 | BQ564944 BQ564944.Y |
| 7 | 330 | 100.0 | 630 13 | BQ564871 BQ564871.Y |
| 8 | 330 | 100.0 | 684 13 | BQ563768 BQ563768.Y |
| 9 | 330 | 100.0 | 696 10 | BB611549 BB611549.Y |
| 10 | 328.4 | 99.5 | 474 13 | BQ565637 BQ565637.Y |
| 11 | 313.8 | 95.1 | 409 13 | BQ566932 BQ566932.Y |
| 12 | 307.6 | 93.2 | 604 13 | BQ565411 BQ565411.Y |
| 13 | 300 | 90.9 | 490 13 | BQ567343 BQ567343.Y |
| 14 | 286.4 | 86.8 | 365 13 | B1232622 B1232622.Y |
| 15 | 244 | 73.9 | 485 13 | BQ565179 BQ565179.Y |
| 16 | 206 | 62.4 | 280 13 | BQ568785 BQ568785.Y |
| 17 | 204 | 61.8 | 588 13 | BQ566776 BQ566776.Y |
| 18 | 196 | 59.4 | 795 13 | B0748241 B0748241.Y |
| 19 | 157.4 | 47.7 | 527 10 | BE236443 BE236443.Y |
| 20 | 142.4 | 43.2 | 677 13 | BQ563227 BQ563227.Y |
| 21 | 142.4 | 43.2 | 3240 11 | AK047965 AK047965.Y |
| 22 | 137.6 | 41.7 | 678 10 | BB647928 BB647928.Y |
| 23 | 137 | 41.5 | 492 9 | AA222797 AA222797.Y |
| 24 | 124.6 | 37.8 | 349 9 | AM023324 AM023324.Y |
| 25 | 122.8 | 37.2 | 533 9 | AL925854 AL925854.Y |
| 26 | 107 | 32.4 | 646 13 | BQ563767 BQ563767.Y |
| 27 | 102.4 | 31.0 | 170 13 | BQ569268 BQ569268.Y |
| 28 | 102 | 30.9 | 186 13 | BQ564457 BQ564457.Y |
| 29 | 101.8 | 30.8 | 338 9 | AM021345 AM021345.Y |
| 30 | 99.2 | 30.1 | 1201 13 | BX418941 BX418941.Y |
| 31 | 98.8 | 29.9 | 978 13 | BX444840 BX444840.Y |
| 32 | 91.8 | 27.8 | 633 14 | CD360404 CD360404.Y |
| 33 | 89.8 | 27.2 | 178 13 | BQ567219 BQ567219.Y |
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| 35 | 81.8 | 24.8 | 615 9 | AL717905 AL717905.Y |
| 36 | 74 | 22.4 | 675 14 | CA370333 CA370333.Y |
| 37 | 68 | 20.6 | 589 9 | AV169321 AV169321.Y |
| 38 | 67.4 | 20.4 | 544 13 | BO208982 BO208982.Y |
| 39 | 67.4 | 20.4 | 594 14 | CA509768 CA509768.Y |
| 40 | 64.4 | 19.5 | 424 14 | CB726570 CB726570.Y |
| 41 | 63.4 | 19.2 | 404 13 | BQ567257 BQ567257.Y |
| 42 | 63.4 | 19.2 | 440 10 | BB749350 BB749350.Y |
| 43 | 63.4 | 19.2 | 449 13 | BQ569338 BQ569338.Y |
| 44 | 63.4 | 19.2 | 464 9 | AI323423 AI323423.Y |
| 45 | 63.4 | 19.2 | 465 9 | AA003262 AA003262.Y |

ALIGNMENTS

RESULT 1
BQ570035
LOCUS
DEFINITION
g1143b10.Y1 Mouse Organ of Corti cDNA plusvescript Mus musculus cDNA
clone g1143b10 5', mRNA sequence.
BQ570035
ACCESSION
BQ570035
VERSION
BQ570035.1 GI:21473352
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 398)

REFERENCE
Kachar, B.
EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
Unpublished
JOURNAL
COMMENT
Contact: Kachar, B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: kachar@nidcd.nih.gov
Place: 143 row: b column: 10
Seq primer: M3RPI reverse primer (ABI).
Location/Qualifiers

FEATURES

source

1. .398
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="BALB/c"
 /db_xref="taxon:10090"
 /clone="g113b10"
 /sex="male and female"
 /dev_stage="Post natal day 5 to 13"
 /clone_lib="Mouse Organ of Corti cDNA pluescript"
 /note="Organ: Organ of Corti; Vector: pluescript. The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR GigaPack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly, 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMuV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pvu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been pre-digested with EcoR I and Xho I. The phagemid was packaged with GigaPack III Gold and, upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's EXSist Intereference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CACGAAACGCTATGAC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in Genbank and have known function; 23% have hits in Genbank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT
 ORIGIN

105 a 69 c 116 g 108 t

Query Match 100.0%; Score 330; DB 13; Length 398;
 Best Local Similarity 100.0%; Pred. No. 3.1e-92;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CATGGTATATTGATATAACTTCTCTTAAGAACTTGTGGATAGAGAGTGTGC 60

Db 67 CATGGTATATTGATATAACTTCTCTTAAGAACTTGTGGATAGAGAGTGTGC 126
 QY 61 TATATATTTCTCTGGCAAGACAGCAAGATTACATATGCCAGACTGTAGTTGATC 120
 Db 127 TATATATTTCTCTGGCAAGACAGCAAGATTACATATGCCAGACTGTAGTTGATC 186
 QY 121 GATGTCAAGAAAGGAGAGATCTATGTTTCTCCAGCTGTATACAGAAAGGAGCT 180
 Db 187 GATGTCAAGAAAGGAGAGATCTATGTTTCTCCAGCTGTATACAGAAAGGAGCT 246
 QY 181 GAGAGCTTTGGCTGGCTGAGTGTATGTTATGTTGACCAAGATGAGATTTGAGGT 240
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 QY 241 TATTTCCAGCACTTGTGAGAGAGCAGCTGTATACAGAGAGCCCAAGAGAGATC 300
 Db 307 TATTTCCAGCACTTGTGAGAGAGCAGCTGTATACAGAGAGCCCAAGAGAGATC 366
 QY 301 CCACACCGCATATTGACTTCTTCTGTGA 330
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RESULT 2

LOCUS

B0564607 488 bp mRNA linear EST 19-JUN-2002
 g119h02.y1 Mouse Organ of Corti cDNA pluescript Mus musculus cDNA
 clone g119h02 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished
 Contact: Kachar, B.
 Structural Cell Biology
 National Institute of Deafness and other Communication Disorders
 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
 Tel: 301-402-1599
 Fax: 301-402-1765
 Email: kacharb@nidcd.nih.gov
 Plate: 19 row: h column: 02
 Seq primer: M13R1 reverse primer (ABI).

FEATURES

source

1. 488

/organism="Mus musculus"

/mol_type="mRNA"

/strain="BALB/c"

/db_xref="taxon:10090"

/clone="g119h02"

/sex="male and female"

/dev_stage="Post natal day 5 to 13"

/clone_lib="Mouse Organ of Corti cDNA pluescript"

/note="Organ: Organ of Corti; Vector: pluescript. The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and

library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of 1 ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XL1 Blue MRF⁺ cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's EXASist interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in Genbank and have known function; 23% have hits in Genbank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified.

BASE COUNT ORIGIN

Query Match 100.0%; Score 330; DB 13; Length 488;
Best Local Similarity 100.0%; Pred. No. 3.5e-92;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1  CATGGTATTTATGATTAACCTTTCTTAAGAGTTGTGGGATGAGAGTGTGTC 60
Db  CATGGTATTTATGATTAACCTTTCTTAAGAGTTGTGGGATGAGAGTGTGTC 60
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Qy  TATACTATTTCTGGCAGAGCAGAGAGATTAACATGCCAGACTGAGGTTATC 120
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121  GATGTCAGAAAGGCGAGAGATCTATGTTTACTCCAACTGCTTAACAGAAACGAGCT 180
Qy  GATGTCAGAAAGGCGAGAGATCTATGTTTACTCCAACTGCTTAACAGAAACGAGCT 180
Db  GATGTCAGAAAGGCGAGAGATCTATGTTTACTCCAACTGCTTAACAGAAACGAGCT 240
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Qy  GGAAGTTTTGGGTGGAGTGTATATGTTACACCAAGATGAGATGGAAATTGATG 240
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Db  TATTTCCCAAGCACTGGTGAAGAGAGGTATATACAGAGAGGCCACCAAGAGATC 300
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Qy  CCAACCAAGGATATGACTTTCTTGTGAA 330
Db  CCAACCAAGGATATGACTTTCTTGTGAA 390

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RESULT 3
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DEFINITION
B0568498
ACCESSION
B0568498
VERSION
B0568498.1
KEYWORDS
EST.
SOURCE
MUS MUSCULUS (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 514)
REFERENCE
Kachar, B.
EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
Unpublished
JOURNAL
COMMENT
Contact: Kachar, B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: kachar@nidcd.nih.gov
Plate: 109 row: c column: 02
Seq primer: M13RPI reverse primer (ABI).
Location/Qualifiers
1..514
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/mol_type="mRNA"
/strain="BALB/c"
/db_xref="taxon:10090"
/clone="g109c02"
/sex="male and female"
/dev_stage="Post natal day 5 to 13"
/clone_lib="Mouse Organ of Corti cDNA Pbluescript"
/note="Organ: Organ of Corti; Vector: Pbluescript; The organ of Corti (OC) was fine dissected from a total of 36 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was clipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA). according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of 1 ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XL1 Blue MRF⁺ cells, the yield of the phage library was estimated to be 11,100,000

recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 µl of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAAACAGCTATGACC) and 25× strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 147 a 85 c 143 g 139 t
ORIGIN:

Query Match 100.0%; Score 330; DB 13; Length 514;
Best Local Similarity 100.0%; Pred. No. 3.7e-92;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATGCTGATTTATGATTAACCTTCTTCTTAAGAGTTGTGCGGATGAGAGTGTGTC 60
DB 59 CATGCTGATTTATGATTAACCTTCTTCTTAAGAGTTGTGCGGATGAGAGTGTGTC 118
QY 61 TATCTCTTTCTCGGAAGACACAGAGATTAACATCCCGACAGCTAGAGTTCATC 120
DB 119 TATACATTTCTCGGAAGACACAGAGATTAACATCCCGACAGCTAGAGTTCATC 178
QY 121 GATGTCAGAAAGGCGACAGATCTATGTTACTCCAGCTGGTAAACAGAAACGGAGCT 180
DB 179 GATGTCAGAAAGGCGACAGATCTATGTTACTCCAGCTGGTAAACAGAAACGGAGCT 238
QY 181 GGAGAGTTTGGGCTGGCACTGTTATGATGACACACAGAGATGAGATTTAGAGT 240
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QY 241 TATTTCCCGCAACTTGTGGAAGAGACCGTGTATACAGAGCCCAAGAGAGATC 300
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QY 301 CCAACACGAGATATTGACTTCTCTGTGAA 330
DB 359 CCAACACGAGATATTGACTTCTCTGTGAA 388

RESULT 4
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DEFINITION clone g111d01 5', mRNA sequence.
ACCESSION B0564134
VERSION B0564134.1 GI:21467451
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 534)
AUTHORS Kachar, B.
TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
JOURNAL Unpublished
COMMENT Contact: Kachar, B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders

FEATURES

50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: kachar@nidcd.nih.gov
Plate: 11 row: d column: 01
Seq primer: MJ3R1 reverse primer (ABI).
Location/Qualifiers
1..534
/organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
/db_xref="taxon:10090"
/clone="g111d01"
/sex="male and female"
/dev_stage="post natal day 5 to 13"
/clone_lib="Mouse Organ of Corti cDNA pBluescript"
/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR GigaPack III Gold Cloning Kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 µg mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase. ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The plasmid was packaged with GigaPack III Gold and, upon titration on XLI Blue MRP cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 µl of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAAACAGCTATGACC) and 25× strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT

155 a 87 c 148 g 144 t

ORIGIN

Query Match 100.0%; Score 330; DB 13; Length 534;
 Best Local Similarity 100.0%; Pred. No. 3.7e-92;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CATGGGTATTTATGATTAACCTTTCTTAAAGATTGTGGCGATGAGAGTGTGTC 60
 57 CATGGGTATTTATGATTAACCTTTCTTAAAGATTGTGGCGATGAGAGTGTGTC 116
 61 TATACATTTCTCTGCGAAGACACAGAAAGATTCAATGCCCGAGCTTTAGTTTATC 120
 117 TATACATTTCTCTGCGAAGACACAGAAAGATTCAATGCCCGAGCTTTAGTTTATC 176
 121 GATGTCAAGAAAGGCGAGACATCTATGTTTACTCCAGCTGGTAAACAGAAACGAGACT 180
 177 GATGTCAAGAAAGGCGAGACATCTATGTTTACTCCAGCTGGTAAACAGAAACGAGACT 236
 181 GGAGAGTTTGGGCTGGCAGTGTATGTTACCCACGAGATGAGATGGAAATTGTAGGT 240
 237 GGAGAGTTTGGGCTGGCAGTGTATGTTACCCACGAGATGAGATGGAAATTGTAGGT 296
 241 TATTTCCCGACGACCTGTGTGAAGAGAGAGGTGTATCCAGAGGCGACCAAGAGATC 300
 297 TATTTCCCGACGACCTGTGTGAAGAGAGAGGTGTATCCAGAGGCGACCAAGAGATC 356
 301 CCACACGAGATTTGACTTCTTCTGTGAA 330
 357 CCACACGAGATTTGACTTCTTCTGTGAA 386

RESULT 5
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 LOCUS g135f01.y1 Mouse Organ of Corti cDNA Bluescript Mus musculus cDNA
 DEFINITION clone g135f01 5', mRNA sequence.
 ACCESSION BQ569741
 VERSION BQ569741.1 GI:21473058
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 560)
 AUTHORS Kachar, B.
 TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing

JOURNAL Unpublished
 COMMENT Contact: Kachar, B.
 Structural Cell Biology
 National Institute of Deafness and other Communication Disorders
 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
 Tel: 301-402-1599
 Fax: 301-402-1765
 Email: KacharB@nidcd.nih.gov
 Plate: 135 row: f column: 01
 Seg primer: M13RP1 reverse primer (ABT).
 Location/Qualifiers

FEATURES

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 /sex="male and female"
 /dev_stage="Post natal day 5 to 13"
 /clone_11b="Mouse Organ of Corti cDNA Bluescript"
 /note="Organ: Organ of Corti; Vector: pbluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla

was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR GigaPack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly, 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with GigaPack III Gold and, upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExaStar Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert6 (TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CACGAAACAGCTATACC) and 25x strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on 96 titered thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified.

BASE COUNT 160 a 92 c 154 g 153 t 1 others

Query Match 100.0%; Score 330; DB 13; Length 560;
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 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 180 GATGTCAAGAAAGGCGAGACATCTATGTTTACTCCAGCTGGTAAACAGAAACGAGACT 239
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 240 GGAGAGTTTGGGCTGGCAGTGTATGTTACCCACGAGATGAGATGGAAATTGTAGGT 299

QY 241 TATTTCCCGACGACCTGTGTGAAGAGCAGCGTGTATACCGAGGCCACCAAGAGATC 300
 DB 300 TATTTCCCGACGACCTGTGTGAAGAGCAGCGTGTATACCGAGGCCACCAAGAGATC 359
 QY 301 CCACACGAGATTTGACTTCTTCTGTGAA 330
 DB 360 CCACACGAGATTTGACTTCTTCTGTGAA 389

RESULT 6
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 LOCUS g127909.y1 Mouse Organ of Corti cDNA pluescript Mus musculus cDNA
 DEFINITION
 B0564944
 B0564944
 B0564944.1 GI:21468261
 EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 608)
 Kachar.B.
 EST analysis of gene expression in the mouse Organ of Corti at the
 onset of hearing
 Unpublished
 Contact: Kachar.B.
 Structural Cell Biology
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 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
 Tel: 301-402-1599
 Fax: 301-402-1765
 Email: kachar@nidcd.nih.gov
 Plate: 27 row: 9 column: 09
 Seq primer: M13RPI reverse primer (ABI).
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 /mol_type="mRNA"
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 /sex="male and female"
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 /note="Organ: Organ of Corti; Vector: pluescript; The
 organ of Corti (OC) was fine dissected from a total of 386
 OC as follows: 102 samples from post-natal (P) day 5; 72
 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
 14 from P12 and 24 from P13. After killing animals by
 cervical dislocation followed by decapitation, the bulla
 was removed and opened in Leibowitz medium. The bony
 capsule of the cochlea was chipped away, stria vascularis
 and spiral ligament were removed and the sensory
 epithelium was carefully dissected out of the modiolus.
 Total RNA was extracted using the micro Fasttrack kit
 (catalog # K1593-02; Invitrogen, Carlsbad, CA), according
 to manufacturer's instructions. Reverse transcription and
 library construction were carried out with the Uni-Zap XR
 vector kit (catalog # 237211, Stratagene) and Uni-Zap XR
 GigaPack III Gold Cloning kit (catalog # 237612), both
 from Stratagene (La Jolla, CA, USA), according to
 manufacturer's instructions. Briefly, 1.5 ug mRNA was
 reverse transcribed using a hybrid oligo(dT) linker-primer
 that contains an Xho I site. First strand synthesis was
 primed with the linker-primer and transcribed using
 Moloney murine leukemia virus reverse transcriptase
 (MMuV-RT) and 5-methyl dCTP. The second strand was
 synthesized with DNA polymerase and RNase H. Complementary
 DNA was blunt ended with Pfu DNA polymerase, ligated with
 EcoR I adapters in the presence of ligase and digested
 over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden)

and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA)
 columns to enrich for cDNAs greater than 400bp and 1000 bp
 , respectively. The cDNA was then directionally ligated to
 the Uni-ZAP XR vector, which had been predigested with
 EcoR I and Xho I. The phagemid was packaged with GigaPack
 III Gold and, upon titration on XLI Blue MRF⁺ cells, the
 yield of the phage library was estimated to be 11,100,000
 recombinants. Stratagene's ExBassist Interference
 resistance helper phage (catalogue # 211203) was adopted
 to rescue plasmid DNA from the phages. Upon plating of the
 rescued library, individual cDNA clones were selected and
 grown in 96-well, 2 ml growth plate. Plasmid DNA was
 purified from 200 ul of saturated culture with the
 Concert96(TM) plasmid purification kit (Invitrogen,
 Carlsbad, CA) as instructed by the manufacturer. ESTs from
 the 5' end of the cDNA clones were generated with the
 universal M13 reverse primer (CAGGAACAGCTTATGACC) and 25x
 strength BigDye terminator sequencing chemistry (Applied
 Biosystems, Foster City, CA). Sequencing reactions were
 performed on MJ Tetrad thermal cyclers (MJ Research,
 Waltham, MA), and analyzed on 3700 automated capillary
 sequencers using POP5 polymer (Applied Biosystems, Foster
 City, CA). The frequency distribution of the library is
 as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10;
 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of
 genes are present in GenBank and have known function; 23%
 have hits in GenBank, but do not have assigned function;
 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 169 a 107 c 166 g 166 t
 ORIGIN
 Query Match 100.0%; Score 330; DB 13; Length 608;
 Best Local Similarity 100.0%; Pred. No. 4e-92; Indels 0; Gaps 0;
 Matches 330; Conservative 0; Mismatches 0;

QY 1 CATGTGTATTATGATATAAAGCTTTCTTACAGAGTTGTGCGGATGAGAGTGTGC 60
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 DB 127 TATACATTTTCTTGCCAGACGACGAGAAATTACAAATGCCAGACTGTAGTTTATC 186
 QY 121 GATGTCAAGAAAGGAGGACGATCTATGTTTCTCCAGCTGTATACAGAAACGAGCT 180
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 QY 181 GGAGAGTTTGGGCTGCGAGTGTATATGTTGACCAACGAGATGAGTGGAAATTGAGGT 240
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 DB 307 TATTTCCCGACGACCTGTGTGAAGAGCAGCGTGTATACCGAGGCCACCAAGAGATC 366
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 DB 367 CCACACGAGATTTGACTTCTTCTGTGAA 396

RESULT 7
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 LOCUS g1108904.y1 Mouse Organ of Corti cDNA pluescript Mus musculus cDNA
 DEFINITION
 B0568471
 B0568471
 B0568471.1 GI:21471788
 EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 630)

AUTHORS TITLE JOURNAL COMMENT

Kachar, B.
EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
Unpublished
Contact: Kachar, B.
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50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: kachar@nidcd.nih.gov
Plate: 108 row: 9 column: 04
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers

FEATURES source

1. 630
/organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
/db_xref="taxon:10090"
/sex="male and female"
/dev_stage="Post natal day 5 to 13"
/clone_lib="Mouse Organ of Corti cDNA plibscript"
/note="Organ: Organ of Corti; Vector: pBluescript; The Organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with GigaPack III Gold and, upon titration on XL1 Blue XRF cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's Exassist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAAACGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster

City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in Genbank and have known function; 23% have hits in Genbank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified.

Query Match 100.0%; Score 330; DB 13; Length 630;
Best Local Similarity 100.0%; Prid. No. 4.1e-92;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN
BASE COUNT
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1 CATGCTATTATGATTAACCTTCTCTTACAGAGTTGTGTGGATGAGAGTGTGTC 60
67 CATGCTATTATGATTAACCTTCTCTTACAGAGTTGTGTGGATGAGAGTGTGTC 126
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127 TATACATTTCTCTGCGAAGAGCAGAGAAATTACATGCCAGCTGTAGCTTATC 186
121 GATGTCAAGAAAGGCGAGATCTATGTTTACTCCAGCTGTACAGAAACGAGCT 180
187 GATGTCAAGAAAGGCGAGATCTATGTTTACTCCAGCTGTACAGAAACGAGCT 246
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247 GGAGAGTTTGGGCTGGCACTGTTTATGTGACCCAGGAGTGGGATTTAGGT 306
241 TATTTCCCGCAACTGTGAGAGAGCGCTGTATACAGAGGCCACCAAGAGATC 300
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301 CCACCAAGGATATGACTTCTCTGTGA 330
367 CCACCAAGGATATGACTTCTCTGTGA 396

RESULT 8
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DEFINITION g106c09.y1 Mouse Organ of Corti cDNA plibscript Mus musculus cDNA
B0563768
B0563768.1 GI:21466749
VERSION
KEYWORDS
SOURCE
ORGANISM
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 684)
Kachar, B.
EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
Unpublished

JOURNAL
COMMENT
Unpublished
Contact: Kachar, B.
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Tel: 301-402-1599
Fax: 301-402-1765
Email: kachar@nidcd.nih.gov
Plate: 06 row: c column: 09
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers

FEATURES source

1. 684
/organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
/db_xref="taxon:10090"
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/sex="male and female"
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/clone.lib="Mouse Organ of Corti cDNA Bluescript"
 /note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5, 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR GigaPack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with GigaPack III Gold and, upon titration on XL1 Blue MRF⁺ cells, the yield of the phage library was estimated to be 1.1e10/100 recombinants. Stratagene's ExSist Interference resistance helper phage (catalogue # 211203) was used to rescue plasmid DNA from the phages. Upon plating of the grown in 96-well, 2 ml growth plate, plasmid DNA was purified from 200 ul of saturated culture with the Concert96 (TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACGCTATACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Watham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 46% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 13% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT
 ORIGIN

Query Match 100.0%; Score 330; DB 13; Length 684;
 Best Local Similarity 100.0%; Pred. No. 4.4e-92;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 67 CATGGTATATTAAGATTAACCTTCTCTAAGAGTTGTGCGATGAGAGGTCTC 126
 61 TATATCTATTTCTCTGCAAGACAGAGATTTCAATGCCAGCTGTAGCTTATC 120
 127 TATATCTATTTCTCTGCAAGACAGAGATTTCAATGCCAGCTGTAGCTTATC 186
 121 GATGTCAGAAAGGCGACAGATCTATGTCTCAAGCGCTGTACAGAAAGCGAGCT 180

Db
 187 GATGTCAGAAAGGCGACAGATCTATGTCTCAAGCGCTGTACAGAAAGCGAGCT 246
 181 GGAGAGTTTGGGCTGGCGAGTCTTTATGTTGACACCGAGATGAGATGGATTTAGCT 240
 247 GGAGAGTTTGGGCTGGCGAGTCTTTATGTTGACACCGAGATGAGATGGATTTAGCT 306
 241 TATTTTCCCGAGACTTGTGTGAAGAGCAGAGTGTATCCAGAGAGCCACCAAGAGATC 300
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 301 CCACCGAGATATGACTTCTTCTGTGA 330
 367 CCACCGAGATATGACTTCTTCTGTGA 396

RESULT 9
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 BB611549 RIKEN full-length enriched, 13 days embryo head Mus
 musculus cDNA clone 3110083012 5', mRNA sequence.
 BB611549
 VERSION
 KEYWORDS
 EST.
 SOURCE
 ORGANISM
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 696)

REFERENCE

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Horii, F., Ishii, Y., Ito, M., Kawai, D., Konno, H., Kouda, M., Koyama, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
 RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
 Unpublished

TITLE

Journal
 Contact: Yoshinobu Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-resgsc.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 Waga, K., Fujisake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
 Watanuki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, D., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
 Hayashizaki, Y.
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Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y., and Hayashizaki, Y.
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Yamakawa, I., Kiyosawa, H., Kondo, S., Saito, T., Shinagawa, A., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, D., Shibata, K., Arakawa, T.,
 Ishii, Y. and Hayashizaki, Y.
 Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.
 Func. Genomics 2 pre, 172-186 (2001).
 Please visit our web site (http://genome.gsc.riken.go.jp) for
 further details.
 e mouse tissues.
 Location/Qualifiers

FEATURES

genes are present in GenBank and have known function; 234
have hits in GenBank, but do not have assigned function;
128 are uncharacterized ESTs and 208 are unidentified."

BASE COUNT
ORIGIN

145 a 78 c 131 g 120 t

Query Match 99.5%; Score 328.4; DB 13; Length 474;
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Matches 326; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CATGTGATTTATGATTAACCTTCTTCTAGAGAGTGTGCGATGAGAGAGTGTGTC 60
DB 68 CATGTGATTTATGATTAACCTTCTTCTAGAGAGTGTGCGATGAGAGAGTGTGTC 127
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DB 128 TATACATTTCTCTGGCAAGACACAGAGATTAACATGCCCCAAGCTGTAGTTCATC 187
QY 121 GATGTCAAGAAAGGCGACAGATCTATGTTTACTCCAGGTGTACAGAAACGAGCT 180
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QY 241 TATTTCCCGCAGCACTGTGTGAAGAGCAGCGCTGTATCCAGAGGCCCAAGAGATC 300
DB 308 TATTTCCCGCAGCACTGTGTGAAGAGCAGCGCTGTATCCAGAGGCCCAAGAGATC 367
QY 301 CCAACCAAGGATTTGACTCTCTCTGTGA 330
DB 368 CCAACCAAGGATTTGACTCTCTCTGTGA 397

RESULT 11
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DEFINITION g173909.y1 Mouse Organ of Corti cDNA pbluescript Mus musculus cDNA
ACCESSION B0566932
VERSION B0566932.1 GI:21470249
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 409)
AUTHORS Kachar, B.
TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
JOURNAL Unpublished
COMMENT Contact: Kachar, B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: kachar@nidcd.nih.gov
Plate: 73 row: 9 column: 09
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/note="Organ: Organ of Corti; Vector: pbluescript. The organ of Corti (OC) was fine dissected from a total of 386

OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR GigaPack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly, 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-100 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with GigaPack III Gold and, upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's Exsist1 Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAAGACGTACGAC) and 254 strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 234 have hits in GenBank, but do not have assigned function; 128 are uncharacterized ESTs and 208 are unidentified."

BASE COUNT
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102 a 75 c 121 g 111 t

Query Match 95.1%; Score 313.8; DB 13; Length 409;
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 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 490)
 Kachar, B.
 EST analysis of gene expression in the mouse Organ of Corti at the
 onset of hearing
 Unpublished
 Contact: Kachar, B.
 Structural Cell Biology
 National Institute of Deafness and other Communication Disorders
 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
 Tel: 301-402-1599
 Fax: 301-402-1765
 Email: kachar@nidcd.nih.gov
 Plate: 37 row: b column: 12
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 FEATURES
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 /note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA) according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary

DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XL1 Blue MRF⁺ cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's Exassist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAAACGCTATGAC) and 254 strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified.

BASE COUNT 191 a 77 c 109 g 112 t 1 others
 ORIGIN
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 Db 261 GATGTCAAGAAAGGGACAGATCTATGTTACTCCAGCTGTATACAGAAACGAGCT 320
 QY 181 GGAGAGTTTGGGCTGCGAGTGTATATGATGACCCAGATGAGATGGAAATTGTAGT 240
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 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
1 (bases 1 to 604)

REFERENCE

Kachar, B.
EST analysis of gene expression in the mouse Organ of Corti at the
onset of hearing

TITLE

Unpublished

JOURNAL

Contact: Kachar, B.

COMMENT

Structural Cell Biology

National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA

Tel: 301-402-1599

Fax: 301-402-1599

Email: kachar@nidcd.nih.gov

Plate: 88 row: d column: 08

Seq primer: M13Rpl reverse primer (ABI).

FEATURES

Location/Qualifiers

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Organ of Corti (OC) was fine dissected from a total of 386
OC as follows: 102 samples from post-natal (P) day 5; 72
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
14 from P12 and 24 from P13. After killing animals by
cervical dislocation followed by decapitation, the bulla
was removed and opened in Leibowitz medium. The bony
capsule of the cochlea was chipped away, stria vascularis
and spiral ligament were removed and the sensory
epithelium was carefully dissected out of the modiolus.
Total RNA was extracted using the micro Fasttrack kit
(catalog # K1593-02; Invitrogen, Carlsbad, CA), according
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library construction were carried out with the Uni-Zap XR
vector kit (catalog # 237211, Stratagene) and Uni-Zap XR
Gigapack III Gold Cloning kit (catalog # 237612), both
from Stratagene (La Jolla, CA, USA) according to
manufacturer's instructions. Briefly: 1.5 ug mRNA was
reverse transcribed using a hybrid oligo(dT) linker-primer
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MMLV-RT and 5-methyl dCTP. The second strand was
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DNA was blunt ended with Pfu DNA polymerase, ligated with
EcoR I adapters in the presence of ligase and digested
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over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden)
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recombinants. Stratagene's EXASist interference
resistance helper phage (catalogue # 211203) was adopted to
rescue plasmid DNA from the phages. Upon plating of the
rescued library, individual cDNA clones were selected and
grown in 96-well, 2 ml growth plate. Plasmid DNA was
purified from 200 ul of saturated culture with the
Concert 6 (TM) plasmid purification kit (Invitrogen,
Carlsbad, CA) as instructed by the manufacturer. ESTs from
the 5' end of the cDNA clones were generated with the
universal M13 reverse primer (CAGGAAACAGCTATGACC) and 25¢
strength BigDye terminator sequencing chemistry (Applied

BASE COUNT

178 a 108 c 152 g 166 t

Query Match

Best Local Similarity 90.9%; Score 300; DB 13; Length 604;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 14

BY232622

LOCUS

BY232622

DEFINITION

BY232622 RIKEN full-length enriched, adult inner ear Mus musculus

ACCESSION

BY232622

VERSION

BY232622.1

KEYWORDS

EST

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

1 (bases 1 to 365)

AUTHORS

Nikazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C.,
Gotohori, T., Baldarelli, R., Hill, D. P., Butt, C., Hume, D. A.,
Quackenbush, J., Schmitt, L. M., Kanapin, A., Matsuda, H., Batalov, S.,
Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V., Chochia, C., Corbani,
L. E., Cousins, S., Dalla, E., Drgant, T. A., Fletcher, C. F., Forrest,
A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A.,
Gough, G., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J.,
Jarvis, E. D., Kanai, A., Kawai, H., Kawasawa, Y., Kedzierski, R. M.,
King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons,
P. A., Meglath, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki,
H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Pertea, G.,
Rachandran, S., Ravasi, T., Reed, J. C., Reed, J. U., Reid, J., Ring,
B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C. A., Setou,
M., Shimada, K., Sultana, R., Takemura, Y., Taylor, M. S., Teasdale,
R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y.,
Watanabe, Y., Wells, C., Wilming, L. G., Wyszynski, A., Yanagisawa,
M., Yang, I., Yang, L., Yuan, Z., Zavalan, M., Zhu, Y., Zimmer, A.,
Carninci, P., Hayashita, N., Hirozane-Kitakawa, T., Kono, H., Nakamura,
M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.

Biosystems, Foster City, CA). Sequencing reactions were
performed on MJ Tetrad thermal cyclers (MJ Research,
Waltham, MA), and analyzed on 3700 automated capillary
sequencers using POPs polymer (Applied Biosystems, Foster
City, CA). The frequency distribution of the library is
as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10;
1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of
genes are present in Genbank and have known function, 23%
have hits in Genbank, but do not have assigned function;
12% are uncharacterized ESTs and 20% are unidentified."

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imorani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

22354683
12466851

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-72 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gscc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/

Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imorani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watanuki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Kirk W. Beisel (Boys Town National Research Hospital 555 North 30th Street Omaha, NE 68131 USA) whose assistance we gratefully acknowledge. Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.
Location/Qualifiers

FEATURES
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Matches 287; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 78 CATGGTGAATTTAGATTAACCTTCTCTAGAGTTGTGCGATGAGAGTGTTC 137
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DB 138 TATATATTTCTCTGCGAAGACAGAGAAATTCAATGCCCGAGCTGTAGTTTCATC 197
QY 121 GATGCAAGAAAGGCGACAGATCTATGTCTTACCTCCAGCTGTGTACGAAACGAGCT 180
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DB 318 TATTTCCCGACACTGGTGAAGAGCAGCCTGTATTCACGAGAGGCC 365

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DEFINITION clone g132a07 5', mRNA sequence.
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VERSION B0565179.1 GI:21468496
KEYWORDS EST
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 485)
Kachar, B.

REFERENCE
EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
Unpublished
Contact: Kachar, B.
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: kachar@nidcd.nih.gov
Plate: 32 row: a column: 07
Seq primer: M13RP1 reverse primer (AB1).

FEATURES
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/note="Organ: Organ of Corti; Vector: pbuiscrpt; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (p) day 5; 72 from p6; 60 from p7; 46 from p8; 18 from p9; 20 from p10; 14 from p12 and 24 from p13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02, Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR GigaPack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was phenolically size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden)

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ORIGIN

Query Match 73.9%; Score 244; DB 13; Length 485;
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Search completed: December 30, 2003, 06:07:16
Job time: 1099.64 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 22:01:01 ; Search time 109.538 Seconds
(without alignment)
8132.484 Million cell updates/sec

Title: US-10-019-455A-25

Sequence: 1 catgtgtgtttatcgtgataa.....atattgactctctctgtgaa 330

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

N_Geneseq_19Jun03:*

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- 2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
- 3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
- 4: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
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- 10: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
- 11: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
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- 14: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
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- 20: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
- 21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
- 22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
- 23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
- 25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | ID | Description |
|------------|-------|--------------------|-----|--------------------|
| 1 | 330 | 100.0 | 330 | Mouse MLP nucleoti |
| 2 | 330 | 100.0 | 384 | Mouse MLP nucleoti |
| 3 | 330 | 100.0 | 947 | Mouse MLP nucleoti |
| 4 | 294.8 | 89.3 | 330 | Rat MLP nucleotide |
| 5 | 294.8 | 89.3 | 384 | Rat MLP nucleotide |
| 6 | 261.8 | 79.3 | 307 | Rat MLP nucleotide |
| 7 | 252.2 | 76.4 | 330 | Human MLP nucleoti |
| 8 | 252.2 | 76.4 | 384 | Human MLP nucleoti |

| | | | | | | |
|----|-------|------|------|----|----------|---------------------|
| 9 | 252.2 | 76.4 | 387 | 24 | AA317583 | DNA encoding novel |
| 10 | 252.2 | 76.4 | 426 | 22 | AAH26341 | Human growth regul |
| 11 | 252.2 | 76.4 | 521 | 24 | ABL95740 | Human angiogenesis |
| 12 | 252.2 | 76.4 | 521 | 24 | ABL68251 | Human PRO9873 CDNA |
| 13 | 252.2 | 76.4 | 521 | 24 | ABK31571 | CDNA encoding huma |
| 14 | 252.2 | 76.4 | 891 | 22 | AAH98226 | Human SST-derived |
| 15 | 252.2 | 76.4 | 891 | 22 | AAH26342 | Human growth regul |
| 16 | 252.2 | 76.4 | 923 | 22 | AAH59083 | Human MLP nucleoti |
| 17 | 252.2 | 76.4 | 1201 | 22 | AAH26343 | Human growth regul |
| 18 | 233.8 | 70.8 | 261 | 22 | AAH59092 | Rat MLP nucleotide |
| 19 | 65 | 19.7 | 581 | 16 | AAQ84052 | Sequence encoding |
| 20 | 60.2 | 18.2 | 433 | 22 | AAH47783 | Recombinant human |
| 21 | 60.2 | 18.2 | 459 | 16 | AAQ84050 | Sequence encoding |
| 22 | 60.2 | 18.2 | 459 | 22 | AAI70083 | Melanoma inhibitor |
| 23 | 60.2 | 18.2 | 459 | 22 | AAI18732 | Human antisease ol |
| 24 | 60.2 | 18.2 | 555 | 23 | ABV59229 | Human prostate exp |
| 25 | 58.6 | 17.8 | 442 | 24 | ABL53602 | Breast cancer rela |
| 26 | 58.6 | 17.8 | 442 | 24 | ABL64012 | Sequence encoding |
| 27 | 55.2 | 16.7 | 330 | 16 | AAQ84061 | Amplified fragment |
| 28 | 52.6 | 15.9 | 305 | 16 | AAQ84055 | Human gene express |
| 29 | 47.2 | 14.3 | 300 | 20 | AAZ14828 | Human protein enco |
| 30 | 47.2 | 14.3 | 417 | 22 | AAH99775 | Human CDNA encodin |
| 31 | 47.2 | 14.3 | 429 | 22 | AAH22695 | Human CDNA encodin |
| 32 | 47.2 | 14.3 | 884 | 22 | AAH22459 | Human CDNA encodin |
| 33 | 47.2 | 14.3 | 1060 | 22 | AAH92140 | Human PRO19670 CDN |
| 34 | 47.2 | 14.3 | 1060 | 24 | ABH74460 | Human CDNA encodin |
| 35 | 47.2 | 14.3 | 1060 | 24 | ABH57328 | Human angiogenesis |
| 36 | 47.2 | 14.3 | 1060 | 24 | ABH88249 | Human PRO19670 CDN |
| 37 | 47.2 | 14.3 | 1060 | 25 | ACA58892 | CDNA encoding huma |
| 38 | 47.2 | 14.3 | 1060 | 25 | ACA58892 | Novel human secret |
| 39 | 47.2 | 14.3 | 1060 | 25 | ACA60445 | CDNA encoding huma |
| 40 | 47.2 | 14.3 | 1060 | 25 | ACA63455 | Human CDNA encodin |
| 41 | 47.2 | 14.3 | 1060 | 25 | ABX98433 | Novel human secret |
| 42 | 47.2 | 14.3 | 1060 | 25 | ABX98935 | Human secreted/tira |
| 43 | 47.2 | 14.3 | 1060 | 25 | ACA05980 | Human PRO polynuci |
| 44 | 47.2 | 14.3 | 1060 | 25 | ABX98024 | Human PRO polynuci |
| 45 | 47.2 | 14.3 | 1060 | 25 | ABX78808 | Human PRO polynuci |

ALIGNMENTS

RESULT 1

AAH59080 standard; DNA; 330 BP.

AAH59080;

23-Apr-2001 (first entry)

Mouse MLP nucleotide sequence SEQ ID NO:25.

MP; MIA; melanoma inhibitory activity; cancer; bone disease;

joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;

cardiant; gene therapy; secretory cell function regulator; promoter;

inhibitor; ds.

Mus musculus.

WO200102564-A1.

11-JAN-2001.

29-JUN-2000; 2000MC-JP04278.

30-JUN-1999; 99JP-0186718.

(TAKE) TAKEDA CHEM IND LTD.

Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K,

Tanaka H,

WPI, 2001-159271/16.

DR P-PSDB; AAB69127.
 XX Safe, low-toxicity secretory cell function-regulatory protein and
 PT encoded DNA, applicable as drugs, in diagnosis and development of
 PT promoters and inhibitors for preventing or treating e.g. bone and joint
 PT diseases -
 XX
 PS Claim 10; Page 98; 11pp; Japanese.
 XX
 CC The present invention describes novel MLP proteins and their encoding
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
 CC activities, and can be used in gene therapy and as secretory cell
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in
 CC the diagnosis and development of promoters and inhibitors for preventing
 CC or treating bone and joint diseases as well as pathologic angiogenesis.
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
 CC in the exemplification of the present invention.
 CC
 XX Sequence 330 BP; 91 A; 60 C; 92 G; 87 T; 0 other;
 SQ
 Query Match 100.0%; Score 330; DB 22; Length 330;
 Best Local Similarity 100.0%; Pred. No. 6,3e-97;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CATGCTGATTTATGATTAACCTTCTTCTAAGAGTGTGTGGATGAGAGTGTGTC 60
 Db 1 CATGCTGATTTATGATTAACCTTCTTCTAAGAGTGTGTGGATGAGAGTGTGTC 60
 QY 61 TATACATATTTCTCTGCGAAGAGCAGAGAAAGATTACATCCCGACAGTGTGATC 120
 Db 61 TATACATATTTCTCTGCGAAGAGCAGAGAAAGATTACATCCCGACAGTGTGATC 120
 QY 121 GATGTCAAGAAAGGCGAGCATGTATGTTTACCTCCAGCTGTGTACAGAAACGAGCT 180
 Db 121 GATGTCAAGAAAGGCGAGCATGTATGTTTACCTCCAGCTGTGTACAGAAACGAGCT 180
 QY 181 GGAGAGTTTGGGCTGGCAGTGTATGTGTGACCAACAGATGAGATTTGAGT 240
 Db 181 GGAGAGTTTGGGCTGGCAGTGTATGTGTGACCAACAGATGAGATTTGAGT 240
 QY 241 TATTTCCCGACCAACTTGTGTGAAGAGCAGCGTGTATACGAGAGGCGACCAAGAGATC 300
 Db 241 TATTTCCCGACCAACTTGTGTGAAGAGCAGCGTGTATACGAGAGGCGACCAAGAGATC 300
 QY 301 CCAACCAAGGATATTGACTTCTTCTGTGA 330
 Db 301 CCAACCAAGGATATTGACTTCTTCTGTGA 330

RESULT 2
 AAF59068
 ID AAF59068 standard; DNA; 384 BP.
 XX
 AC AAF59068;
 XX
 DT 23-APR-2001 (first entry)
 XX
 DE Mouse MLP nucleotide sequence SEQ ID NO:10.
 XX
 KM MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
 KM joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
 KM cardiant; gene therapy; secretory cell function regulator; promoter;
 KM inhibitor; ds.
 XX
 OS Mus musculus.
 XX
 PN WO200102564-A1.
 XX
 PD 11-JAN-2001.
 XX
 PF 29-JUN-2000; 2000MO-JP04278.
 XX
 PR 30-JUN-1999; 99JP-0186718.

XX (TAKEDA CHEM IND LTD.
 PA
 XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
 PI Tanaka H;
 XX
 DR WPI; 2001-159271/16.
 DR P-PSDB; AAB69125.
 XX
 PT Safe, low-toxicity secretory cell function-regulatory protein and
 PT encoded DNA, applicable as drugs, in diagnosis and development of
 PT promoters and inhibitors for preventing or treating e.g. bone and joint
 PT diseases -
 XX
 PS Claim 11; Page 93; 11pp; Japanese.
 XX
 CC The present invention describes novel MLP proteins and their encoding
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
 CC activities, and can be used in gene therapy and as secretory cell
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in
 CC the diagnosis and development of promoters and inhibitors for preventing
 CC or treating bone and joint diseases as well as pathologic angiogenesis.
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
 CC in the exemplification of the present invention.
 CC
 XX Sequence 384 BP; 98 A; 68 C; 111 G; 107 T; 0 other;
 SQ
 Query Match 100.0%; Score 330; DB 22; Length 384;
 Best Local Similarity 100.0%; Pred. No. 6,7e-97;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CATGCTGATTTATGATTAACCTTCTTCTAAGAGTGTGTGGATGAGAGTGTGTC 60
 Db 55 CATGCTGATTTATGATTAACCTTCTTCTAAGAGTGTGTGGATGAGAGTGTGTC 114
 QY 61 TATACATATTTCTCTGCGAAGAGCAGAGAAAGATTACATCCCGACAGTGTGATC 120
 Db 115 TATACATATTTCTCTGCGAAGAGCAGAGAAAGATTACATCCCGACAGTGTGATC 174
 QY 121 GATGTCAAGAAAGGCGAGCATGTATGTTTACCTCCAGCTGTGTACAGAAACGAGCT 180
 Db 175 GATGTCAAGAAAGGCGAGCATGTATGTTTACCTCCAGCTGTGTACAGAAACGAGCT 234
 QY 181 GGAGAGTTTGGGCTGGCAGTGTATGTGTGACCAACAGATGAGATTTGAGT 240
 Db 235 GGAGAGTTTGGGCTGGCAGTGTATGTGTGACCAACAGATGAGATTTGAGT 294
 QY 241 TATTTCCCGACCAACTTGTGTGAAGAGCAGCGTGTATCCAGAGGCGACCAAGAGATC 300
 Db 295 TATTTCCCGACCAACTTGTGTGAAGAGCAGCGTGTATCCAGAGGCGACCAAGAGATC 354
 QY 301 CCAACCAAGGATATTGACTTCTTCTGTGA 330
 Db 355 CCAACCAAGGATATTGACTTCTTCTGTGA 384

RESULT 3
 AAF59084
 ID AAF59084 standard; DNA; 947 BP.
 XX
 AC AAF59084;
 XX
 DT 23-APR-2001 (first entry)
 XX
 DE Mouse MLP nucleotide sequence SEQ ID NO:30.
 XX
 KM MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
 KM joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
 KM cardiant; gene therapy; secretory cell function regulator; promoter;
 KM inhibitor; ds.
 XX
 OS Mus musculus.

PN WO200102564-A1.
 XX 11-JAN-2001.
 XX 29-JUN-2000; 2000WO-JP04278.
 XX 30-JUN-1999; 99JP-0186718.
 PR (TAKE) TAKEDA CHEM IND LTD.
 XX Itch Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
 PI Tanaka H;
 PI WPI; 2001-159271/16.
 DR
 XX Safe, low-toxicity secretory cell function-regulatory protein and
 PT encoded DNA, applicable as drugs, in diagnosis and development of
 PT promoters and inhibitors for preventing or treating e.g. bone and joint
 PT diseases -
 XX
 XX Example 2; Page 100-101; 11pp; Japanese.
 XX
 CC The present invention describes novel MLP proteins and their encoding
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
 CC activities, and can be used in gene therapy and as secretory cell
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in
 CC the diagnosis and development of promoters and inhibitors for preventing
 CC or treating bone and joint diseases as well as pathologic angiogenesis.
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
 CC in the exemplification of the present invention.
 XX
 XX Sequence 947 BP; 279 A; 158 C; 221 G; 289 T; 0 other;
 SQ
 Query Match 100.0%; Score 330; DB 22; Length 947;
 Best Local Similarity 100.0%; Pred. No. 9.9e-97;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CATGGTGTATTATGATATAAATTCTTCTTAAGAAGTTGTGCGATGAGAGTGTGC 60
 DB 65 CATGGTGTATTATGATATAAATTCTTCTTAAGAAGTTGTGCGATGAGAGTGTGC 124
 QY 61 TATATCTATTTCTCTGGCAAGACACAGAGATTACAAATGCCCAAGCTGTAGTTCATC 120
 DB 125 TATATCTATTTCTCTGGCAAGACACAGAGATTACAAATGCCCAAGCTGTAGTTCATC 184
 QY 121 GATGTCAGAAAGGCGCAGACATCTATGTTTACTCCAGCTGTACAGAAACGGAGCT 180
 DB 185 GATGTCAGAAAGGCGCAGACATCTATGTTTACTCCAGCTGTACAGAAACGGAGCT 244
 QY 181 GGAGAGTTTGGGCTGGCAGTGTATGTTATGTCACCCAGATGATGGGAATTGTAGT 240
 DB 245 GGAGAGTTTGGGCTGGCAGTGTATGTTATGTCACCCAGATGATGGGAATTGTAGT 304
 QY 241 TATTTCCCAAGCACTTGTGTAAGAGAGCGGTGTATACCAAGAGCCCAAGAGATC 300
 DB 305 TATTTCCCAAGCACTTGTGTAAGAGAGCGGTGTATACCAAGAGCCCAAGAGATC 364
 QY 301 CCAACCAAGGATATGACTTCTTCTGTGAA 330
 DB 365 CCAACCAAGGATATGACTTCTTCTGTGAA 394
 RESULT 4
 ID AAF59099 standard; DNA; 330 BP.
 AC AAF59099;
 XX
 DT 23-APR-2001 (first entry)
 XX
 XX Rat MLP nucleotide sequence SEQ ID NO:48.
 XX
 KW MLP; MIA; melanoma inhibitory activity; cancer; bone disease;

KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
 KW cardiant; gene therapy; secretory cell function regulator; promoter;
 KW inhibitor; ds.
 XX
 OS Rattus sp.
 XX
 XX WO200102564-A1.
 XX 11-JAN-2001.
 XX 29-JUN-2000; 2000WO-JP04278.
 XX 30-JUN-1999; 99JP-0186718.
 PR (TAKE) TAKEDA CHEM IND LTD.
 XX Itch Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
 PI Tanaka H;
 PI WPI; 2001-159271/16.
 DR P-PSDB; AAB69131.
 XX
 PT Safe, low-toxicity secretory cell function-regulatory protein and
 PT encoded DNA, applicable as drugs, in diagnosis and development of
 PT promoters and inhibitors for preventing or treating e.g. bone and joint
 PT diseases -
 XX
 XX Claim 12; Page 107; 11pp; Japanese.
 XX
 CC The present invention describes novel MLP proteins and their encoding
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
 CC activities, and can be used in gene therapy and as secretory cell
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in
 CC the diagnosis and development of promoters and inhibitors for preventing
 CC or treating bone and joint diseases as well as pathologic angiogenesis.
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
 CC in the exemplification of the present invention.
 XX
 XX Sequence 330 BP; 91 A; 62 C; 91 G; 86 T; 0 other;
 SQ
 Query Match 89.3%; Score 294.8; DB 22; Length 330;
 Best Local Similarity 93.3%; Pred. No. 1.7e-85;
 Matches 308; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
 QY 1 CATGGTGTATTATGATATAAATTCTTCTTAAGAAGTTGTGCGATGAGAGTGTGC 60
 DB 1 CATGGTGTATTATGATATAAATTCTTCTTAAGAAGTTGTGCGATGAGAGTGTGC 60
 QY 61 TATATCTATTTCTCTGGCAAGACACAGAGATTACAAATGCCCAAGCTGTAGTTCATC 120
 DB 61 TATATCTATTTCTCTGGCAAGACACAGAGATTACAAATGCCCAAGCTGTAGTTCATC 120
 QY 121 GATGTCAGAAAGGCGCAGACATCTATGTTTACTCCAGCTGTACAGAAACGGAGCT 180
 DB 121 AATGTCAAGAAAGGCGCAGACATCTATGTTTATTCCAAGCTGTACAGAAATGGAGCT 180
 QY 181 GGAGAGTTTGGGCTGGCAGTGTATGTTATGTCACCCAGATGATGGGAATTGTAGT 240
 DB 181 GGAGAGTTTGGGCTGGCAGTGTATGTTATGTCACCCAGATGATGGGAATTGTAGT 240
 QY 241 TATTTCCCAAGCACTTGTGTAAGAGAGCGGTGTATACCAAGAGCCCAAGAGATC 300
 DB 241 TATTTCCCAAGCACTTGTGTAAGAGAGCGGTGTATACCAAGAGCCCAAGAGATC 300
 QY 301 CCAACCAAGGATATGACTTCTTCTGTGAA 330
 DB 301 CCAACCAAGGATATGACTTCTTCTGTGAA 330
 RESULT 5
 ID AAF59098 standard; DNA; 384 BP.
 AC AAF59098;
 XX

AC AAF59098;
 XX 23-APR-2001 (first entry)
 DT Rat MLP nucleotide sequence SEQ ID NO:46.
 XX
 XX
 XX MIP; MIA; melanoma inhibitory activity; cancer; bone disease;
 KM joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
 KM cardiant; gene therapy; secretory cell function regulator; promoter;
 KM inhibitor; ds.
 XX
 XX Rattus sp.
 XX
 XX W0200102564-A1.
 XX
 XX 11-JAN-2001.
 PD
 XX 29-JUN-2000; 2000MO-JP04278.
 PF
 XX 30-JUN-1999; 99JP-0186718.
 PR
 XX (TAKE) TAKEDA CHEM IND LTD.
 PA
 XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
 PI Tanaka H;
 XX
 XX WPI; 2001-159271/16.
 DR P-PSDB; AAB69130.
 XX
 XX Safe, low-toxicity secretory cell function-regulatory protein and
 PT encoded DNA, applicable as drugs, in diagnosis and development of
 PT promoters and inhibitors for preventing or treating e.g. bone and joint
 PT diseases -
 PS
 XX Claim 13; Page 105-106; 111pp; Japanese.
 PS
 XX The present invention describes novel MLP proteins and their encoding
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
 CC activities, and can be used in gene therapy and as secretory cell
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in
 CC the diagnosis and development of promoters and inhibitors for preventing
 CC or treating bone and joint diseases as well as pathologic angiogenesis.
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
 CC in the exemplification of the present invention.
 CC
 XX
 XX Sequence 384 BP; 98 A; 72 C; 109 G; 105 T; 0 other;
 SQ
 Query Match 89.3%; Score 294.8; DB 22; Length 384;
 Best Local Similarity 93.3%; Pred. No. 1.8e-85;
 Matches 308; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

DB 355 CCAACCAAGATATTGACTTCTGTGAA 384
 RESULT 6
 AAF59093
 ID AAF59093 standard; DNA; 307 BP.
 XX
 XX AAF59093;
 AC
 XX 23-APR-2001 (first entry)
 DT
 XX Rat MLP nucleotide sequence SEQ ID NO:41.
 DE
 XX
 XX MIP; MIA; melanoma inhibitory activity; cancer; bone disease;
 KM joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
 KM cardiant; gene therapy; secretory cell function regulator; promoter;
 KM inhibitor; ds.
 XX
 XX Rattus sp.
 OS
 XX
 XX W0200102564-A1.
 XX
 XX 11-JAN-2001.
 PD
 XX 29-JUN-2000; 2000MO-JP04278.
 PF
 XX 30-JUN-1999; 99JP-0186718.
 PR
 XX (TAKE) TAKEDA CHEM IND LTD.
 PA
 XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
 PI Tanaka H;
 XX
 XX WPI; 2001-159271/16.
 DR
 XX
 XX Safe, low-toxicity secretory cell function-regulatory protein and
 PT encoded DNA, applicable as drugs, in diagnosis and development of
 PT promoters and inhibitors for preventing or treating e.g. bone and joint
 PT diseases -
 PS
 XX Example 9; Page 104; 111pp; Japanese.
 PS
 XX The present invention describes novel MLP proteins and their encoding
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
 CC activities, and can be used in gene therapy and as secretory cell
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in
 CC the diagnosis and development of promoters and inhibitors for preventing
 CC or treating bone and joint diseases as well as pathologic angiogenesis.
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
 CC in the exemplification of the present invention.
 CC
 XX
 XX Sequence 307 BP; 84 A; 56 C; 90 G; 77 T; 0 other;
 SQ
 Query Match 79.3%; Score 261.8; DB 22; Length 307;
 Best Local Similarity 94.0%; Pred. No. 8.5e-75;
 Matches 283; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

QY 241 TATTCCCGACGACTGTGTAAGAGCAGCTGTATACCGAGA-GGCCACCAAGAGAT 299
 Db 247 TATTCCCGACGAACTGTGTTAGAGCAAGAGTATACCAAGAGGCCACCAAGAGAT 306
 QY 300 C 300
 Db 307 C 307

RESULT 7
 ID AAF59079 standard; DNA; 330 BP.
 AC AAF59079;
 XX
 DT 23-APR-2001 (first entry)
 DE Human MLP nucleotide sequence SEQ ID NO:23.
 XX
 KM MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
 KM joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
 KM cardiant; gene therapy; secretory cell function regulator; promoter;
 KM inhibitor; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200102564-A1.
 XX
 PD 11-JAN-2001.
 XX
 PF 29-JUN-2000; 2000WO-JP04278.
 XX
 PR 30-JUN-1999; 99JP-0186718.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K,
 PI Tanaka H;
 DR WPI: 2001-159271/16.
 DR P-PSDB; AAB69126.
 XX
 PT Safe, low-toxicity secretory cell function-regulatory protein and
 PT encoded DNA, applicable as drugs, in diagnosis and development of
 PT promoters and inhibitors for preventing or treating e.g. bone and joint
 PT diseases -
 XX
 PS Claim 8; Page 97; 11pp; Japanese.
 XX
 CC The present invention describes novel MLP proteins and their encoding
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
 CC activities, and can be used in gene therapy and as secretory cell
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in
 CC the diagnosis and development of promoters and inhibitors for preventing
 CC or treating bone and joint diseases as well as pathologic angiogenesis.
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
 CC in the exemplification of the present invention.
 XX
 SQ Sequence 330 BP; 91 A; 60 C; 91 G; 88 T; 0 other;

Query Match 76.4%; Score 252.2; DB 22; Length 330;
 Best Local Similarity 85.4%; Pred. No. 1.2e-71;
 Matches 281; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 CATGCTATTATATGATTAACCTTCTCTAAGAGTTGTGCGAGTGAAGATGTGTC 60
 Db 1 CATGCAATATTATTAAGACCGCTCTAGCTTCCAGAGCTCTGTGCAATGATGATGTC 60

QY 61 TATACCTTTCTCTGGAAGAGACACAGAGATTACATATCCCAAGCTGTAGCTTATC 120
 Db 61 TATACCTATTCTCTGCTAGTGTCAAGAGATTATATGCCCCGAGCTGTAGATTCAAT 120

QY 121 GATGTCAAGAAAGGAGAGATCTATGTTTACTCCAGCTGTAAACAGAAAGGAGCT 180

Db 121 AACGTTAAAAAGGCGACAGATCTATGTACTAAAGCTGTGTAAAGAAATGAGACT 180
 QY 181 GGAGAGTTTGGGCTGGCAGTGTATTATGTGACCAACAGATGAGATGGAAATGTAGCT 240
 Db 181 GGAGAAATTTGGGCTGGCAGTGTATTATGTGATGGCCAGACAGATGGAGTCTGGCT 240

QY 241 TATTCCCGACGAACTGTGTAAGAGCAGCTGTATACCGAGAGCCACCAAGAGATC 300
 Db 241 TATTCCCGACGAACTGTGTAAGAGCAGCTGTATACCGAGAGCCACCAAGAGATC 300

QY 301 CCACACAGATATTGACTTCTCTGTGA 329
 Db 301 CCACACAGATATTGACTTCTCTGTGA 329

RESULT 8
 ID AAF59065 standard; DNA; 384 BP.
 AC AAF59065;
 XX
 DT 23-APR-2001 (first entry)
 DE Human MLP nucleotide sequence SEQ ID NO:4.
 XX
 KM MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
 KM joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
 KM cardiant; gene therapy; secretory cell function regulator; promoter;
 KM inhibitor; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200102564-A1.
 XX
 PD 11-JAN-2001.
 XX
 PF 29-JUN-2000; 2000WO-JP04278.
 XX
 PR 30-JUN-1999; 99JP-0186718.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K,
 PI Tanaka H;
 DR WPI: 2001-159271/16.
 DR P-PSDB; AAB69123.
 XX
 PT Safe, low-toxicity secretory cell function-regulatory protein and
 PT encoded DNA, applicable as drugs, in diagnosis and development of
 PT promoters and inhibitors for preventing or treating e.g. bone and joint
 PT diseases -
 XX
 PS Example 1; Page 91; 11pp; Japanese.
 XX
 CC The present invention describes novel MLP proteins and their encoding
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
 CC activities, and can be used in gene therapy and as secretory cell
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in
 CC the diagnosis and development of promoters and inhibitors for preventing
 CC or treating bone and joint diseases as well as pathologic angiogenesis.
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
 CC in the exemplification of the present invention.
 XX
 SQ Sequence 384 BP; 99 A; 70 C; 106 G; 109 T; 0 other;

Query Match 76.4%; Score 252.2; DB 22; Length 384;
 Best Local Similarity 85.4%; Pred. No. 1.2e-71;
 Matches 281; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 CATGCTATTATATGATTAACCTTCTCTAAGAGTTGTGCGAGTGAAGATGTGTC 60

PI Drmanac RT:
 XX WPI, 2001-483233/52.
 XX
 XX Isolated human growth regulatory-like polypeptide useful for treating
 PT e.g. Alzheimer's disease, cancer, autoimmune disorders,
 PT hyperproliferative disorders, coagulation disorders, and nervous system
 PT disorders -
 XX
 XX Example 1; Page 114; 119pp; English.
 XX
 CC The present sequence is that of Hysed clone identification number
 CC 16372272, which was obtained from a human thymus cDNA library
 CC using standard PCR with primers specific for vector sequences
 CC flanking the inserts, sequencing by hybridisation sequence
 CC signature analysis, and Sanger sequencing techniques. This
 CC expressed sequence tag was used in the assembly of a full-length
 CC cDNA sequence (see AAH26343) encoding a novel human growth
 CC regulatory-like polypeptide (GRLP, see AAB82671). The GRLP
 CC belongs to the same protein family as growth regulatory proteins,
 CC growth factors, human melanoma derived growth regulatory protein
 CC precursor (64% similarity and 45% identity over 111 amino acids)
 CC or melanoma inhibitory activity, cattle cartilage-derived
 CC retinoic acid sensitive protein (CD-RAP, 44% identity and 64%
 CC similarity over 126 amino acids) and other retinoic acid-sensitive
 CC proteins. GRP polypeptides and polynucleotides of the invention
 CC can be used in the prophylaxis, treatment (including gene therapy)
 CC and diagnosis of disorders and diseases caused by, or involving,
 CC cartilage development and maintenance, inhibition of melanoma cell
 CC growth and tumours, including neuroectodermal tumours such as
 CC gliomas. The polynucleotides can also be used to design probes
 CC and primers, for chromosome and gene mapping, in the recombinant
 CC production of protein, in the generation of antisense, ribozyme and
 CC peptide-nucleic acid molecules, and to produce transgenic animals.
 CC
 XX Sequence 426 BP; 119 A; 73 C; 113 G; 120 T; 1 other;
 SO
 Query Match 76.4%; Score 252.2; DB 22; Length 426;
 Best Local Similarity 85.4%; Pred. No. 1.3e-71;
 Matches 281; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
 QY 1 CATGCTGATTTATGATTAACCTTTCTTTPAAGAGTTGGTGGATGAGAGTGTGC 60
 Db 73 CATGGAATATTATGACCGCTCTAGCTTCAAGAGCTGTGAGATGATGATGTGC 132
 QY 61 TATACTATTTCTCGGACAGACAGAGAGATTACATGCCAGCTGATGCTTCATC 120
 Db 133 TATACTATTTCTCGGCTAGTCTCAAGAGATTATATGCCCGGCTGTAGATTCAIT 192
 QY 121 GATGTCAGAAAGGGGACAGATCTATGTTTACTCCAGCTGGTAACAGAAAGGAGCT 180
 Db 193 AACCTTAAAAAGGACAGATCTATGTTACTCAAAAGCTGTAAAGAAATGAGAGCT 252
 QY 181 GGAGAGTTTGGGCTGGCAGTGTATGATGACACCCAGAGATGAGATGAGATTGAGCT 240
 Db 253 GGAGAAATTTGGGCTGGCAGTGTATGATGACAGAGACAGATGGAGTGGAGCT 312
 QY 241 TATTTCCCGACAGACTGTGAGAGAGAGAGCGGTATATCCAGAGGACCAAGAGATC 300
 Db 313 TATTTCCCGACAGACTGTGAGAGAGAGAGCGGTATATCCAGAGGAGTCAAGAGAGT 372
 QY 301 CCAACCAAGGATATGACTCTCTCTGTA 329
 Db 373 CCCACCAAGGATATGACTCTCTCTGGA 401

RESULT 11
 ABL95740
 ID ABL95740 standard; cDNA; 521 BP.
 XX
 AC ABL95740;
 XX
 DT 19-JUL-2002 (first entry)

XX
 DE Human angiogenesis related cDNA PRO9873 SEQ ID NO: 359.
 XX
 KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
 KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
 KW cadent; cytosolic; antiangiogenic; hypotensive; vulnery;
 KW antiarteriosclerotic; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200208284-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 09-JUL-2001; 2001WO-US21735.
 XX
 PR 20-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 25-JUL-2000; 2000US-220664P.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 02-AUG-2000; 2000US-22265P.
 PR 17-AUG-2000; 2000US-0643657.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23528.
 PR 07-SEP-2000; 2000US-230978P.
 PR 15-SEP-2000; 2000US-000000P.
 PR 18-SEP-2000; 2000US-0664610.
 PR 18-SEP-2000; 2000US-0665350.
 PR 24-OCT-2000; 2000US-242922P.
 PR 08-NOV-2000; 2000US-0709238.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000US-0747259.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 22-JAN-2001; 2001US-0767609.
 PR 28-FEB-2001; 2001US-0796498.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0808689.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0834208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 30-MAY-2001; 2001US-0870574.
 PR 30-MAY-2001; 2001WO-US17443.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 28-JUN-2001; 2001WO-US00000.
 XX
 PA (GERTH) GENENTECH INC.
 PA (BAKE/) BAKER K P.
 PA (FERB/) FERRARA N.
 PA (GERB/) GERBER H.
 PA (GERR/) GERRITSEN M E.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GURN/) GURNEY A L.
 PA (HILL/) HILLAN K J.
 PA (MARS/) MARSTERS S A.
 PA (PANT/) PAN J.
 PA (PAON/) PAONI N F.
 PA (STEP/) STEPHAN J F.
 PA (WATA/) WATANABE C K.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;

Query Match 76.4%; Score 252.2; DB 24; Length 521;
 Best Local Similarity 85.4%; Pred. No. 1.4e-71;
 Matches 281; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

```

QY 1 CAGGCGTATTGATGATAAATCTTCTTCAAGATGTCGCGATGAGAGTGTCTC 60
DB 92 CAGGAAATATTATGACCTCTAGCTTCCAGAGGCTGTGCAATGATGTGTCTC 151
QY 61 TATATATTCTCTGCGAAGAGCAGAGATTAACATGCCAGACTGATGATTC 120
DB 152 TATATATTCTCTGCGTGTGCTCAAGAGATTAATATGCCGAGCTGTGATTCAT 211
QY 121 GATGTCAAGAAAGGCGACAGATCTATGTTTACTCCAAGCTGTAAACAGAAACGAGCT 180
DB 212 AACGTTAAAAAGGCGACAGATCTATGTACTCAAAAGCTGTAAAGAAATGAGCT 271
QY 181 GGAGAGTTTGGGCTGGCATGTTTATGTCACCAAGATGATGGAATTTAGT 240
DB 272 GGAGAAATTTGGGCTGGCATGTTTATGTCAGCCAGAGATGGAATGCGGCT 331
QY 241 TATTTCCCGCAACTTGTGTAAGAGACGCTGTATACAGAGAGGCCAACAGAGATC 300
DB 332 TATTTCCCGCAACTTGTGTAAGAGACGCTGTATACAGAGATCTCAAGAGATTT 391
QY 301 CCAACCAAGGATATGACTTCTTCTGTA 329
DB 392 CCCACCAAGGATATGACTTCTTCTGTA 420

```

RESULT 13
 ABK33571
 ID ABK33571 standard; cDNA; 521 BP.

XX
 AC ABK33571;

XX DT 08-MAY-2002 (first entry)

XX DE cDNA encoding human PRO protein. Seq ID No 71.

XX KM Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
 breast cancer; prostate tumour; rectal tumour; liver tumour;
 pericyte cell proliferation; chondrocyte cell proliferation;
 tumour necrosis factor-alpha; gene; ss.

XX OS Homo sapiens.

XX PN W0200208288-A2.

XX PD 31-JAN-2002.

XX PF 29-JUN-2001; 2001WO-US21066.

XX XX 20-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220585P.
 PR 25-JUL-2000; 2000US-220605P.
 PR 25-JUL-2000; 2000US-220607P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 25-JUL-2000; 2000US-220638P.
 PR 25-JUL-2000; 2000US-220664P.
 PR 25-JUL-2000; 2000US-220666P.
 PR 26-JUL-2000; 2000US-220893P.
 PR 26-JUL-2000; 2000WO-US20710.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 15-SEP-2000; 2000US-000000P.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 28-NOV-2000; 2000US-253646P.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000US-0747259.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001WO-US17092.

XX (GENTH) GENENTECH INC.
 PA Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WT;
 XX WPI; 2002-172001/22.
 DR P-PSDB; AAU83627.

PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful for treating a PRO related disorder and for diagnosing tumours
 PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
 PT tumour or liver tumour -
 PS Claim 2; Figure 71; 35pp; English.

XX The invention relates to one hundred and twenty two nucleic acids
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
 CC agonists and antagonists are useful for treating a PRO related disorder.
 CC The PRO polypeptides are useful for diagnosing tumours, especially lung
 CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. The PRO polypeptides are useful for stimulating the
 CC proliferation of, or gene expression, in pericyte cells, for stimulating
 CC the proliferation or differentiation of chondrocyte cells, for
 CC stimulating the release of tumour necrosis factor-alpha from human blood,
 CC for stimulating or inhibiting the proliferation of normal human dermal
 CC fibroblast cells. The PRO polypeptide may also be used as molecular
 CC weight markers and for tissue typing. The PRO nucleic acids have
 CC applications in molecular biology, including use as hybridisation probes,
 CC and in chromosome and gene mapping. ABK33571-ABK33657 represent human
 CC PRO protein coding sequences of the invention.

XX SQ Sequence 521 BP; 167 A; 86 C; 131 G; 137 T; 0 other;

Query Match 76.4%; Score 252.2; DB 24; Length 521;
 Best Local Similarity 85.4%; Pred. No. 1.4e-71;
 Matches 281; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

```

QY 1 CAGGCGTATTGATGATAAATCTTCTTCAAGATGTCGCGATGAGAGTGTCTC 60
DB 92 CAGGAAATATTATGACCCGCTAGCTTCCAGAGGCTGTGCAATGATGTGTCTC 151
QY 61 TATATATTCTCTGCGAAGAGCAGAGATTAACATGCCAGACTGATGATTC 120
DB 152 TATATATTCTCTGCGTGTGCTCAAGAGATTAATATGCCGAGCTGTGATTCAT 211
QY 121 GATGTCAAGAAAGGCGACAGATCTATGTTTACTCCAAGCTGTAAACAGAAACGAGCT 180
DB 212 AACGTTAAAAAGGCGACAGATCTATGTACTCAAAAGCTGTAAAGAAATGAGACT 271
QY 181 GGAGAGTTTGGGCTGGCATGTTTATGTCACCAAGATGATGGAATTTAGT 240
DB 272 GGAGAAATTTGGGCTGGCATGTTTATGTCAGCCAGAGATGGAATGCGGCT 331
QY 241 TATTTCCCGCAACTTGTGTAAGAGACGCTGTATACAGAGAGGCCAACAGAGATC 300
DB 332 TATTTCCCGCAACTTGTGTAAGAGACGCTGTATACAGAGATCTCAAGAGATTT 391
QY 301 CCAACCAAGGATATGACTTCTTCTGTA 329
DB 392 CCCACCAAGGATATGACTTCTTCTGTA 420

```

RESULT 14

ID AAH98228 standard; cDNA; 891 BP.

XX AC AAH98228;

XX DT 12-OCT-2001 (first entry)

DE Human EST-derived coding sequence SEQ ID NO: 85.

XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
 KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
 KW diagnostics; forensic test; gene mapping; genetic disorder;
 KW biodiversity; gene therapy; nutrition; ss.
 OS Homo sapiens.
 XX MO200154477-A2.
 XX 02-AUG-2001.
 XX 25-JAN-2001; 2001WO-US02687.
 XX 25-JAN-2000; 2000US-0491404.
 XX 17-JUL-2000; 2000US-0617746.
 XX 03-AUG-2000; 2000US-0631451.
 XX 15-SEP-2000; 2000US-0663870.
 XX (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
 PI Cao Y, Dmanac RA, Zhang J, Wehrman T;
 XX WPI; 2001-476164/51.
 XX P-PSDB; AAM23569.
 XX Isolated polypeptide for treatment of diseases, diagnostics, raising
 PT antibodies and research use -
 PS Claim 1; Page 236; 1275pp; English.
 XX The present invention provides the protein and coding sequences of novel
 CC proteins from a variety of organisms, including human, dog, cat, horse,
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
 CC from the organism of interest. They can be used in diagnostics,
 CC forensics, gene mapping, identification of mutations, to assess
 CC biodiversity and for nutritional purposes. The present sequence is a cDNA
 CC of the invention.
 CC
 SQ Sequence 891 BP; 272 A; 146 C; 214 G; 259 T; 0 other;
 XX
 XX Query Match 76.4%; Score 252.2; DB 22; Length 891;
 XX Best Local Similarity 85.4%; Pred. No. 1.8e-71;
 XX Matches 281; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
 QY 1 CATGCTGATTTATGATGAACCTTCTCTTAAGAAGTTGTGGGAGTAGAGAGTGTGC 60
 DB 73 CATGGAATATTTATGAGCCGCTCTAGCTTCCAAGAAGCTCTGTGAGATGATGATGTGTC 132
 QY 61 TATATCTATTTCTCTGCGCAAGCAGCAGAGAAATTACAAATGCCCCAGACTGTAGTTATC 120
 DB 133 TATATCTATTTCTCTGCGTAGTGCTCCAAAGATTATATAGCCCGGACTGTAGTTATT 192
 QY 121 GATGTCAGAAAAGGCGACAGATCTATGTTTCTCAAGCTGTGTAAAGAAAAGCGAGCT 180
 DB 193 AATCGTTAAAAAGGCGACAGATCTATGTTGATCTCAAGCTGTGTAAAAAGAAAAGCGAGCT 252
 QY 181 GAGAGATTTTGGGCTGCGAGTGTATATGATGACCAAGCAGATGAGATGGGATTTAGGT 240
 DB 253 GAGAGATTTTGGGCTGCGAGTGTATATGATGACCAAGCAGATGAGATGGGATTTAGGT 312
 QY 241 TATTTTCCCACTTGTGTAAAGAGAGCGTGTATACCAAGAGGCGCACCAGAGATC 300
 DB 313 TATTTTCCCACTTGTGTCAAGGAAAGCGTGTATACCAAGAGGATTTAGGATTT 372
 QY 301 CCAACCAAGGATTTGATCTTCTGTGA 329
 DB 373 CCAACCAAGGATTTGATCTTCTGTGA 401

AAH26342
 ID AAH26342 standard; cDNA; 891 BP.
 XX
 XX AAH26342;
 AC
 XX 02-OCT-2001 (first entry)
 DT
 XX Human growth regulatory-like polypeptide partial cDNA clone.
 DE
 XX Growth regulatory-like polypeptide; human; cartilage; melanoma;
 KW neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;
 KW ss.
 XX
 XX Homo sapiens.
 XX MO200155332-A2.
 XX 02-AUG-2001.
 XX 25-JAN-2001; 2001WO-US02455.
 XX 25-JAN-2000; 2000US-0491404.
 XX 02-MAY-2000; 2000US-0563786.
 XX (HYSE-) HYSEQ INC.
 XX Mize NK, Boyle BJ, Ford JE, Atterburn MC, Tang YT, Liu C;
 PI Dmanac RT;
 XX WPI; 2001-483233/52.
 XX Isolated human growth regulatory-like polypeptide useful for treating
 PT e.g. Alzheimer's disease, cancer, autoimmune disorders, and
 PT hyperproliferative disorders, coagulation disorders, and nervous system
 PT disorders -
 PS Claim 1; Page 115; 119pp; English.
 XX The present sequence is that of a novel nucleic acid that was
 CC assembled from human thymus cDNA library-derived Hyseq clone
 CC identification number 16372272 (see AAH26341). A recursive
 CC algorithm was used to extend the clone by pulling additional
 CC sequences from different databases. A full-length sequence (see
 CC AAH26343) encoding novel human growth regulatory-like polypeptide
 CC (GRLP, see AAH2671) was subsequently obtained. Human GRLP
 CC belongs to the same protein family as growth regulatory proteins,
 CC growth factors, human melanoma derived growth regulatory protein
 CC precursor (64% similarity and 45% identity over 111 amino acids)
 CC or melanoma inhibitory activity, cattle cartilage-derived
 CC retinoic acid sensitive protein (CD-RAP, 44% identity and 64%
 CC similarity over 126 amino acids) and other retinoic acid-sensitive
 CC proteins. GRLP polypeptides and polynucleotides of the invention
 CC can be used in the prophylaxis, treatment (including gene therapy)
 CC and diagnosis of disorders and diseases caused by, or involving,
 CC cartilage development and maintenance, inhibition of melanoma cell
 CC growth and tumour, including neuroectodermal tumours such as
 CC gliomas. The polynucleotides can also be used to design probes
 CC and primers, for chromosome and gene mapping, in the recombinant
 CC production of protein, in the generation of antisense, ribozyme and
 CC peptide-nucleic acid molecules, and to produce transgenic animals.
 CC
 SQ Sequence 891 BP; 272 A; 146 C; 214 G; 259 T; 0 other;
 XX
 XX Query Match 76.4%; Score 252.2; DB 22; Length 891;
 XX Best Local Similarity 85.4%; Pred. No. 1.8e-71;
 XX Matches 281; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
 QY 1 CATGCTGATTTATGATGAACCTTCTCTTAAGAAGTTGTGGGAGTAGAGAGTGTGC 60
 DB 73 CATGGAATATTTATGAGCCGCTCTAGCTTCCAAGAAGCTCTGTGAGATGATGATGTGTC 132
 QY 61 TATATCTATTTCTCTGCGCAAGCAGCAGAGAAATTACAAATGCCCCAGACTGTAGTTATC 120

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Db      133 TATACATTTCTCTGCTAGTCTCAAGAAATATAATGCCGAGCTGATTCATT 192
Qy      121 GATGTCAGAAAGGCGAGCAGATCTATGTTTACTCCAACTGGTAACAGAAAAACGAGCT 180
Db      193 AACGTTAAAAAGGCGAGCAGATCTATGTTACTCAAGCTGGTAAGAAAAATGAGACT 252
Qy      181 GGAGAGCTTTGGGCTGGCAGTGTATGTGACCAACAGATGAGATGGAAATTGAGT 240
Db      253 GGAGATTTTGGGCTGGCAGTGTATGTGATGGCCAGAGATGGAGTCTGGGT 312
Qy      241 TATTTCCCGCAGCACTTGGTGAAGAGCAGCGTATACCAAGAGGCCACCAAGAGATC 300
Db      313 TATTTCCCGCAGCACTTGGTCAAGAGACAGCGTGTGTACCAAGAGCTTACCAAGAGATT 372
Qy      301 CCAACACGAGATATGACTTCTTCTGTGA 329
Db      373 CCCACACGAGATATGACTTCTTGGCA 401
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
4172.254 Million cell updates/sec

Title: US-10-019-455A-25

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Searched: 2244575 seqs, 173117285 residues

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 252.2 | 76.4 | 426 | 15 | US-10-216-038-1 |
| 2 | 252.2 | 76.4 | 521 | 13 | US-10-216-163-71 |
| 3 | 252.2 | 76.4 | 521 | 13 | US-10-218-765-71 |
| 4 | 252.2 | 76.4 | 521 | 13 | US-10-219-063-71 |
| 5 | 252.2 | 76.4 | 521 | 13 | US-10-219-066-71 |
| 6 | 252.2 | 76.4 | 521 | 13 | US-10-219-067-71 |
| 7 | 252.2 | 76.4 | 521 | 13 | US-10-219-068-71 |
| 8 | 252.2 | 76.4 | 521 | 13 | US-10-219-069-71 |
| 9 | 252.2 | 76.4 | 521 | 13 | US-10-219-073-71 |
| 10 | 252.2 | 76.4 | 521 | 13 | US-10-219-475-71 |
| 11 | 252.2 | 76.4 | 521 | 13 | US-10-219-480-71 |
| 12 | 252.2 | 76.4 | 521 | 13 | US-10-219-483-71 |
| 13 | 252.2 | 76.4 | 521 | 13 | US-10-219-525-71 |
| 14 | 252.2 | 76.4 | 521 | 13 | US-10-219-526-71 |
| 15 | 252.2 | 76.4 | 521 | 13 | US-10-219-530-71 |

| | | | | | | |
|----|-------|------|-----|----|-------------------|--------------------|
| 16 | 252.2 | 76.4 | 521 | 13 | US-10-219-531-71 | Sequence 71, Appl |
| 17 | 252.2 | 76.4 | 521 | 13 | US-10-219-532-71 | Sequence 71, Appl |
| 18 | 252.2 | 76.4 | 521 | 13 | US-10-219-533-71 | Sequence 71, Appl |
| 19 | 252.2 | 76.4 | 521 | 13 | US-10-223-081-359 | Sequence 359, Appl |
| 20 | 252.2 | 76.4 | 521 | 13 | US-10-230-437-71 | Sequence 71, Appl |
| 21 | 252.2 | 76.4 | 521 | 13 | US-10-232-228-71 | Sequence 71, Appl |
| 22 | 252.2 | 76.4 | 521 | 13 | US-10-223-082-359 | Sequence 359, Appl |
| 23 | 252.2 | 76.4 | 521 | 15 | US-10-227-884-71 | Sequence 71, Appl |
| 24 | 252.2 | 76.4 | 521 | 15 | US-10-230-163-71 | Sequence 71, Appl |
| 25 | 252.2 | 76.4 | 521 | 15 | US-10-230-338-71 | Sequence 71, Appl |
| 26 | 252.2 | 76.4 | 521 | 15 | US-10-218-631-71 | Sequence 71, Appl |
| 27 | 252.2 | 76.4 | 521 | 15 | US-10-230-414-71 | Sequence 71, Appl |
| 28 | 252.2 | 76.4 | 521 | 15 | US-10-216-159A-71 | Sequence 71, Appl |
| 29 | 252.2 | 76.4 | 521 | 15 | US-10-218-849-71 | Sequence 71, Appl |
| 30 | 252.2 | 76.4 | 521 | 15 | US-10-227-873-71 | Sequence 71, Appl |
| 31 | 252.2 | 76.4 | 521 | 15 | US-10-227-883-71 | Sequence 71, Appl |
| 32 | 252.2 | 76.4 | 521 | 15 | US-10-219-076-71 | Sequence 71, Appl |
| 33 | 252.2 | 76.4 | 521 | 15 | US-10-230-434-71 | Sequence 71, Appl |
| 34 | 252.2 | 76.4 | 521 | 15 | US-10-219-481-71 | Sequence 71, Appl |
| 35 | 252.2 | 76.4 | 521 | 15 | US-10-219-075-71 | Sequence 71, Appl |
| 36 | 252.2 | 76.4 | 521 | 15 | US-10-219-464-71 | Sequence 71, Appl |
| 37 | 252.2 | 76.4 | 521 | 15 | US-10-219-466-71 | Sequence 71, Appl |
| 38 | 252.2 | 76.4 | 521 | 15 | US-10-219-479-71 | Sequence 71, Appl |
| 39 | 252.2 | 76.4 | 521 | 15 | US-10-219-481-71 | Sequence 71, Appl |
| 40 | 252.2 | 76.4 | 521 | 15 | US-10-230-260-71 | Sequence 71, Appl |
| 41 | 252.2 | 76.4 | 521 | 15 | US-10-232-231-71 | Sequence 71, Appl |
| 42 | 252.2 | 76.4 | 521 | 15 | US-10-232-233-71 | Sequence 71, Appl |
| 43 | 252.2 | 76.4 | 521 | 15 | US-10-216-165-71 | Sequence 71, Appl |
| 44 | 252.2 | 76.4 | 521 | 15 | US-10-218-956-71 | Sequence 71, Appl |
| 45 | 252.2 | 76.4 | 521 | 15 | US-10-219-468-71 | Sequence 71, Appl |

ALIGNMENTS

RESULT 1
US-10-216-038-1
Sequence 1, Application US/10216038
Publication No. US20030124573A1
GENERAL INFORMATION:
APPLICANT: Mize, Nancy K
APPLICANT: Boyle, Bryan J
APPLICANT: Ford, John E
APPLICANT: Atreidurn, Matthew C
APPLICANT: Tang, Y Tom
APPLICANT: Liu, Chenghua
APPLICANT: Drmanac, Radolje T
APPLICANT: Song, Yong
TITLE OF INVENTION: Methods and Materials Relating to No. US20030124573A1 Growth F
TITLE OF INVENTION: Polypeptides and Polynucleotides
FILE REFERENCE: HVS-7CIP
CURRENT APPLICATION NUMBER: US/10/216,038
PRIOR APPLICATION NUMBER: US 09/563,786
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: US 09/491,404
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 426
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (426)..(426)
OTHER INFORMATION: n = A, T, G, or C
US-10-216-038-1
Query Match 76.4%; Score 252.2; DB 15; Length 426;
Best Local Similarity 85.4%; Pred. No. 1.1e-76;
Matches 281; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/086392
PRIOR FILING DATE: 1998-05-22
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PRIOR FILING DATE: 1998-09-10
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PRIOR FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: 60/100385
PRIOR FILING DATE: 1998-09-15
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PRIOR FILING DATE: 1998-09-17
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PRIOR FILING DATE: 1998-09-24
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PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/106178
PRIOR FILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: 60/106248
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 60/106464
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 60/106905
PRIOR FILING DATE: 1998-11-03
PRIOR APPLICATION NUMBER: 60/108787
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/108801
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/108849
PRIOR FILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: 60/112422
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/112966
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/113605
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113621
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/115558
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115565
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115733
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/119549
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/123618
PRIOR FILING DATE: 1999-03-10
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PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 60/126773
PRIOR FILING DATE: 1999-03-29
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PRIOR FILING DATE: 1999-04-05
PRIOR APPLICATION NUMBER: 60/130232
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/131022
PRIOR FILING DATE: 1999-04-26
PRIOR APPLICATION NUMBER: 60/131270
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131291
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131445
PRIOR FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 60/134287
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/140650
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/140723
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/141037
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 60/144758
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/145698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: 60/146222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: 60/146963
PRIOR FILING DATE: 1999-08-03
PRIOR APPLICATION NUMBER: 60/149320

PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/149638
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/151733
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/164418
PRIOR FILING DATE: 1999-11-09
PRIOR APPLICATION NUMBER: 60/166361
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: 60/169445
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169495
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169835

Query Match 76.4%; Score 252.2; DB 13; Length 521;
Best Local Similarity 85.4%; Pred. No. 1.2e-76;
Matches 281; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 CATGCTATTTATGATTAACCTTTCTTCTAAGAGTTGTGGGATGAGAGTGTGC 60
DB 92 CATGAAATATTTATGACCGCTCTAGCTTCCAGAAAGCTGTGTGAGATGATGATGTC 151
QY 61 TATACTATTTCTGTGCAAGACAGAGAGATTACAATGCCCGAGCTGTAGTTATC 120
DB 152 TATACTATTTCTGTGCTAGTGTCTCAAGATTTATATGCCCCGAGCTGTAGTTATT 211
QY 121 GATGCAAGAAAGGCGACAGATCTATGTTTACTCCAAAGCTGTGTAACAGAAACGAGCT 180
DB 212 AACGTTAAAAAGGCGACAGATCTATGTTACTCAAAAGCTGTGTAAGAAATGAGACT 271
QY 181 GAGAGTTTGGGCTGGAGTGTATTATGATGACCAAGAGATGAGATGAGATTTGAGT 240
DB 272 GAGAGATTTTGGCTGGAGTGTATTATGATGATGCGCAGAGATGAGATGAGTGTGAGT 331
QY 241 TATTTCCCGACCACTGTGTGAAGAGAGCGTGTATACCGAGAGCGACCAAGAGATC 300
DB 332 TATTTCCCGACCACTGTGTGAAGAGAGCGTGTATACCGAGAGCGTGTATACCGAGAGATC 391
QY 301 CCAACCCAGATATTGACTTCTTGTGA 329
DB 392 CCAACCCAGATATTGACTTCTTGTGA 420

RESULT 4

US-10-219-063-71
Sequence 71, Application US/10219063
Publication No. US20030187202A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C24
CURRENT FILING DATE: 2002-08-13
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28

PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 71
LENGTH: 521
TYPE: DNA
ORGANISM: Homo Sapien
US-10-219-063-71

Query Match 76.4%; Score 252.2; DB 13; Length 521;
Best Local Similarity 85.4%; Pred. No. 1.2e-76;
Matches 281; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 CATGCTATTTATGATTAACCTTTCTTCTAAGAGTTGTGGGATGAGAGTGTGC 60
DB 92 CATGAAATATTTATGACCGCTCTAGCTTCCAGAAAGCTGTGTGAGATGATGATGTC 151
QY 61 TATACTATTTCTGTGCAAGACAGAGATTTACAATGCCCGAGCTGTAGTTATC 120
DB 152 TATACTATTTCTGTGCTAGTGTCTCAAGATTTATATGCCCCGAGCTGTAGTTATT 211
QY 121 GATGCAAGAAAGGCGACAGATCTATGTTTACTCCAAAGCTGTGTAACAGAAACGAGCT 180
DB 212 AACGTTAAAAAGGCGACAGATCTATGTTACTCAAAAGCTGTGTAAGAAATGAGACT 271
QY 181 GAGAGTTTGGGCTGGAGTGTATTATGATGACCAAGAGATGAGATGAGATTTGAGT 240
DB 272 GAGAGATTTTGGCTGGAGTGTATTATGATGATGCGCAGAGATGAGATGAGTGTGAGT 331
QY 241 TATTTCCCGACCACTGTGTGAAGAGAGCGTGTATACCGAGAGCGACCAAGAGATC 300
DB 332 TATTTCCCGACCACTGTGTGAAGAGAGCGTGTATACCGAGAGCGTGTATACCGAGAGATC 391
QY 301 CCAACCCAGATATTGACTTCTTGTGA 329
DB 392 CCAACCCAGATATTGACTTCTTGTGA 420

RESULT 5

US-10-219-066-71
Sequence 71, Application US/10219066
Publication No. US20030187203A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C27
CURRENT FILING DATE: 2002-08-13
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113

PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 71
LENGTH: 521
TYPE: DNA
ORGANISM: Homo Sapien
US-10-219-066-71

Query Match 76.4%; Score 252.2; DB 13; Length 521;
Best Local Similarity 85.4%; Pred. No. 1.2e-76;
Matches 281; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 CATGGTATTTATGATAAATTTCTTCTAGAGTTGTGCGATGAGAGTGTCTC 60
DB 92 CATGGATATTTATGACCGCTAGCTTCCAGAGCTGTGTGATGATGATGTCTC 151
QY 61 TATACATTTCTCTGCGAAGACACAGAAATTCATGCCCACTGTAGCTTCATC 120
DB 152 TATACATTTCTCTGCGTAGTGTCTCAAGAAATTAATATGCCCCGAGCTAGATTCATT 211
QY 121 GATGTCAGAAAGGCGAGATCTATGTTACTCCAGCTGTATACAGAAACGAGCT 180
DB 212 AACGTTAAAGGCGAGATCTATGTTACTCCAGCTGTATACAGAAATGAGCT 271
QY 181 GGAAGATTTGGCTGGCACTGTTTATGTCACACAGATGAGATGGAATTGAGCT 240
DB 272 GGAAGATTTGGCTGGCACTGTTTATGTCACAGATGGAAGATGGAAGCTGAGCT 331
QY 241 TATTTCCCGACAACTGTTGTAAGAGACAGCTGTATACAGAGAGCCCAAGAGATC 300
DB 332 TATTTCCCGACAACTGTTGTAAGAGACAGCTGTATACAGAGAGCTGCAAGAGATT 391
QY 301 CCAACCCAGATATTGACTTCTTCTGTGA 329
DB 392 CCCACCCAGATATTGACTTCTTCTGTGA 420

RESULT 6
US-10-219-067-71
Sequence 71, Application US/10219067
Publication No. US20030187204A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerltisen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PIC51

CURRENT APPLICATION NUMBER: US/10/219,067
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 71
LENGTH: 521
TYPE: DNA
ORGANISM: Homo Sapien
US-10-219-067-71

Query Match 76.4%; Score 252.2; DB 13; Length 521;
Best Local Similarity 85.4%; Pred. No. 1.2e-76;
Matches 281; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 CATGGTATTTATGATAAATTTCTTCTAGAGTTGTGCGATGAGAGTGTCTC 60
DB 92 CATGGATATTTATGACCGCTAGCTTCCAGAGCTGTGTGATGATGATGTCTC 151
QY 61 TATACATTTCTCTGCGAAGACACAGAAATTCATGCCCACTGTAGCTTCATC 120
DB 152 TATACATTTCTCTGCGTAGTGTCTCAAGAAATTAATATGCCCCGAGCTAGATTCATT 211
QY 121 GATGTCAGAAAGGCGAGATCTATGTTACTCCAGCTGTATACAGAAACGAGCT 180
DB 212 AACGTTAAAGGCGAGATCTATGTTACTCCAGCTGTATACAGAAATGAGCT 271
QY 181 GGAAGATTTGGCTGGCACTGTTTATGTCACACAGATGAGATGGAATTGAGCT 240
DB 272 GGAAGATTTGGCTGGCACTGTTTATGTCACAGATGGAAGATGGAAGCTGAGCT 331
QY 241 TATTTCCCGACAACTGTTGTAAGAGACAGCTGTATACAGAGAGCCCAAGAGATC 300
DB 332 TATTTCCCGACAACTGTTGTAAGAGACAGCTGTATACAGAGAGCTGCAAGAGATT 391
QY 301 CCAACCCAGATATTGACTTCTTCTGTGA 329
DB 392 CCCACCCAGATATTGACTTCTTCTGTGA 420

RESULT 7
US-10-219-068-71
Sequence 71, Application US/10219068
Publication No. US20030187205A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerltisen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.

APPLICANT: Watanabe, Colin I.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C31
CURRENT APPLICATION NUMBER: US/10/219,068
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO: 71
LENGTH: 521
TYPE: DNA
ORGANISM: Homo Sapien
US-10-219-068-71

Query Match 76.4%; Score 252.2; DB 13; Length 521;
Best Local Similarity 85.4%; Pred. No. 1.2e-76;
Matches 281; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 CATGCTGATTTATGATTAACCTTCTCTAAGAGTTGTGCGAGTGAAGAGTGTGTC 60
DB 92 CATGGAATATTTATGAGCCGCTTACCTCCAAAGAGCTCTGTGAGATGATGTGTC 151
QY 61 TATACATTTCTCTGCGAAGAGCAGAGAAATTACATGCCCCAGACTGTAGTTCATC 120
DB 152 TATACATTTCTCTGCGTAGTCTCAAGAAATTAATGCCCCGAGCTGTAGTTCATC 211
QY 121 GATGTCAGAAAGGCGCAGCAGATCTATGTTTACTCAAAGCTGTGTACAGAAAAGCGAGCT 180
DB 212 AACGTTAAAAAGGCGCAGCAGATCTATGTTTACTCAAAGCTGTGTAAAAAGAAATGAGAGCT 271
QY 181 GGAGAGTTTGGGCTGGCAGTGTATGATGTCACCCAGATGAGATGAGATTTGATAGT 240
DB 272 GGAGAAATTTGGGCTGGCAGTGTATGATGTCACCCAGATGAGATGAGATTTGATAGT 331
QY 241 TATTTCCCGAGCACTTGTGAAGAGCAGCGTGTATACAGAGGCCCAAGAGAGATC 300
DB 332 TATTTCCCGAGCACTTGTGTCAAGAGACAGCGTGTGTACAGAGAGCTACCAAGAGAGTT 391
QY 301 CCAACCAAGGATTTGACTTCTTCTGTGA 329
DB 392 CCCACCAAGGATTTGACTTCTTCTGTGA 420

RESULT 8
US-10-219-069-71
Sequence 71, Application US/10219069
Publication No. US20030187206A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gertsen, Mary
APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin I.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C40
CURRENT APPLICATION NUMBER: US/10/219,069
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO: 71
LENGTH: 521
TYPE: DNA
ORGANISM: Homo Sapien
US-10-219-069-71

Query Match 76.4%; Score 252.2; DB 13; Length 521;
Best Local Similarity 85.4%; Pred. No. 1.2e-76;
Matches 281; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 CATGCTGATTTATGATTAACCTTCTCTAAGAGTTGTGCGAGTGAAGAGTGTGTC 60
DB 92 CATGGAATATTTATGAGCCGCTTACCTCCAAAGAGCTCTGTGAGATGATGTGTC 151
QY 61 TATACATTTCTCTGCGAAGAGCAGAGAAATTACATGCCCCAGACTGTAGTTCATC 120
DB 152 TATACATTTCTCTGCGTAGTCTCAAGAAATTAATGCCCCGAGCTGTAGTTCATC 211
QY 121 GATGTCAGAAAGGCGCAGCAGATCTATGTTTACTCAAAGCTGTGTACAGAAAAGCGAGCT 180
DB 212 AACGTTAAAAAGGCGCAGCAGATCTATGTTTACTCAAAGCTGTGTAAAAAGAAATGAGAGCT 271
QY 181 GGAGAGTTTGGGCTGGCAGTGTATGATGTCACCCAGATGAGATGAGATTTGATAGT 240
DB 272 GGAGAAATTTGGGCTGGCAGTGTATGATGTCACCCAGATGAGATGAGATTTGATAGT 331
QY 241 TATTTCCCGAGCACTTGTGAAGAGCAGCGTGTATACAGAGGCCCAAGAGAGATC 300
DB 332 TATTTCCCGAGCACTTGTGTCAAGAGACAGCGTGTGTACAGAGAGCTACCAAGAGAGTT 391
QY 301 CCAACCAAGGATTTGACTTCTTCTGTGA 329
DB 392 CCCACCAAGGATTTGACTTCTTCTGTGA 420

RESULT 9
US-10-219-073-71
Sequence 71, Application US/10219073
Publication No. US20030187207A1

GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C52
CURRENT FILING DATE: 2002-08-14
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 71
LENGTH: 521
TYPE: DNA
ORGANISM: Homo Sapien
US-10-219-073-71

Query Match 76.4%; Score 252.2; DB 13; Length 521;
Best Local Similarity 85.4%; Pred. No. 1.2e-76;
Matches 281; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 CATGCTGATTTATGATAAACTTCTTCTAAGAGTTGTGGGATGAGAGTGTGTC 60
DB 92 CATGGAATATTTATGACCGCTTAGCTTCAAGAACTGTGTCAGATGATGTGTGTC 151
QY 61 TATACATTTCTCTGGCAAGACAGAGAGATTACATGCCCACTGTAGTTTCATC 120
DB 152 TATACATTTCTCTGGCTAGTGTCTCAAGAGATTATATGCCCCGAGCTGTATATTCATT 211
QY 121 GATGTCAGAAAGGGGACAGATCTATGTTTACTTCCAGCTGTGTACAGAAAAGAGCT 180
DB 212 AAGCTTAAAAAAGGGGACAGATCTATGTGTACTCAAGCTGTGTAAAAAGAAAAGAGCT 271
QY 181 GGAGAGTTTGGGCTGGCAGTGTGTTATGTTGACACAGAGATGAGATGGGAATTTAGGT 240
DB 272 GGAGAAATTTGGGCTGGCAGTGTGTTATGTTGATGCGACAGATGGAGTGGAGCT 331
QY 241 TATTTCCCGCAACTGTTGGAGAGACAGCTGTATACAGAGAGCCACAGAGAGATC 300
DB 332 TATTTCCCGCAACTGTTGGAGAGACAGCTGTATACAGAGAGCTACCAAGAGAT 391
QY 301 CCAACACAGATATGACTTCTCTGTGA 329
DB 392 CCAACACAGATATGACTTCTCTGTGA 420

RESULT 10
US-10-219-475-71
Sequence 71, Application US/10219475
Publication No. US20030187208A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C49
CURRENT FILING DATE: 2002-08-13
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 71
LENGTH: 521
TYPE: DNA
ORGANISM: Homo Sapien
US-10-219-475-71

Query Match 76.4%; Score 252.2; DB 13; Length 521;
Best Local Similarity 85.4%; Pred. No. 1.2e-76;
Matches 281; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 CATGCTGATTTATGATAAACTTCTTCTAAGAGTTGTGGGATGAGAGTGTGTC 60
DB 92 CATGGAATATTTATGACCGCTTAGCTTCAAGAACTGTGTCAGATGATGTGTGTC 151
QY 61 TATACATTTCTCTGGCAAGACAGAGAGATTACATGCCCACTGTAGTTTCATC 120
DB 152 TATACATTTCTCTGGCTAGTGTCTCAAGAGATTATATGCCCCGAGCTGTATATTCATT 211
QY 121 GATGTCAGAAAGGGGACAGATCTATGTTTACTTCCAGCTGTGTACAGAAAAGAGCT 180
DB 212 AAGCTTAAAAAAGGGGACAGATCTATGTGTACTCAAGCTGTGTAAAAAGAAAAGAGCT 271
QY 181 GGAGAGTTTGGGCTGGCAGTGTGTTATGTTGACACAGAGATGAGATGGGAATTTAGGT 240
DB 272 GGAGAAATTTGGGCTGGCAGTGTGTTATGTTGATGCGACAGATGGAGTGGAGCT 331
QY 241 TATTTCCCGCAACTGTTGGAGAGACAGCTGTATACAGAGAGCCACAGAGAGATC 300
DB 332 TATTTCCCGCAACTGTTGGAGAGACAGCTGTATACAGAGAGCTACCAAGAGAT 391

QY 301 CCAACACGATATGACTTCTTGTGA 329
DB 392 CCCACACGATATGACTTCTTGTGCA 420

RESULT 11
US-10-219-480-71
Sequence 71, Application US/10219480
Publication No. US20030187209A1
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey J.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530P1C38
CURRENT APPLICATION NUMBER: US/10/219,480
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 71
LENGTH: 521
TYPE: DNA
ORGANISM: Homo Sapien
US-10-219-480-71

Query Match 76.4%; Score 252.2; DB 13; Length 521;
Best Local Similarity 85.4%; Pred. No. 1.2e-76;
Matches 281; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 CANGGTGATTTATGATAAAGTTCTTGAAGAAAGTTGTGCGATGAGAGTGTGTC 60
DB 92 CATGGAATATTATGAGCCGCTGAGCTTCCAGAAAGCTGTGCGATGATGAGTGTGTC 151
QY 61 TATACATTTCTCTGCGAAGACAGAGATTACATGCCACAGCTGTAGTTGATC 120
DB 152 TATACATTTCTCTGCGTGTGCTCAAGAAAGATTAAAGCCCGAGCTGTAGTTGATC 211
QY 121 GATGTCAAGAAAGGAGCAGATCTATGTTTACTCCAGCTGTGTAACAAAAAGGAGCT 180
DB 212 AACGTAAAAAAGGAGCAGATCTATGTTTACTCAAGCTGTGTAAGAAAAAGGAGCT 271
QY 181 GGAGAGTTTGGGCTGGGAGTGTATTGTGACACAGAGATGAGATGGAAATTGAGCT 240

DB 272 GGAGATTTTGGGCTGGGAGTGTATTGTGATGCGCAGAGACGATGGAGTGTGCT 331

QY 241 TATTTCCCGCAACTTGTGTAAGAGCGGTATATACAGAGGCGCACCAAGAGATC 300
DB 332 TATTTCCCGCAACTTGTGTAAGAGCGGTATATACAGAGGCGCACCAAGAGATC 391

QY 301 CCAACACGATATGACTTCTTGTGA 329
DB 392 CCCACACGATATGACTTCTTGTGCA 420

RESULT 12
US-10-219-483-71
Sequence 71, Application US/10219483
Publication No. US20030187210A1
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey J.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530P1C43
CURRENT APPLICATION NUMBER: US/10/219,483
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 71
LENGTH: 521
TYPE: DNA
ORGANISM: Homo Sapien
US-10-219-483-71

Query Match 76.4%; Score 252.2; DB 13; Length 521;
Best Local Similarity 85.4%; Pred. No. 1.2e-76;
Matches 281; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 CANGGTGATTTATGATAAAGTTCTTGAAGAAAGTTGTGCGATGAGAGTGTGTC 60
DB 92 CATGGAATATTATGAGCCGCTGAGCTTCCAGAAAGCTGTGCGATGATGAGTGTGTC 151
QY 61 TATACATTTCTCTGCGAAGACAGAGATTACATGCCACAGCTGTAGTTGATC 120
DB 152 TATACATTTCTCTGCGTGTGCTCAAGAAAGATTAAAGCCCGAGCTGTAGTTGATC 211
QY 121 GATGTCAAGAAAGGAGCAGATCTATGTTTACTCCAGCTGTGTAACAAAAAGGAGCT 180

Db 212 AAGGTAAAAAGGCGCAGATCTATGTACTCAAGCTGGTAAAGAAATGAGATC 271
QY 181 GGAGAGTTTGGGCTGGCACTGTTTATGTGACACACAGAGATGAGATGGAAATGAGATC 240
Db 272 GGAGAAATTTGGGCTGGCACTGTTTATGTGATGGCCAGAGACAGATGGAGTGGGCT 331
QY 241 TATTTCCCGACGAACCTGTTGTAAGAGAGAGCGGTATACCAAGAGCCCAACAGAGATC 300
Db 332 TATTTCCCGACGAACCTGTTGTAAGAGAGAGCGGTATACCAAGAGATC 391
QY 301 CCAACCGAGATATGACTTCTTCTGTGA 329
Db 392 CCCACCGAGATATGACTTCTTCTGTGA 420

RESULT 13

US-10-219-525-71
; Sequence 71, Application US/10219525
; Publication No. US2003018721A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Geritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C29
; CURRENT APPLICATION NUMBER: US/10/219,525
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-525-71

Query Match 76.4%; Score 252.2; DB 13; Length 521;
Best Local Similarity 85.4%; Pred. No. 1,2e-76;
Matches 281; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
QY 1 CATGCTGATTTATGATTAACCTTTCTTCTAAGAGTGTGTGGGATGAGAGATGCTC 60
Db 92 CATGGAATTTATGACCGCTTACCTTCAAGAGAGCTGTGTGAGATGAGATGCTC 151

QY 61 TATATATTTCTCTGGCAAGACACAGAGATTAACATGCCCCAGACTGTAGTTATC 120
Db 132 TATATATTTCTCTGGCTAGTGTCAAGAGATTAATATGCCCGAGCTGTAGATTCATT 211
QY 121 GATGTCAGAAAGGCGCAGATCTATGTTTACTCAAGCTGTGTACAGAAACCGACT 180
Db 212 AACGTAAAAAGGCGCAGATCTATGTATCTCAAGAGCTGTAAAAAGAAATGGAGCT 271
QY 181 GGAGAGTTTGGGCTGGCACTGTTTATGTGACACACAGAGATGAGATGGAAATGAGATC 240
Db 272 GGAGAAATTTGGGCTGGCACTGTTTATGTGATGGCCAGAGACAGATGGAGTGGGCT 331
QY 241 TATTTCCCGACGAACCTGTTGTAAGAGAGAGCGGTATACCAAGAGCCCAACAGAGATC 300
Db 332 TATTTCCCGACGAACCTGTTGTAAGAGAGAGCGGTATACCAAGAGATC 391
QY 301 CCAACCGAGATATGACTTCTTCTGTGA 329
Db 392 CCCACCGAGATATGACTTCTTCTGTGA 420

RESULT 14

US-10-219-526-71
; Sequence 71, Application US/10219526
; Publication No. US2003018721A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Geritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C41
; CURRENT APPLICATION NUMBER: US/10/219,526
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-526-71

Query Match 76.4%; Score 252.2; DB 13; Length 521;
Best Local Similarity 85.4%; Pred. No. 1,2e-76;
Matches 281; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 30, 2003, 01:34:27 ; Search time 26.6527 Seconds
(Without alignments)
5464.987 Million cell updates/sec

Title: US-10-019-455A-25

Perfect score: 330
Sequence: 1 catggtctattatgatataa.....atatgactctctctgtgaa 330

Scoring table: IDENTITY NUC
Gapop 10*0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*
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2: /cgn2_6/ptodata/2/ina/5B.COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A.COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCtus.COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 65 | 19.7 | 581 | 1 | US-08-578-649-4 |
| 2 | 60.2 | 18.2 | 459 | 1 | US-08-578-649-1 |
| 3 | 55.2 | 16.7 | 330 | 1 | US-08-578-649-18 |
| 4 | 52.6 | 15.9 | 305 | 1 | US-08-578-649-8 |
| 5 | 35.6 | 10.8 | 596 | 1 | US-08-578-649-24 |
| 6 | 35.6 | 10.8 | 3565 | 1 | US-08-578-649-3 |
| 7 | 34.4 | 10.4 | 2644 | 4 | US-09-328-731-35 |
| 8 | 34.4 | 10.4 | 2644 | 4 | US-09-298-731-35 |
| 9 | 34.4 | 10.4 | 7218 | 1 | US-08-232-463-14 |
| 10 | 32.6 | 9.9 | 5822 | 3 | US-08-899-595-5 |
| 11 | 32.6 | 9.8 | 202001 | 4 | US-09-734-674-3 |
| 12 | 32.2 | 9.8 | 654 | 4 | US-09-280-116-57 |
| 13 | 31.8 | 9.6 | 683 | 4 | US-09-088-651-3 |
| 14 | 31.8 | 9.6 | 980 | 4 | US-09-023-942A-30 |
| 15 | 31.8 | 9.6 | 1109 | 3 | US-09-088-651-1 |
| 16 | 31.8 | 9.6 | 1109 | 3 | US-09-088-651-6 |
| 17 | 31.8 | 9.6 | 1110 | 4 | US-09-386-653A-1 |
| 18 | 31.8 | 9.6 | 1130 | 4 | US-09-386-653A-8 |
| 19 | 31.8 | 9.6 | 1212 | 4 | US-09-620-312D-431 |
| 20 | 31.8 | 9.6 | 1751 | 4 | US-09-453-702B-223 |
| 21 | 31.6 | 9.6 | 464 | 4 | US-09-615-192A-236 |
| 22 | 30.8 | 9.3 | 1778 | 1 | US-08-416-870C-3 |
| 23 | 30.4 | 9.2 | 8789 | 1 | US-08-328-254-5 |
| 24 | 30.4 | 9.2 | 10136 | 1 | US-08-353-700-2 |
| 25 | 30.4 | 9.2 | 10136 | 5 | PCT-US95-16216-2 |
| 26 | 30.4 | 9.1 | 13158 | 2 | US-08-687-080-105 |
| 27 | 30 | | | | |

| | | | | | | |
|----|------|-----|-------|---|---------------------|-------------------|
| 28 | 30 | 9.1 | 36412 | 4 | US-08-311-731A-132 | Sequence 132, App |
| 29 | 29.8 | 9.0 | 1500 | 4 | US-09-252-991A-4920 | Sequence 4920, Ap |
| 30 | 29.8 | 9.0 | 1620 | 4 | US-09-252-991A-4922 | Sequence 4922, Ap |
| 31 | 29.8 | 9.0 | 2800 | 3 | US-08-714-918-35 | Sequence 35, Appl |
| 32 | 29.8 | 9.0 | 2800 | 3 | US-09-265-315-35 | Sequence 35, Appl |
| 33 | 29.8 | 9.0 | 2800 | 3 | US-09-265-315-35 | Sequence 35, Appl |
| 34 | 29.8 | 9.0 | 2800 | 3 | US-09-266-417-35 | Sequence 35, Appl |
| 35 | 29.6 | 9.0 | 1425 | 4 | US-09-325-932A-200 | Sequence 200, App |
| 36 | 29.6 | 9.0 | 1878 | 3 | US-08-996-139-14 | Sequence 14, Appl |
| 37 | 29.6 | 9.0 | 1878 | 3 | US-08-996-139-14 | Sequence 14, Appl |
| 38 | 29.6 | 9.0 | 1878 | 3 | US-09-215-649A-14 | Sequence 14, Appl |
| 39 | 29.6 | 9.0 | 1878 | 4 | US-09-577-780-14 | Sequence 14, Appl |
| 40 | 29.6 | 9.0 | 1878 | 4 | US-09-577-800-14 | Sequence 14, Appl |
| 41 | 29.6 | 9.0 | 1878 | 4 | US-09-466-496-14 | Sequence 14, Appl |
| 42 | 29.6 | 9.0 | 1878 | 4 | US-09-871-856-14 | Sequence 14, Appl |
| 43 | 29.6 | 9.0 | 1878 | 4 | US-09-871-291-14 | Sequence 14, Appl |
| 44 | 29.6 | 9.0 | 2938 | 3 | US-08-969-815-3 | Sequence 3, Appl |
| 45 | 29.6 | 9.0 | 2938 | 3 | US-09-120-025-3 | Sequence 3, Appl |

ALIGNMENTS

RESULT 1
US-08-578-649-4
Sequence 4, Application US/08578649
Patent No. 570365
GENERAL INFORMATION:
APPLICANT: Ulrich Bogdan
APPLICANT: Reinhard Butner
APPLICANT: Brigitte Kaluza
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felle & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 MB storage diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-July-1993
ATTORNEY/AGENT INFORMATION:
NAME: Andrew L. Tiajolo
REGISTRATION NUMBER: 31,575
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3864
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 581 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 110..499
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 110..178
FEATURE:

NAME/KEY: mat peptide
LOCATION: 179..499
US-08-578-649-4

Query Match 19.7%; Score 65; DB 1; Length 581;
Best Local Similarity 54.4%; Pred. No. 9.6e-12;
Matches 178; Conservative 0; Mismatches 140; Indels 9; Gaps 2;

QY 3 TGGTGTATTTTGTGATAACTTTCTTCAAGAGTGTGCGATGAGAGTGTCTA 62
DB 175 TGATCGAGCTATGCCCCAGCTGCGTACTGAGAGCTGTGCGACAGAGAGAGCCCA 234
QY 63 TACTATTCTCTGCGACAGACAGAGAGATTACATGCCCCAGACTGTAGTTTATGCA 122
DB 235 TCTATCTCCATGCTGTGCGCTTCCAGAGACTAGTGGCCCCCTATTGCGCTTGTAC 294
QY 123 TGTCAAGAAAGGCGACAGATCTATGTTTACTCCAGCTGTGAACAGAAAACGAGCTGG 182
DB 295 TATATATAGGGGCGCAAGTGTGTATGTCTCTCCAAAGTTG-----AAGGCGCTGGGCG 348
QY 183 AGAGTTTGGGCTGGCACTGTTTATGNGACACACAGATGAGAGGA---ATTGTAG 239
DB 349 CTTTTCGCGGAGGAGGCTTACAGGAGTTTACTATGAGAGCTGCGAGCCCCCTGG 408
QY 240 TTATTTCCCGACACTGTGTGAAGAGCAGCGTGTATACAGAGGCCACCAAGAGAT 299
DB 408 CTATTTCCCGACACTGTGTGCGGAGAGCCTGAACTGCAAACTGGCAAAATTGATAT 468
QY 300 CCCAACACGAGTATGACTTCTTCTG 326
DB 469 GAAAGCCGATCAATGGGATTTCTACTG 495

RESULT 2
US-08-578-649-1
Sequence 1, Application US/08578649
Patent No. 5770366

GENERAL INFORMATION:
APPLICANT: Ulrich Bogdan
APPLICANT: Reinhard Buttner
APPLICANT: Brigitte Kaluza
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-July-1993
ATTORNEY/AGENT INFORMATION:
NAME: Andrew L. Tiajoleff
REGISTRATION NUMBER: 31,575
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 459 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 40..432
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 40..111
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 112..432
US-08-578-649-1

Query Match 18.2%; Score 60.2; DB 1; Length 459;
Best Local Similarity 56.8%; Pred. No. 3.2e-10;
Matches 154; Conservative 0; Mismatches 108; Indels 9; Gaps 2;

QY 4 GGTGATTTATGATTAACCTTTCTTCAAGAGTGTGCGATGAGAGTGTCTAT 63
DB 109 GGTGATTTATGATTAACCTTTCTTCAAGAGTGTGCGATGAGAGTGTCTAT 168
QY 64 ACTATTTCTGCGACAGACAGAGAGATTACATGCCCCAGACTGTAGTTTATGAT 123
DB 169 CTTATCTCCATGCTGTGCGCTTCCAGAGCTAGTGGCCCCGAGATTTCTGACC 228
QY 124 GTCAAGAAAGGCGACAGATCTATGTTTACTCCAGCTGTGAACAGAAAACGAGCTGA 183
DB 229 ATTCACCGGGGCGCAAGTGTGTATGTCTCTCCAAAGTTG-----AAGGCGCTGGGCGG 282
QY 184 GAGTTTGGGCTGGCACTGTTTATGTTGACCCAGAGATGAGATGAGAAATT---GTAGGT 240
DB 283 CTCCTTGGGAGAGCAGCGCTTCAAGAGATTACTATGAGATGTGCTGCTGCTGGGC 342
QY 241 TATTTCCCGACACTGTGTGAAGAGCAGC 271
DB 343 TATTTCCCGACACTGTGTGCGAGAGACC 373

RESULT 3
US-08-578-649-18
Sequence 18, Application US/08578649
Patent No. 5770366

GENERAL INFORMATION:
APPLICANT: Ulrich Bogdan
APPLICANT: Reinhard Buttner
APPLICANT: Brigitte Kaluza
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-July-1993
ATTORNEY/AGENT INFORMATION:
NAME: Andrew L. Tiajoleff
REGISTRATION NUMBER: 31,575
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
TELECOMMUNICATION INFORMATION:

ATTORNEY/AGENT INFORMATION:

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: DE P 43 24 247.2
;; FILING DATE: 20-July-1993

ATTORNEY/AGENT INFORMATION:
NAME: Andrew L. Tiajolo
REGISTRATION NUMBER: 31,575
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 596 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: join(40..111, 40..166, 214..347, 393..503, 549
LOCATION: ..569)
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 40..111
FEATURE:
NAME/KEY: exon
LOCATION: 40..166
FEATURE:
NAME/KEY: exon
LOCATION: 214..347
FEATURE:
NAME/KEY: exon
LOCATION: 393..503
FEATURE:
NAME/KEY: exon
LOCATION: 549..569
NAME/KEY:
LOCATION: one-of(194, 369, 527)
OTHER INFORMATION: /note="N in positions 194, 369
OTHER INFORMATION: and 527 denotes an indefinite number and sequence
OTHER INFORMATION: of nucleotides"
US-08-578-649-24
Query Match 10.8% Score 35.6; DB 1; Length 596;
Best Local Similarity 60.2%; Pred. No. 0.043; 39; Indels 0; Gaps 0;
Matches 59; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
QY 65 CTATTTCCTGGCAAGACAGAGCAAGATTACATGCCCCGACTGTGTTTCATCGATG 124
DB 217 CTATCTCCATGGCTGTGGCCCTTCAGACTACATGCCCCCGACTGCGATTCCAGACCA 276
QY 125 TCAGAAAGGGCAGCAGATCTATGTTTACTCCAGCTG 162
DB 277 TTCACCGGGCCCAAGTGTATGTTCTTCCAGCTG 314

COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-July-1993
ATTORNEY/AGENT INFORMATION:
NAME: Andrew L. Tiajolo
REGISTRATION NUMBER: 31,575
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3565 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 1378..1449
FEATURE:
NAME/KEY: exon
LOCATION: 1378..1504
FEATURE:
NAME/KEY: exon
LOCATION: 1586..1719
FEATURE:
NAME/KEY: exon
LOCATION: 2804..2914
FEATURE:
NAME/KEY: exon
LOCATION: 3232..3252
NAME/KEY:
LOCATION: one-of(2216)
OTHER INFORMATION: /note="N in position 2216
OTHER INFORMATION: denotes an indefinite number and sequence of
OTHER INFORMATION: nucleotides"
US-08-578-649-3
Query Match 10.8% Score 35.6; DB 1; Length 3565;
Best Local Similarity 60.2%; Pred. No. 0.1; 39; Indels 0; Gaps 0;
Matches 59; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
QY 65 CTATTTCCTGGCAAGACAGAGCAAGATTACATGCCCCGACTGTGTTTCATCGATG 124
DB 1589 CTATCTCCATGGCTGTGGCCCTTCAGACTACATGCCCCCGACTGCGATTCCAGACCA 1648
QY 125 TCAGAAAGGGCAGCAGATCTATGTTTACTCCAGCTG 162
DB 1649 TTCACCGGGCCCAAGTGTATGTTCTTCCAGCTG 1686

RESULT 7
US-09-399-913-35
Sequence 35, Application US/09399913
Patent No. 6361971
GENERAL INFORMATION:
APPLICANT: Rhodes, Kenneth
APPLICANT: Betty, Maria
APPLICANT: Ling, Hual-Ping
APPLICANT: An, Wengian
TITLE OF INVENTION: POTASSIUM CHANNEL INTERACTORS AND USES THEREFOR
FILE REFERENCE: KWI-070CP2
CURRENT APPLICATION NUMBER: US/09/399,913
CURRENT FILING DATE: 1999-09-21

| Query Match | Score | DB | Length |
|-----------------|-------|----|------------|
| Best Similarity | 52.1% | | |
| Best Local | 52.1% | | |
| Matches | 100 | 0 | Mismatches |
| | | 91 | Indels |
| | | 1 | Gaps |

| Qy | 133 | GGACGACAGATTCATCTTACTTCACAGCTGTGTAACGAAAAGGAGCTGGAGATTGG | 192 |
|----|------|--|------|
| Db | 1940 | GGATTGGAAGGCCACGTTTAACTTAAGCTGAGAGCTGAGGCTTGAAGGAGCCTGTA | 1996 |

91 GATTACAATGCCCACT
QY

| | Query Match | Similarity | Score | DB L | Length | Best Local | Mismatches | Gaps |
|----|-------------|--|--------------|---------|---------|------------|------------|------|
| | | 10.4% | 34.4 | 1 | 7218 | 2.9% | 157 | 0 |
| | | | Pred. No. | 0.35 | | | Indels | |
| | | | Conservative | | | | | |
| | | | | | | | | |
| QY | 31 | AAGAAGTGTGCGGATGGAGAGTGCTACTATTCTCTGCACAGACAGAA | 90 | | | | | |
| | | ::::::: | ::::::: | ::::::: | ::::::: | | | |
| Dd | 1333 | RR | 127 | | | | | |
| QY | 91 | GATTCGAATGCCCCAGACTGTAGTTCATCAGTCGAAGAGGACAGCATATGTT | 150 | | | | | |
| | | ::::::: | ::::::: | ::::::: | ::::::: | | | |
| Dd | 1273 | RRR | 121 | | | | | |

QY 151 TACTCCAGCTGTGTAACAGAAAGCGAGCTGGAGTTTGGCTGCGAGTTTATGCT 210
DB 1213 RRR 1154
QY 211 GACCACGAGTGTGATGTAGTATTGATTTCCTCCAGCACTGTGTAGAGAGCAG 270
DB 1153 RRR 1094
QY 271 CGGTATACGAGAGCGCCAGCAGAGATCCCAACAC 308
DB 1093 RRR 1056

RESULT 10
US-08-899-595-4/C
Sequence 4, Application US/08899595
Patent No. 6111072

GENERAL INFORMATION:
APPLICANT: Narumiya, Shuh
APPLICANT: Takahashi, No. 6111072uaki
TITLE OF INVENTION: RHO TARGET PROTEIN HUMAN MDIA AND GENE
TITLE OF INVENTION: ENCODING SAME
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,595
FILING DATE: 24-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-242701
FILING DATE: 26-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 9-90170
FILING DATE: 25-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Stephen A. Bent
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 049441/0112
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 5822 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Human
FEATURE:
NAME/KEY: CDS
LOCATION: 28..3972
US-08-899-595-4

Query Match 9.9%; Score 32.6; DB 3; Length 5822;
Best Local Similarity 48.6%; Pred. No. 1.2;
Matches 89; Conservative 0; Mismatches 94; Indels 0; Gaps 0;
QY 114 GTTCATCATGTGTAAGAAAGGCGAGCATCTATCTTACTCCAGCTGTGTAAGAAAA 173

DB 2066 GTACCTCCAGGTAAAGAGGGGGTGAAGATGCAAAACACCCCGAGGCAAGAGCTGCA 2007
QY 174 CGAGCTGAGAGCTTTGGGCTGCGAGCTTTATGCTGACACCGAGATGAGATGGGAT 233
DB 2006 GGAGGAGGAGGAGGAGGAGGAGAGAGAGTGTACTATCCCGAGAGAGCTGTGT 1947
QY 234 TGTAGTTATTTCCCGAGCACTGTGTGAGAGCAGCTGTATACAGAGGCCACCA 293
DB 1946 GGAATATATGTGCGAGAGTCCACAGTAAAGAGGGCGAGGGGAAACAGACGACACTA 1887
QY 294 GGA 296
DB 1886 GGA 1884

RESULT 11
US-08-899-595-5
Sequence 5, Application US/08899595
Patent No. 6111072

GENERAL INFORMATION:
APPLICANT: Narumiya, Shuh
APPLICANT: Takahashi, No. 6111072uaki
TITLE OF INVENTION: RHO TARGET PROTEIN HUMAN MDIA AND GENE
TITLE OF INVENTION: ENCODING SAME
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,595
FILING DATE: 24-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-242701
FILING DATE: 26-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 9-90170
FILING DATE: 25-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Stephen A. Bent
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 049441/0112
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 5822 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ANTI-SENSE: YES
ORIGINAL SOURCE:
ORGANISM: Human
US-08-899-595-5

Query Match 9.9%; Score 32.6; DB 3; Length 5822;
Best Local Similarity 48.6%; Pred. No. 1.2;
Matches 89; Conservative 0; Mismatches 94; Indels 0; Gaps 0;
QY 114 GTTCATCATGTGTAAGAAAGGCGAGCATCTATCTTACTCCAGCTGTGTAAGAAAA 173

Db 3757 GTACCTCCAGGTAAGAGAGGGGCTGAGAGATGCCAAACCCCCAGCAAGAGGTGCA 3816
QY 174 CGAGAGCTGAGAGATTTTGGCTGCGAGTGTATGTTGACACACAGATGAGATGGAAAT 233
Db 3817 GGAGGAG 3876
QY 234 TGAAGTATTTTCCCGACCACTTGTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 293
Db 3877 GGAATTAATAGTCCAGAGTCAACAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAG 3936
QY 294 GGA 296
Db 3937 GGA 3939

RESULT 12

US-09-734-674-3
Sequence 3, Application US/09734674
Patent No. 6498022
GENERAL INFORMATION:
APPLICANT: WEI, Ming-Hui et al
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLO01018
CURRENT APPLICATION NUMBER: US/09/734,674
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 202001
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)...(202001)
OTHER INFORMATION: n = A,T,C or G
US-09-734-674-3

Query Match 9.8%; Score 32.2; DB 4; Length 202001;
Best Local Similarity 49.7%; Pred. No. 8.9;
Matches 82; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 65 CTATTTCTGTGCGAAG 124
Db 183409 CTAGAACTCAG 183468
QY 125 TCAG 184
Db 183469 GAAAGTCAG 183528
QY 185 AGTTTGGGCTGAG 229
Db 183529 AGTCCAG 183573

RESULT 13

US-09-280-116-57/C
Sequence 57, Application US/09280116A
Patent No. 6331427
GENERAL INFORMATION:
APPLICANT: ROBISON, Keith E.
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
FILE REFERENCE: 5800-24, 035800/176965
CURRENT APPLICATION NUMBER: US/09/280,116A
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 268
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 57
LENGTH: 654
TYPE: DNA
ORGANISM: Homo sapiens

FEATURE:
OTHER INFORMATION: trypsin-like serine proteases
US-09-280-116-57

Query Match 9.6%; Score 31.8; DB 4; Length 654;
Best Local Similarity 59.3%; Pred. No. 0.79;
Matches 54; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 198 CAGTGTATGAGTACCAAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 257
Db 625 CGGTGTCTTGTGTGAG 566
QY 258 CGTGAAG 288
Db 565 TCTGAGAGATCCGCGGTTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 535

RESULT 14

US-09-088-651-3/C
Sequence 3, Application US/09088651
Patent No. 6165771
GENERAL INFORMATION:
APPLICANT: BURGESS, NICOLA A.
APPLICANT: CLINKENBEARD, HELEN E.
APPLICANT: SOUTHAN, CHRISTOPHER D.
TITLE OF INVENTION: NOVEL COMPOUNDS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: RATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088,651
FILING DATE: JUNE 1, 1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB9712088.5
FILING DATE: 10-JUNE-1997
APPLICATION NUMBER: EP 97308295.1
FILING DATE: 17-OCT-1997
APPLICATION NUMBER: GB 9803650.2
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F.
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH30358
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 683 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-088-651-3

Query Match 9.6%; Score 31.8; DB 3; Length 683;
Best Local Similarity 59.3%; Pred. No. 0.81;
Matches 54; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 198 CAGTGTATGAGTACCAAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 257

DB 369 CGGTGCTTCTGCTAGACGACGAGTTGCACTTGCGTGTGTCGATGATGCGGACACGCGAGTT 310

QY 258 GGTGAGAGACGACCGCTGTATACGAGAGGCC 288

DB 309 TCTGACGAGATCCGCGCTTCGGGACGAGAGGTC 279

RESULT 15

US-09-023-942A-30/C

; Sequence 30, Application US/09023942A

; Patent No. 6479274

; GENERAL INFORMATION:

; APPLICANT: (US only) ANTALIS Toni Marie and HOOVER John David

; TITLE OF INVENTION: NOVEL MOLECULES

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER

; STREET: 400 GARDEN CITY PLAZA

; CITY: GARDEN CITY

; STATE: NEW YORK

; COUNTRY: USA

; ZIP: 11530

; COMPUTER READABLE FORM:

; MEDIUM TYPE: floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/023,942A

; FILING DATE: 13-FEB-1998

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: POS101/97

; FILING DATE: 13-FEB-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: P0422/97

; FILING DATE: 18-NOV-1997

; PRIOR APPLICATION DATA: International PCT Application

; APPLICATION NUMBER:

; FILING DATE: 13-FEB-1998

; ATTORNEY/AGENT INFORMATION:

; NAME: DIGILIO, FRANK S

; REGISTRATION NUMBER: 31,346

; REFERENCE/DOCKET NUMBER: 11168

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (516) 742 4343

; TELEFAX: (516) 742 4366

; TELEX: 230 901 SANS UR

; INFORMATION FOR SEQ ID NO: 30:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 980 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

; US-09-023-942A-30

; Query Match 9.6%; Score 31.8; DB 4; Length 980;

; Best Local Similarity 59.3%; Pred. No. 0.96;

; Matches 54; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 198 CAGTGTATTAGTACACACAGAGATGAGATGCGAATTGATTTTCCCGAGCACTT 257

DB 525 CGGTGCTTCTGCTAGACGACGTTGCACTTGCGTGTGTCGATGATGCGGACACGCGAGTT 466

QY 258 GGTGAGAGACGACCGCTGTATACGAGAGGCC 288

DB 465 TCTGACGAGATCCGCGCTTCGGGACGAGAGGTC 435

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OM protein - protein search, using sw model

Run on: December 29, 2003, 16:03:18 ; Search time 11.4006 Seconds
(without alignments)
927.898 Million cell updates/sec

Title: US-10-019-455A-26

Perfect score: 591
Sequence: 1 HGVPMDKLSKKLCADCECV.....RVYQATKEIPTDIDFCE 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length DB | ID | Description |
|------------|-------|---------------|-----------|----|---------------------------|
| 1 | 261.5 | 44.2 | 131 | 2 | 138019 melanoma-derived g |
| 2 | 91.5 | 15.5 | 844 | 1 | TVMSV transforming prote |
| 3 | 89.5 | 15.1 | 839 | 1 | TVHVV transforming prote |
| 4 | 84.5 | 14.3 | 878 | 2 | IS1940 gene VAV2 protein |
| 5 | 81.5 | 13.8 | 1215 | 2 | T32734 myosin-1A - Acanth |
| 6 | 78.5 | 13.3 | 1589 | 1 | RCBVC5 cell division cont |
| 7 | 77 | 13.0 | 695 | 2 | SG6662 protein-glutamine |
| 8 | 74.5 | 12.6 | 1097 | 2 | T31504 hypothetical prote |
| 9 | 73 | 12.4 | 994 | 2 | T21356 hypothetical prote |
| 10 | 72 | 12.2 | 308 | 2 | T48525 hypothetical prote |
| 11 | 72 | 12.2 | 585 | 2 | G96995 ATP-dependent RNA |
| 12 | 72 | 12.2 | 636 | 2 | T06793 receptor kinase ho |
| 13 | 71.5 | 12.1 | 847 | 1 | A53800 mixed-lineage prot |
| 14 | 71 | 12.0 | 259 | 2 | C64427 hypothetical prote |
| 15 | 71 | 12.0 | 373 | 2 | T36655 VHS domain contain |
| 16 | 70.5 | 11.9 | 303 | 2 | A84055 transcritpion regu |
| 17 | 70.5 | 11.9 | 535 | 1 | S24550 protein-tyrosine k |
| 18 | 70.5 | 11.9 | 506 | 1 | S24553 protein-tyrosine k |
| 19 | 70.5 | 11.9 | 718 | 2 | T03310 hypothetical prote |
| 20 | 70.5 | 11.9 | 839 | 2 | G96719 probable chromet |
| 21 | 70.5 | 11.9 | 859 | 2 | S13030 3',5'-cyclic-GMP p |
| 22 | 70 | 11.8 | 486 | 2 | S29302 allin lyase (EC 4 |
| 23 | 70 | 11.8 | 722 | 2 | G86746 hypothetical prote |
| 24 | 69.5 | 11.8 | 344 | 2 | C81920 S-receptor kinase |
| 25 | 69.5 | 11.8 | 413 | 2 | T03696 probable peroxisom |
| 26 | 69 | 11.7 | 288 | 2 | T38696 probable signal tr |
| 27 | 69 | 11.7 | 670 | 2 | S67383 hypothetical prote |
| 28 | 69 | 11.7 | 816 | 2 | T17257 hypothetical prote |
| 29 | 68.5 | 11.6 | 164 | 2 | F96968 hypothetical prote |

| | | | | | |
|----|------|------|------|---|---------------------------|
| 30 | 68.5 | 11.6 | 377 | 2 | S08636 nck protein - huma |
| 31 | 68.5 | 11.6 | 461 | 2 | AF2340 sugar ABC transpor |
| 32 | 68.5 | 11.6 | 618 | 2 | G59432 MacGAP protein (Im |
| 33 | 68 | 11.5 | 413 | 2 | T31051 transposase homolo |
| 34 | 68 | 11.5 | 415 | 2 | AG0391 conserved hypothet |
| 35 | 68 | 11.5 | 680 | 2 | UC5133 protein-glutamine |
| 36 | 68 | 11.5 | 954 | 1 | S68178 mixed-lineage prot |
| 37 | 68 | 11.5 | 1077 | 2 | A96533 probable zinc meta |
| 38 | 67.5 | 11.4 | 339 | 2 | UT0668 hypothetical 38.8K |
| 39 | 67.5 | 11.4 | 383 | 2 | S24156 polygalacturonase |
| 40 | 67.5 | 11.4 | 1560 | 2 | T30282 calcium-binding pr |
| 41 | 67 | 11.3 | 1173 | 2 | T08610 major core capsid |
| 42 | 66.5 | 11.3 | 496 | 2 | A12354 hypothetical prote |
| 43 | 66.5 | 11.3 | 505 | 2 | I37206 protein-tyrosine k |
| 44 | 66.5 | 11.3 | 540 | 2 | A70358 topoisomerase I - |
| 45 | 66.5 | 11.3 | 616 | 2 | T03027 receptor-like prot |

ALIGNMENTS

RESULT 1
138019
melanoma-derived growth regulatory protein M1A - human
C:Species: Homo sapiens (man)
C>Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 04-Mar-2000
C:Accession: I38019; S40238
R:Blesch, A.; Bossehoff, A.K.; Apfel, R.; Behl, C.; Hesseoerfer, B.; Schmitt, A.; Jac
Cancer Res. 54, 5695-5701, 1994
A>Title: Cloning of a novel malignant melanoma-derived growth-regulatory protein, M1A.
A:Reference number: I38019; MUID:95007612; PMID:7923218
A:Accession: I38019
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-131 <RES>
A:Cross-references: EMBL:X75450; NID:9438057; PIDN:CAAS3203.1; PID:9438058
C:Genetics:
A:Gene: mla
C:Superfamily: human melanoma-derived growth regulatory protein M1A

Query Match 44.2% Score 261.5; DB 2; Length 131;
Best Local Similarity 45.4%; Pred. No. 4.3e-20;
Matches 49; Conservative 24; Mismatches 30; Indels 5; Gaps 3;

| | | |
|----|----|---|
| Oy | 5 | MDKLSKKLCADCECVTTISLAPQBDYNAPDCRFIDVKKGQIYYYSKLVTEGAGE-F 63 |
| Db | 27 | MPLIADPKLCADQCSHPISMAVALQDYAPDCRFILIRHGQVYVFSKL---KGRGLF 83 |
| Oy | 64 | WAGSVYGDHODEMGI-VGYPFSLVKEQRYQATKEIPTDIDFCE 110 |
| Db | 84 | WGSVQGDYVDLAARLGFPPSSIVREDQTLKSGKVDVKTDMDFYQO 131 |

RESULT 2

TVMSV
transforming protein vav - mouse
C:Species: Mus musculus (house mouse)
C>Date: 03-May-1994 #sequence_revision 16-Feb-1996 #text_change 18-Jun-1999
C:Accession: A61187; A39576; S36941; S23669
R:Coppola, J.; Bryant, S.; Koda, T.; Conway, D.; Barbacid, M.
Cell Growth Differ. 2, 95-105, 1991
A>Title: Mechanism of activation of the vav protooncogene.
A:Reference number: A61187; MUID:91299578; PMID:2069873
A:Accession: A61187
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
R:Katayev, S.; Cleveland, J.L.; Heslop, H.E.; Pulido, D.
Mol. Cell. Biol. 11, 1912-1920, 1991
A>Title: Loss of the amino-terminal helix-loop-helix domain of the vav proto-oncogene
A:Reference number: A39576; MUID:91172176; PMID:2005887
A:Accession: A39576
A:Molecule type: mRNA

A:Residues: 1-28, 'E', 30-93 <KAT>
 A:Cross-references: GB:MS9833; NID:9202343; PIDN:AAA63402.1; PID:9202344
 R:Adams, J.M.
 A:Note: Submitted to the EMBL Data Library, January 1992
 A:Reference number: S36941
 A:Accession: S36941
 A:Molecule type: mRNA
 A:Residues: 1-523, 'D', 'L', 'M', 'P', 'M', 'O', 'V', 'L', 'K', 'Y', 'H', 'L', 'L', 'Q', 'E', 'L', 'V', 'K', '346-347, 'Q', 'D', 'A', 'T', '352, 'K', '354, 'N', '355-453, 'R', '45
 A:Cross-references: EMBL:X64361; NID:955220; PIDN:CAA5713.1; PID:955221
 R:Adams, J.M.; Houston, H.; Allen, J.; Lints, T.; Harvey, R.
 A:Note: The hematopoietically expressed vav proto-oncogene shares homology with the dbl
 A:Reference number: S36659; MUID:92228488; PMID:1565462
 A:Accession: S36659
 A:Reference number: S36659; MUID:92228488; PMID:1565462
 A:Note: The complete sequence was submitted to Genbank; see S36941
 A:Gene: vav
 C:Superfamily: vav transforming protein; CDC24 homology; protein kinase C zinc-binding
 C:Keywords: phosphoprotein; transforming protein; zinc finger
 F:132-102/Region: leucine-rich
 F:132-176/Region: acidic
 F:194-458/Domain: CDC24 homology <CD24>
 F:336-340/Region: proline-rich
 F:486-493/Region: nuclear location signal
 F:515-563/Region: protein kinase C zinc-binding repeat homology <KZ1>
 F:528-548/Region: zinc finger CCCC motif
 F:553-566/Region: zinc finger HCHC motif
 F:575-582/Region: nuclear location signal
 F:604-654/Domain: SH3 homology <SH3A>
 F:606-609/Region: proline-rich
 F:670-761/Domain: SH2 homology <SH2>
 F:788-836/Domain: SH3 homology <SH3B>
 F:439/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

Query Match 15.5%; Score 91.5; DB 1; Length 844;
 Best Local Similarity 32.9%; Pred. No. 0.2;
 Matches 23; Conservative 14; Mismatches 20; Indels 13; Gaps 3;

QY 26 ARAQEDYNAPDCRFIDVKKGQGIYYSKLVTEGAGFEWAGSVYGDHDEMGIVGYFSPN 85
 DB 786 AKARYDFPCARDRELSLKEGDII---KILNKKGGQGMWKGELIYGR-----IGWFPAN 834

QY 86 LVKEGRVYGE 95
 DB 835 YVEED--YSE 842

RESULT 3
 Transforming protein vav - human (fragments)
 N:Alternate names: finger protein vav
 C:Species: Homo sapiens (man)
 C:Date: 31-Mar-1991 #sequence_revision 03-May-1996 #ext_change 18-Jun-1999
 A:Accession: B39576; S05382
 R:Katzav, S.; Cleveland, J.L.; Heslop, H.E.; Pulido, D.
 A:Title: Loss of the amino-terminal helix-loop-helix domain of the vav proto-oncogene ac
 A:Reference number: A39576; MUID:91172176; PMID:2005867
 A:Accession: B39576
 A:Molecule type: mRNA
 A:Residues: 1-61 <KAT>
 A:Cross-references: GB:MS9834; NID:9340189; PIDN:AAA63267.1; PID:9340190
 A:Note: The authors translated the codon CAA for residue 6 as Gln, CAG for residue 13 as
 R:Katzav, S.; Martin-Zanca, D.; Barbacid, M.
 EMBL J. 8, 2283-2290, 1989
 A:Title: vav, a novel human oncogene derived from a locus ubiquitously expressed in hema
 A:Reference number: S05382; MUID:90005433; PMID:2477241
 A:Accession: S05382
 A:Molecule type: mRNA
 A:Residues: 62-839 <KAT2>
 A:Cross-references: EMBL:X16316
 R:Adams, J.M.; Houston, H.; Allen, J.; Lints, T.; Harvey, R.
 Oncogene 7, 611-618, 1992

A:Title: The hematopoietically expressed vav proto-oncogene shares homology with the d
 A:Reference number: S23669; MUID:92228488; PMID:1565462
 A:Accession: S23669
 A:Note: In the sequence from mouse the authors find three additional nucleotides that
 occurred in the published human sequences
 C:Comment: In comparing these sequences with the mouse (see PIR:TVMSV), there appear
 C:Genetics:
 A:Gene: GDB:VAV1; VAV
 A:Cross-references: GDB:127112; OMIM:164875
 A:Map position: 19p13.3-19p13.3
 C:Superfamily: vav transforming protein; CDC24 homology; protein kinase C zinc-binding
 C:Keywords: phosphoprotein; transforming protein; zinc finger
 F:126-170/Region: acidic
 F:188-452/Domain: CDC24 homology <CD24>
 F:509-557/Domain: protein kinase C zinc-binding repeat homology <KZ2>
 F:522-542/Region: zinc finger CCCC motif
 F:547-560/Region: zinc finger HCHC motif
 F:598-648/Domain: SH3 homology <SH3A>
 F:664-756/Domain: SH2 homology <SH2>
 F:783-831/Domain: SH3 homology <SH3B>
 F:433/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

Query Match 15.1%; Score 89.5; DB 1; Length 839;
 Best Local Similarity 32.9%; Pred. No. 0.32;
 Matches 23; Conservative 14; Mismatches 20; Indels 13; Gaps 3;

QY 26 ARAQEDYNAPDCRFIDVKKGQGIYYSKLVTEGAGFEWAGSVYGDHDEMGIVGYFSPN 85
 DB 781 AKARYDFPCARDRELSLKEGDII---KILNKKGGQGMWKGELIYGR-----VGWFPAN 829

QY 86 LVKEGRVYGE 95
 DB 830 YVEED--YSE 837

RESULT 4
 VAV2 protein - human
 C:Species: Homo sapiens (man)
 C:Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #ext_change 16-Jul-1999
 A:Accession: I51940
 R:Henske, E.P.; Short, M.P.; Jozwiak, S.; Bovey, C.M.; Ramlakhan, S.; Haines, J.L.; Kw
 Ann. Hum. Genet. 59, 25-37, 1995
 A:Title: Identification of VAV2 on 9q34 and its exclusion as the tubercous sclerosis ge
 A:Reference number: I51940; MUID:95283235; PMID:7762962
 A:Accession: I51940
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-878 <RES>
 A:Cross-references: GB:S76992; NID:9133345; PIDN:AA834377.1; PID:9133346
 C:Genetics:
 A:Gene: GDB:VAV2
 A:Cross-references: GDB:370880; OMIM:600428
 A:Map position: 9q34-q34
 C:Superfamily: vav transforming protein; CDC24 homology; protein kinase C zinc-binding
 F:198-462/Domain: CDC24 homology <CD24>
 F:524-572/Domain: protein kinase C zinc-binding repeat homology <KZ2>
 F:673-764/Domain: SH2 homology <SH2>
 F:823-872/Domain: SH3 homology <SH3>

Query Match 14.3%; Score 84.5; DB 2; Length 878;
 Best Local Similarity 27.6%; Pred. No. 1.1;
 Matches 21; Conservative 20; Mismatches 22; Indels 13; Gaps 3;

QY 20 VYT---ISLAQEDYNAPDCRFIDVKKGQGIYYSKLVTEGAGFEWAGSVYGDHDEMG 76
 DB 812 VETPVVIGTAVARVYFALPDWEISLRGQDVYRYSRIGGQG---WKKG-----ETN 861

QY 77 GIVGYFSPNIVKEGRV 92
 DB 862 GRIGWFPSTVYEEBGI 877

RESULT 5
T32734
A:Gene: myosin-1A - Acanthamoeba castellanii
C:Species: Acanthamoeba castellanii
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 08-Sep-2000
C:Accession: T32734
R:Lee, W.L.; Ostap, E.M.; Zot, H.G.; Pollard, T.D.
Submitted to the EMBL Data Library, August 1998
A:Description: Hydrodynamic and ligand binding properties of Acanthamoeba myosin-1A GFA/
A:Reference number: Z21216
A:Accession: T32734
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1215 <UEB>
A:Cross-references: EMBL:AF085185; NID:g3599477; PID:g3599478; PIDN:AA03357.1
A:Experimental source: strain Neff
A:Genetics:
A:Gene: MYA
A:Initiators: 1/3; 41/3; 72/2; 103/2; 162/3; 184/1; 217/1; 296/1; 340/3; 390/3; 447/3; 500/3
A:Superfamily: protozoan myosin heavy chain IB; myosin motor domain homology; SH3 homolo
F;14-674/Domain: myosin motor domain homology <MMO>
Query Match 13.8%; Score 81.5; DB 2; Length 1215;
Best Local Similarity 30.0%; Pred. No. 3.3;
Matches 21; Conservative 13; Mismatches 23; Indels 13; Gaps 2;
OY 20 VYTSLARAEEDYNAPOCRFDYKKGQIYYSKLVTEENGAEFFWAGSYVGDHDEMGIV 79
Db 1158 VPTGRCRALYDYGAGADELTLAGDVIVDICK-----SGEWEGTILNGK-----T 1204
OY 80 GYFSPNTLWKE 89
Db 1205 GVDPANVYED 1214
RESULT 6
RGBYCS
cell division control protein CDC25 - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein L2142.6; protein YLR310C
C:Species: Saccharomyces cerevisiae
C>Date: 31-Mar-1988 #sequence_revision 31-Mar-1993 #text_change 21-Jul-2000
C:Accession: A26596; S51442; A23444; S43051; S47990
R:Broek, D.; Toda, T.; Michaeli, T.; Levin, L.; Bitchmeier, C.; Zoller, M.; Powers, S.;
Cell 48; 789-799, 1987
A>Title: The S. cerevisiae CDC25 gene product regulates the PAS/adenylylate cyclase pathwa
A:Reference number: A26596; MUID:87131091; PMID:355497
A:Accession: A26596
A:Molecule type: DNA
A:Residues: 1-1589 <BRO>
A:Cross-references: EMBL:M15458; NID:g171184; PIDN:AAA4478.1; PID:g171185
R:Pauley, A.
Submitted to the EMBL Data Library, November 1994
A:Description: The sequence of S. cerevisiae cosmid L2142.
A:Reference number: S51437
A:Accession: S51442
A:Molecule type: DNA
A:Residues: 1-1589 <PAU>
A:Cross-references: EMBL:U17247; NID:g577216; PIDN:AA067360.1; PID:g577222; GSPDB:GN0001
R:Caumont, J.H.; Kalekine, W.; Gondre, B.; Garreau, H.; Boy-Marcotte, E.; Jaquet, M.
EMBO J. 5; 375-380, 1986
A>Title: Characterization, cloning and sequence analysis of the CDC25 gene which control
A:Reference number: A23444; MUID:86220116; PMID:3011405
A:Accession: A23444
A:Molecule type: DNA
A:Residues: 1-496, 'Y', 498-953, 'LSVINMISR', 964-1589 <CAN>
A:Cross-references: EMBL:X03579; NID:g3483; PIDN:CAA2759.1; PID:g3484
R:Daniel, J.H.
Curr. Genet. 10; 879-885, 1986
A>Title: The CDC25 "Start" gene of Saccharomyces cerevisiae: sequencing of the active C-
A:Reference number: S43051; MUID:88194639; PMID:3329037
A:Accession: S43051
A:Molecule type: DNA
A:Residues: 877-1589 <DAN>

A:Cross-references: EMBL:X03579
A:Genetics:
A:Gene: SGD:CD25; CTN1; MIPS:YLR310C
A:Cross-references: SGD:S0004301; MIPS:YLR310C
A:Map position: 12R
A:Function:
A:Description: positive control of level of cellular cAMP at the stage at which the ce
C:Superfamily: budding yeast CDC25; CDC25-type guanine nucleotide exchange activator h
C:Keywords: cell cycle control; transmembrane protein
P;65123/Domain: SH3 homology <SH3>
F;1301-1542/Domain: CDC25-type guanine nucleotide exchange activator homology <SOS>
Query Match 13.3%; Score 78.5; DB 1; Length 1589;
Best Local Similarity 27.0%; Pred. No. 9.3;
Matches 24; Conservative 18; Mismatches 36; Indels 11; Gaps 4;
OY 8 ISSKLCADDEECVYTSILARAQEDYNAP-----DCRFDYKKGQIYYSKLVTEENGAE 62
Db 45 ISSSTSELTISIRDIGVVAAPFNYPRIKDDSSQLLSVOGGETIYLNK-----NSSG- 99
OY 63 FWAGSYVGDHDEMGIVGYFSPNTLWKEOR 91
Db 100 WWDGLVIDDSNGKVN-RGWFQNGRPLR 127
RESULT 7
S6662
protein-glutamine gamma-glutamyltransferase (EC 2.3.2.13) - red sea bream
N:Alternate names: transglutaminase
C:Species: Chrysophrys major (red sea bream)
C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 18-Jun-1999
C:Accession: S66662
R:Yasuda, H.; Nakaniishi, K.; Kumazawa, Y.; Nagase, K.; Mocchi, M.; Matsui, H.
Eur. J. Biochem. 232; 411-419, 1995
A>Title: Tissue-type transglutaminase from red sea bream (Pagrus major). Sequence anal
A:Reference number: S66662; MUID:96035874; PMID:7556189
A:Accession: S66662
A:Molecule type: mRNA
A:Residues: 1-695 <YAS>
A:Cross-references: GB:S79761; NID:g1176434; PIDN:AA03570.1; PID:g1176435
C:Superfamily: protein-glutamine gamma-glutamyltransferase
C:Keywords: aminoacyltransferase
F;212/Active site: Cys #status predicted
Query Match 13.0%; Score 77; DB 2; Length 695;
Best Local Similarity 27.5%; Pred. No. 5.3;
Matches 22; Conservative 20; Mismatches 28; Indels 10; Gaps 3;
OY 31 DYNAPDCRFIDYKKGQIYYSKLVTEENGAG---EFWAGSYVGDHDEMGIVGYFSPNTLV 87
Db 393 EVNADTYWIVQDQGR-----RKITHASVGNKISTKSYVGNHREDVTLHYKYPEGSG 447
OY 88 KEORVYGEATFKET--PTTDI 105
Db 448 KEREVYKAGRRVTEPSNEI 467
RESULT 8
T31504
hypothetical protein Y116A8C.36 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T31504
R:McMurray, A.
Submitted to the EMBL Data Library, October 1999
A:Reference number: Z21041
A:Accession: T31504
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1097 <MIL>
A:Cross-references: EMBL:AL117204; PIDN:CA055138.1; CESP:Y116A8C.36
A:Experimental source: clone Y116A8C
A:Genetics:

A:Gene: CESP:Y116A8C.36
A:Introns: 50/3; 245/3; 411/3; 486/3; 697/1; 820/3; 926/2

Query Match 12.6%; Score 74.5; DB 2; Length 1097;

Best Local Similarity 29.7%; Pred. No. 16;

Matches 22; Conservative 10; Mismatches 33; Indels 9; Gaps 2;

QY 17 EECVYITSLARAQEDYNAPDCRFIDVKKGOQIYYVSKLTVNGAGFEFMAGSVYGDHODEM 76
DB 1033 EEAASPARATAVVDYEAASQPDGLGXTGDIYI-----IVIDKSAEWMNS-----GHRQDP 1083

QY 77 GIVGVFPPSNLYKEQ 90
DB 1084 SKSGIFPSNYVOQ 1097

RESULT 9
T21356
Hypothetical protein F25H2.13 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999

C:Accession: T21356; T21540

R:Wilkinson, J.

submitted to the EMBL Data Library, September 1996

A:Reference number: Z19411

A:Accession: T21356

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-994 <W12>

A:Cross-references: EMBL:Z79754; PIDN:CA802102.1; GSPDB:GN00019; CESP:F25H2.13

A:Experimental source: clone F25H2

R:Wilkinson, J.

submitted to the EMBL Data Library, December 1996

A:Reference number: Z19437

A:Accession: T21540

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-994 <W12>

A:Cross-references: EMBL:Z83224; PIDN:CA805720.1; GSPDB:GN00019; CESP:F25H2.13

A:Experimental source: clone F29C6

C:Genetics:

A:Gene: CESP:F25H2.13

A:Map position: 1

A:Introns: 129/2; 177/1; 206/2; 349/3; 436/3; 506/2; 626/3; 689/3; 772/3; 845/3; 903/3;

Query Match 12.4%; Score 73; DB 2; Length 994;

Best Local Similarity 27.6%; Pred. No. 21;

Matches 37; Conservative 20; Mismatches 45; Indels 32; Gaps 9;

QY 5 MDKLSSKKL-----CADECYVITSLARAQEDYNAPDCRFIDVKKGOQIYYVSK- 53

DB 339 MDKLSSKKLSSVPLSGASDGE-ILLETAKAGFDANSVE-RLVLDLRDAISYLSKN 396

QY 54 ---LVTEAGAG-----EFWAGSVYGDH-QDEMGITG-----YFPSNLYKEQRYQE 95

DB 397 EEVALTEKDGKMEKVADEFL-LSYSTHADVAANAAGETVTKLVDRVDKTVARNKCLYIQ 455

QY 96 ATKETPTTIDFFC 109

DB 456 KDKMEKLTIKYFC 469

RESULT 10

T48525
Hypothetical protein T22P22.50 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000

C:Accession: T48525

R:Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft,

submitted to the Protein Sequence Database, April 2000

A:Reference number: Z24490

A:Accession: T48525

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-308 <BEV>

A:Cross-references: EMBL:AL163814

A:Experimental source: cultivar Columbia; BAC clone T22P22

C:Genetics:

A:Map position: 5

A:Introns: 63/3; 117/3; 135/3; 180/3

A:Note: T22P22.50

Query Match 12.2%; Score 72; DB 2; Length 308;

Best Local Similarity 37.2%; Pred. No. 7;

Matches 16; Conservative 6; Mismatches 19; Indels 2; Gaps 1;

QY 44 KGOQIYYVSKLTVNGAGFEFMAGSVYGDHODEMGITGVYFPSNL 86
DB 168 KGOQIYYVSKLTVNGAGFEFMAGSVYGDHODEMGITGVYFPSNL 208

RESULT 11

G96995
ATP-dependent RNA helicase, superfamily II [imported] - Clostridium acetobutylicum

C:Species: Clostridium acetobutylicum

C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001

C:Accession: G96995

R:Nolling, U.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Le

J. Bacteriol. 183, 4823-4838, 2001

J. Daily, M.C.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C

A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: G96995

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-585 <KDM>

A:Cross-references: GB:AE001437; PIDN:AAK78754.1; PID:G15023664; GSPDB:GN00168

A:Experimental source: Clostridium acetobutylicum ATCC824

C:Genetics:

A:Gene: CAC0778

Query Match 12.2%; Score 72; DB 2; Length 585;

Best Local Similarity 29.4%; Pred. No. 14;

Matches 30; Conservative 13; Mismatches 22; Gaps 5;

QY 12 KLCADG---ECVYITSLARAQEDYNAPDCRFIDVKKGOQIYYVSK---LVTEAGAG 62

DB 272 KCCEDEYEIKYKRAIPIEVEDSEFN-----YKDKEGDAVVFSSKVLLEAQSARQ 326

QY 63 FNAAGSVYGDHODEMGITGVYFPSNLVKEQRYQATKEIPTTD 104

DB 327 IKASITVGDLPPEVRKQIY-----EQTIKKE-TKLVTTD 360

RESULT 12

T06793
receptor kinase homolog LrK10 - wheat

N:Alternate names: rust resistance kinase Lr10

C:Species: Triticum aestivum (common wheat)

C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000

C:Accession: T06793

R:Feuillet, C.; Schachermayer, G.; Keller, B.

Plant J. 11, 45-52, 1997

A:Title: A novel class of receptor-like kinase mapping to the Lr10 locus in wheat.

A:Reference number: Z15819; MUID:97177795; PMID:9025301

A:Accession: T06793

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-636 <FEU>

A:Cross-references: EMBL:U51330; NID:G1680685; PIDN:AAC49629.1; PID:G1680686

A:Experimental source: leaf

C:Genetics:

A:Gene: LrK10

A:Map position: 1

A:Introns: 272/1; 280/1

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homc

Query Match 12.2%; Score 72; DB 2; Length 636;
 Best Local Similarity 25.4%; Pred. No. 16;
 Matches 29; Conservative 20; Mismatches 49; Indels 16; Gaps 5;

QY 1 HGVFMD----KLS--KLCADBECCYTTSLARQEDYNAPDC--RFIDVKKGGQIY 49
 Db 470 HNILDLYFNFKISDFGLAKCARDQSIVTLTAARGTGYAPLAYSRRNFGVSYKADVY 529

QY 50 VYSKLVNENGAGFWMAGSVYGDHODEMGIVGFPSPNVKEQRYQATKEIPTT 103
 Db 530 SFGMLVYEMVSGRRNSDPRIQS-QDDV---YLPBWYIEKYNGEELALITLETT 578

RESULT 13

A53800
 mixed-lineage protein kinase (EC 2.7.1.-) 3 - human
 A:Accession: A53800; EMBL:U07747; NID:9464027; PIDN:AA19647.1; PID:9464028
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-847 <GAL>
 A:Cross-references: GB:U07747; NID:9464027; PIDN:AA19647.1; PID:9464028
 R:Ring, Y.L.; Leung, I.W.; Heng, H.H.; Tsui, L.C.; Lassam, N.J.
 Oncogene 9, 1745-1750, 1994
 A:Title: MLK-3: identification of a widely-expressed protein kinase bearing an SH3 domain
 A:Reference number: 158395; MUID:94239754; PMID:8183572
 A:Accession: 158395
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-847 <RES>
 A:Cross-references: GB:LJ2976; NID:9488295; PIDN:AA59859.1; PID:9488296

C:Genetics:
 A:Gene: GDB:MLK3; PTK1; SPRK
 A:Cross-references: GDB:134755; OMIM:600050
 A:Map position: 11q13.1-11q13.3
 C:Superfamily: mixed-lineage protein kinase 3; protein kinase homology; SH3 homology
 C:Keywords: ATP; leucine zipper; phosphotransferase; serine/threonine-specific protein X
 F:48-100/Domain: SH3 homology <SH3>
 F:115-383/Domain: protein kinase homology <KIN>
 F:123-131/Region: protein kinase ATP-binding motif
 F:403-424/Region: leucine zipper motif
 F:438-459/Region: leucine zipper motif
 F:468-482/Region: basic

Query Match 12.1%; Score 71.5; DB 1; Length 847;
 Best Local Similarity 33.3%; Pred. No. 25;
 Matches 19; Conservative 8; Mismatches 23; Indels 7; Gaps 1;

QY 31 DYNAPCRFIDVKKGGQIYYSKLVNENGAGFWMAGSVYGDHODEMGIVGFPSPNV 87
 Db 51 DYPSGODELARKGRVEVLSRDAISGDEGWMAGVGGQ-----VGIFPSNV 100

RESULT 14

C64427
 hypothetical protein MJ020 - Methanococcus jannaschii
 C:Species: Methanococcus jannaschii
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
 C:Accession: C64427
 R:Butt, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
 ; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weisscock, K.G.; Merrick, J.M.; Glodok, A.;
 rsen, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, W.A.
 Science 273, 1058-1073, 1996
 A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
 A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii

A:Reference number: A64300; MUID:96337999; PMID:8688087
 A:Accession: C64427
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-259 <BUL>
 A:Cross-references: GB:U67544; GB:L77117; NID:91591671; PIDN:AA89024.1; PID:91591678;
 C:Genetics:
 A:Map position: FOR950420-951199

Query Match 12.0%; Score 71; DB 2; Length 259;
 Best Local Similarity 25.5%; Pred. No. 7.3;
 Matches 26; Conservative 17; Mismatches 41; Indels 18; Gaps 3;

QY 2 GVFMDLSK---KLCADBECCYTTSLARQEDYNAPDCRFIDVKKGGQIYYSKLVTE 57
 Db 169 GTDMDGRSRIPICKKCYDHSASASIER-----VEIKGDEKPIQIEVLIS 216

QY 58 NGAGFWMAGSVYGDHODEMGIVGFP--SNLYKEQRYQATKE 97
 Db 217 NEAGIFQIQEVLGEXIKMSGIRKMYSVVARVEKEKVFEEIT 258

RESULT 15

T39655
 VHS domain containing, signal transducing adaptor STAW-like protein - fission yeast (S
 C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 07-Dec-1999
 C:Accession: T39655
 R:Lyme, M.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.
 submitted to the EMBL Data Library, October 1998
 A:Reference number: 221868
 A:Accession: T39655
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-373 <LYN>
 A:Cross-references: EMBL:AL031856; PIDN:CAA21302.1; GSPDB:GNO0067; SPDB:SPBC1734.08
 A:Experimental source: strain 972n-; cosmid c1734
 C:Genetics:
 A:Gene: SPDB:SPBC1734.08
 A:Map position: 2
 A:introns: 43/2; 68/3; 142/1

Query Match 12.0%; Score 71; DB 2; Length 373;
 Best Local Similarity 32.1%; Pred. No. 11;
 Matches 25; Conservative 10; Mismatches 29; Indels 14; Gaps 3;

QY 22 TISLARQEDYNAPDCRFIDVKKGGQIYYSKLVNENGAGFWMAGSVYGDHODEMGIVGY 81
 Db 216 TVSRVRLVDPAAATEGSELFRKGDII-----LVLSVYKDWKSGSC-----KNAVGI 263

QY 82 FPSNVKEQRYQATKE 99
 Db 264 FPNVIV--QRVVEPTIEQ 279

Search completed: December 29, 2003, 16:10:40
 Job time: 11.4006 secs

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OM protein - protein search, using sw model

Run on: December 29, 2003, 16:03:18 : Search time 4.3173 Seconds
(without alignments)
1199.181 Million cell updates/sec

Title: US-10-019-455a-26

Sequence: 1 HGVEFMDKLSKKLCADECV.....RYQETATKEPTTIDFCE 110

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_41*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 591 | 100.0 | 128 | 1 | OTOR_MOUSE |
| 2 | 547 | 92.6 | 128 | 1 | OTOR_HUMAN |
| 3 | 465.5 | 78.8 | 132 | 1 | OTOR_CHICK |
| 4 | 399 | 67.5 | 133 | 1 | OTOR_RANCA |
| 5 | 261.5 | 44.2 | 131 | 1 | MIA_HUMAN |
| 6 | 260.5 | 44.1 | 130 | 1 | MIA_RAT |
| 7 | 259.5 | 43.9 | 130 | 1 | MIA_BOVIN |
| 8 | 245.5 | 41.5 | 130 | 1 | MIA_MOUSE |
| 9 | 91.5 | 15.5 | 843 | 1 | VAV_RAT |
| 10 | 91.5 | 15.5 | 845 | 1 | VAV_MOUSE |
| 11 | 91.5 | 15.5 | 847 | 1 | VAV_HUMAN |
| 12 | 89.5 | 15.1 | 847 | 1 | VAV3_HUMAN |
| 13 | 89.5 | 15.1 | 847 | 1 | VAV2_MOUSE |
| 14 | 85.5 | 14.5 | 868 | 1 | VAV2_MOUSE |
| 15 | 84.5 | 14.3 | 878 | 1 | CC25_YEAST |
| 16 | 78.5 | 13.3 | 1589 | 1 | TGM2_PIGMA |
| 17 | 77 | 13.0 | 695 | 1 | SHK1_HUMAN |
| 18 | 77 | 13.0 | 2161 | 1 | SHK1_RAT |
| 19 | 75 | 12.7 | 2167 | 1 | SHK1_RAT |
| 20 | 74 | 12.5 | 1217 | 1 | ITN1_RAT |
| 21 | 71.5 | 12.1 | 1696 | 1 | ITN2_HUMAN |
| 22 | 71 | 12.0 | 259 | 1 | YAZO_METUA |
| 23 | 71 | 12.0 | 1714 | 1 | ITN1_MOUSE |
| 24 | 71 | 12.0 | 1721 | 1 | ITN1_HUMAN |
| 25 | 71 | 12.0 | 1815 | 1 | SHK3_RAT |
| 26 | 70.5 | 11.9 | 505 | 1 | SRK1_SPOLA |
| 27 | 70.5 | 11.9 | 506 | 1 | SRK4_SPOLA |
| 28 | 70.5 | 11.9 | 858 | 1 | CNRA_MOUSE |
| 29 | 70 | 11.8 | 486 | 1 | ALIN_ALISA |
| 30 | 69 | 11.7 | 670 | 1 | YBY2_SCHRO |
| 31 | 68.5 | 11.6 | 377 | 1 | NCK1_HUMAN |
| 32 | 68 | 11.5 | 427 | 1 | AROQ_STRP8 |
| 33 | 68 | 11.5 | 430 | 1 | AROQ_STRBY |

| | | | | | | |
|----|------|------|------|---|-------------|--------------------|
| 34 | 68 | 11.5 | 733 | 1 | VINE_MOUSE | Q9128 mus musculus |
| 35 | 68 | 11.5 | 954 | 1 | M3KA_HUMAN | Q0279 homo sapien |
| 36 | 67.5 | 11.4 | 643 | 1 | PGL3_ASPNG | Q1254 aspergillus |
| 37 | 67.5 | 11.4 | 643 | 1 | SGLT_ARATH | Q1255 arabidopsis |
| 38 | 67.5 | 11.4 | 1658 | 1 | ITN2_MOUSE | Q9206 mus musculus |
| 39 | 67 | 11.3 | 671 | 1 | VINE_HUMAN | Q60504 homo sapien |
| 40 | 66.5 | 11.3 | 496 | 1 | Y7J3_ANASP | Q05070 anabaena sp |
| 41 | 66.5 | 11.3 | 504 | 1 | BLK_HUMAN | P51451 homo sapien |
| 42 | 66.5 | 11.3 | 540 | 1 | TOPI_AQUAE | P66893 aquifex aeo |
| 43 | 66.5 | 11.3 | 727 | 1 | IP2M_HUMAN | P46199 homo sapien |
| 44 | 66 | 11.2 | 328 | 1 | COAD_THERYO | Q97bq0 thermoplasm |
| 45 | 66 | 11.2 | 380 | 1 | NCK2_HUMAN | Q43639 homo sapien |

ALIGNMENTS

| RESULT 1 | ID | OTOR_MOUSE | STANDARD | PRT | 128 AA. |
|----------|--|------------|----------|-----|------------|
| AC | Q91E3 | | | | |
| DT | 16-OCT-2001 (Rel. 40, Created) | | | | |
| DT | 16-OCT-2001 (Rel. 40, Last sequence update) | | | | |
| DT | 28-FEB-2003 (Rel. 41, Last annotation update) | | | | |
| DE | Otoraplin precursor (Melanoma inhibitory activity-like protein). | | | | |
| GN | OTOR OR MIAL. | | | | |
| OS | Mus musculus (Mouse). | | | | |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | | |
| OX | NCBI_TaxID=10090; | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RX | MEDLINE=20334619; PubMed=10873378; | | | | |
| RA | Robertson N.G., Heller S., Jin J.S., Resendes B.L., Weremowicz S., | | | | |
| RA | Denis C.S., Bell A.M., Hudspeth A.J., Morton C.C.; | | | | |
| RT | "A novel conserved cochlear gene, OTOR: identification, expression | | | | |
| RT | analysis, and chromosomal mapping."; | | | | |
| RL | Genomics 66:242-248 (2000). | | | | |
| RN | [2] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | TISSUE=Fetal; | | | | |
| RX | MEDLINE=21100875; PubMed=11161796; | | | | |
| RA | Rendtorff N.D., Frodin M., Attie-Bitach T., Vekemans M., Tommerup N.; | | | | |
| RT | "Identification and characterization of an inner ear-expressed human | | | | |
| RT | melanoma inhibitory activity (MIA)-like gene (MIAL) with a frequent | | | | |
| RT | polymorphism that abolishes translation."; | | | | |
| RL | Genomics 71:40-52 (2001). | | | | |
| CC | - SUBCELLULAR LOCATION: Secreted (Potential). | | | | |
| CC | - TISSUE SPECIFICITY: HIGHLY EXPRESSED IN COCHLEA. | | | | |
| CC | - SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY. | | | | |
| CC | - SIMILARITY: Contains 1 SH3 domain. | | | | |
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| CC | ----- | | | | |
| EMBL | AF233333; AAF82079.1; - | | | | |
| EMBL | AF243939; CAC27444.1; - | | | | |
| HSSP | Q16674; 111J. | | | | |
| MGD | WGI:188678; Otor. | | | | |
| GO | GO:0001502; P:cartilage condensation; IMP. | | | | |
| InterPro | IPR001452; SH3. | | | | |
| Pfam | PF00018; SH3; 1. | | | | |
| SMART | SM00326; SH3; 1. | | | | |
| PROSITE | PS50002; SH3; 1. | | | | |
| SIGNAL | 1 | | | | POTENTIAL. |
| CHAIN | 19 | | | | OTORAPLIN. |
| FT | 128 | | | | |
| DOMAIN | 39 | | | | SH3. |

```

FT DISUFLD 32 37 BY SIMILARITY.
FT DISUFLD 55 127 BY SIMILARITY.
SQ SEQUENCE 128 AA; 14328 MW; 3DD47D4C77C4A7FD CRC64;
Query Match 100.0%; Score 591; DB 1; Length 128;
Best Local Similarity 100.0%; Pred. No. 1.9e-53;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGVMMDKLSKSKKLCADEECVYTISLARAQEDYNAPDCRFIDVKKGOQIYYYSKLVTENGA 60
DQ 19 HGVMMDKLSKSKKLCADEECVYTISLARAQEDYNAPDCRFIDVKKGOQIYYYSKLVTENGA 78
QY 61 GEFNAGSYGQDHODEMGIVGFFPSNLVKEGCVYQATKEIPTTIDPFCE 110
DQ 79 GEFNAGSYGQDHODEMGIVGFFPSNLVKEGCVYQATKEIPTTIDPFCE 128

RESULT 2
OTOR HUMAN STANDARD; PRT; 128 AA.
AC Q9NRC9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Otoraplin precursor (Fibrocyte-derived protein) (Melanoma inhibitory
DE activity like protein).
GN OTOR OR FDP OR MIAL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cochlea;
RX MEDLINE=20334619; PubMed=10873378;
RA Robertson N.G., Heller S., Lin J.S., Resendes B.L., Wernowicz S.,
RA Denis C.S., Bell A.M., Hudspeth A.J., Morton C.C.;
RA "A novel conserved cochlear gene, OTOR: identification, expression
RT analysis, and chromosomal mapping.";
RL Genomics 66:242-248(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20568254; PubMed=10998416;
RA Cohen-Salmon N., Frenx D., Liu W., Verpy E., Voegelting S., Petit C.;
RA "Fdp, a new fibrocyte-derived protein related to MIA/CD-RAP, has an
RT in vitro effect on the early differentiation of the inner ear
RT mesenchyme.";
RL J. Biol. Chem. 275:40036-40041(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, and Cochlea;
RX MEDLINE=21100875; PubMed=1161796;
RA Wendorff N.D., Frodin M., Attie-Bitach T., Vekemans M., Tommerup N.;
RA "Identification and characterization of an inner ear-expressed human
RT melanoma inhibitory activity (MIA)-like gene (MIAL) with a frequent
RT polymorphism that abolishes translation.";
RL Genomics 71:40-52(2001).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052;
RA Delouis P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.W., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Copley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Griffiths D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.W., King A., Knights A., Laird G.K., Lawlor S.,

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RA Lehaesajaho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McLeay K., McMurtry A.A.,
RA Milne S.A., Misty D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Philimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Rose M.T., Scott C.E., Senta H.K., Showken R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilmig L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
CC - SUBCELLULAR LOCATION: Secreted (potential).
CC - TISSUE SPECIFICITY: HIGHLY EXPRESSED IN COCHLEA.
CC - SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
CC - SIMILARITY: Contains 1 SH3 domain.
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DR EMBL; AF233261; AAF82078.1; -
DR EMBL; AF243505; AAG42356.1; -
DR EMBL; AJ242552; CAC27443.1; -
DR EMBL; AJ252324; CAC28085.1; -
DR EMBL; AJ252325; CAC28085.1; JOINED.
DR EMBL; AJ252326; CAC28085.1; JOINED.
DR EMBL; AJ252327; CAC28085.1; JOINED.
DR HSPB; AL034428; CAC16848.1; -
DR HSPB; Q16674; 111J.
DR Genew; HGNC:8517; OTOR.
DR MIM; 606067; -
DR GO; GO:0007605; P:hearing; TAS.
DR InterPro; IPR001452; SH3.
DR Pfam; PF00018; SH3; 1.
DR SMART; SMO0326; SH3; 1.
DR PROSITE; PS50002; SH3; FALSE_NEG.
DR KMW; 18
FT SIGNAL 18 POTENTIAL.
FT CHAIN 39 OTORAPLIN.
FT DOMAIN 19 110 SH3.
FT DISUFLD 32 37 BY SIMILARITY.
FT DISUFLD 55 127 BY SIMILARITY.
SQ SEQUENCE 128 AA; 14332 MW; 9BB52C7F5D4FB700 CRC64;
Query Match 92.6%; Score 547; DB 1; Length 128;
Best Local Similarity 90.0%; Pred. No. 5.9e-49;
Matches 99; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 HGVMMDKLSKSKKLCADEECVYTISLARAQEDYNAPDCRFIDVKKGOQIYYYSKLVTENGA 60
DQ 19 HGVMMDKLSKSKKLCADEECVYTISLARAQEDYNAPDCRFIDVKKGOQIYYYSKLVTENGA 78
QY 61 GEFNAGSYGQDHODEMGIVGFFPSNLVKEGCVYQATKEIPTTIDPFCE 110
DQ 79 GEFNAGSYGQDHODEMGIVGFFPSNLVKEGCVYQATKEIPTTIDPFCE 128

RESULT 3
OTOR CHICK STANDARD; PRT; 132 AA.
AC Q9IBP6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Otoraplin precursor.
GN OTOR.

```


OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 CC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20334619; PubMed=10873378;
 RA Robertson N.G., Heller S., Lin J.S., Resendes B.L., Weremowicz S.,
 RA Denis C.S., Bell A.M., Hudepeth A.J., Morton C.C.;
 RA "A novel conserved cochlear gene, OTOR: identification, expression
 RT analysis, and chromosomal mapping.";
 RT Genomics 66:242-248(2000).
 CC -1- SUBCELLULAR LOCATION: Secreted (potential).
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN COCHLEA.
 CC -1- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
 CC -1- SIMILARITY: Contains 1 SH3 domain.
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 CC EMBL: AF233518; AAF82727.1; -
 CC HSSP: Q16674; 111J.
 CC InterPro: IPR001452; SH3.
 CC SMART: SMO0326; SH3; 1.
 CC PROSITE: PS50002; SH3; 1.
 CC SIGNAL; SH3 domain.
 CC FT CHAIN 1 23 POTENTIAL.
 CC FT DOMAIN 24 132 OTORAPLIN.
 CC FT DISULFID 35 40 SH3.
 CC FT DISULFID 58 132 BY SIMILARITY.
 CC FT DISULFID 132 AA; 15177 MW; 9D1CB07FD353CE1C CRC64;
 CC SQ SEQUENCE 132 AA; 15177 MW; 9D1CB07FD353CE1C CRC64;
 CC
 CC Query Match 78.8%; Score 465.5; DB 1; Length 132;
 CC Best Local Similarity 77.3%; Pred. No. 1,2e-40;
 CC Matches 85; Conservative 12; Mismatches 12; Indels 1; Gaps 1;
 CC
 CC QY 2 GVPMFKLSKKLCADEECVTTISLARAQEDYNAPDCRFIVKGGQIYYYSKLVTENGAG 61
 CC DB 23 GIPMDKASKKLCADDDCVYITSLVRAEDYNAPDCRFINIKKGQILYYYSKLVKEKESG 82
 CC QY 62 EFPAAGSVYGD-HQDEMGIYGFPPSNLYVEQRYQATKEIPTDIDPFCE 110
 CC DB 83 EFPAAGSVYGEYEDHMGTVGFPPSLVSEQHVIOEANKTIPPTDIDPFCE 132
 CC
 CC RESULT 4
 CC ID OTOR_RANCA STANDARD; PRT; 133 AA.
 CC AC Q918P5;
 CC DT 16-OCT-2001 (Rel. 40, Created)
 CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE Otoraplin precursor.
 CC GN OTOR.
 CC OS Rana catesbeiana (Bull frog).
 CC CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 CC NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20334619; PubMed=10873378;
 RA Robertson N.G., Heller S., Lin J.S., Resendes B.L., Weremowicz S.,
 RA Denis C.S., Bell A.M., Hudepeth A.J., Morton C.C.;
 RA "A novel conserved cochlear gene, OTOR: identification, expression
 RT analysis, and chromosomal mapping.";
 RT Genomics 66:242-248(2000).
 CC

CC -1- SUBCELLULAR LOCATION: Secreted (potential).
 CC -1- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
 CC -1- SIMILARITY: Contains 1 SH3 domain.
 CC -----
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 CC -----
 CC EMBL: AF233519; AAF82728.1; -
 CC HSSP: Q16674; 111J.
 CC InterPro: IPR001452; SH3.
 CC SMART: SMO0326; SH3; 1.
 CC PROSITE: PS50002; SH3; 1.
 CC SIGNAL; SH3 domain.
 CC FT CHAIN 1 23 POTENTIAL.
 CC FT DOMAIN 24 132 OTORAPLIN.
 CC FT DISULFID 35 40 SH3.
 CC FT DISULFID 58 132 BY SIMILARITY.
 CC FT DISULFID 133 AA; 15243 MW; 25440C1A3CF911AE CRC64;
 CC SQ SEQUENCE 133 AA; 15243 MW; 25440C1A3CF911AE CRC64;
 CC
 CC Query Match 67.5%; Score 399; DB 1; Length 133;
 CC Best Local Similarity 60.7%; Pred. No. 7.6e-34;
 CC Matches 68; Conservative 26; Mismatches 16; Indels 2; Gaps 2;
 CC
 CC QY 1 HGVMFKLSKKLCADEECVTTISLARAQEDYNAPDCRFIVKGGQIYYYSKLVTENGAG 59
 CC DB 22 YGVYMQKLSIDKRLCADEECVTTISLARAQEDYNAPDCRFIVKGGQIYYYSKLVTENGAG 81
 CC QY 60 AGEFPAAGSVYGD-HQDEMGIYGFPPSNLYVEQRYQATKEIPTDIDPFCE 110
 CC DB 82 AGEFPAAGSVYSDQYRDQGLVGFPPSLVTELTYYKDELQELPTTAVDFYCD 133
 CC
 CC RESULT 5
 CC ID MIA_HUMAN STANDARD; PRT; 131 AA.
 CC AC Q16674;
 CC DT 01-NOV-1997 (Rel. 35, Created)
 CC DT 01-NOV-1997 (Rel. 35, Last sequence update)
 CC DT 15-SEP-2003 (Rel. 42, Last annotation update)
 CC DE Melanoma derived growth regulatory protein precursor (Melanoma
 CC inhibitory activity).
 CC GN MIA.
 CC OS Homo sapiens (Human).
 CC CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RA MEDLINE=95007612; PubMed=7923218;
 RA Blesch A., Bosserhoff A.-K., Apfel R., Behl C., Heesdoerfer B.,
 RA Schmitt A., Jachimeczak P., Lottspeich F., Buetner R., Bogdahn U.;
 RA "Cloning of a novel malignant melanoma-derived growth-regulatory
 RT protein, MIA.";
 RT Cancer Res. 54:5695-5701(1994).
 CC
 CC [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=96132947; PubMed=8550608;
 RA Bosserhoff A.-K., Hein R., Bogdahn U., Buetner R.;
 RT "Structure and promoter analysis of the gene encoding the human
 RT melanoma-inhibiting protein MIA.";
 RT J. Biol. Chem. 271:490-495(1996).
 CC
 CC [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RX MEDLINE=2338257; PubMed=12477932;
 CC

RA Strausberg R.L., Feigold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.D., Abramson R.D., Mullen S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huylk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buttefield Y.S.N., Krzywinski M.I., Skalska U., Smalpus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [4]
 RL X-RAY CRYSTALLOGRAPHY (1.39 ANGSTROMS) OF 25-131.
 RP MEDLINE=2124635; PubMed=11331761;
 RX Loughhead J.C., Holton J.M., Alber T., Bazan J.F., Handel T.M.,
 RA "Structure of melanoma inhibitory activity protein, a member of a
 RT recently identified family of secreted proteins."
 Proc. Natl. Acad. Sci. U.S.A. 98:5515-5520(2001).
 CC -1- FUNCTION: ELICITS GROWTH INHIBITION ON MELANOMA CELLS IN VITRO
 CC AS WELL AS SOME OTHER NEUROECTODERMAL TUMORS, INCLUDING GLIOMAS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: ALL MALIGNANT MELANOMA CELL LINES TESTED AND
 CC INDEPENDENTLY IN GLIOMA CELL LINES.
 CC -1- PTM: MAY POSSESS TWO INTRAMOLECULAR DISULFIDE BONDS.
 CC -1- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
 CC -1- SIMILARITY: Contains 1 SH3 domain.
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 CC -----
 CC EMBL: X75450; CA53203.1; -
 DR EMBL: X84707; CA59195.1; -
 DR EMBL: BC005910; AA05910.1; -
 DR PIR: I38019; I38019.
 DR PDB: 1IJU; 16-MAY-01.
 DR PDB: 1HJD; 29-JAN-02.
 DR PDB: 1K0X; 24-JUL-02.
 DR Genew; HGNC:7076; MIA.
 DR MIM: 601340; -
 DR GO: GO:0005615; C:extracellular space; TAS.
 DR GO: GO:0008283; P:cell proliferation; TAS.
 DR InterPro: IPR001452; SH3.
 DR SMART; SMO0326; SH3; 1.
 DR PROSITE; PSS0002; SH3; 1.
 KW Growth factor; signal; SH3 domain; 3D-structure.
 FT SIGNAL 1 24
 FT CHAIN 25 131 MELANOMA DERIVED GROWTH REGULATORY
 FT PROTEIN. SH3.
 FT DOMAIN 43 113
 FT DISULFID 36 41
 FT DISULFID 59 130
 FT STRAND 33 36
 FT TURN 39 40
 FT STRAND 46 50
 FT STRAND 54 54
 FT TURN 59 60
 FT STRAND 61 61
 FT STRAND 64 64

FT TURN 66 67
 FT STRAND 69 76
 FT HELIX 78 80
 FT TURN 81 82
 FT STRAND 83 89
 FT TURN 93 94
 FT STRAND 96 96
 FT STRAND 101 104
 FT STRAND 105 107
 FT HELIX 108 113
 FT STRAND 119 122
 FT STRAND 126 128
 FT HELIX 126 128
 SQ SEQUENCE 131 AA; 14509 MW; 4D3B30BD6008BDC CRC64;
 Query Match 44.2%; Score 261.5; DB 1; Length 131;
 Best Local Similarity 45.4%; Pred. No. 7.7e-20;
 Matches 49; Conservative 24; Mismatches 30; Indels 5; Gaps 3;
 QY 5 MDKSSKLCADDECVTISLARAQEDYNAPDPRIDPKGQIYVSKLYTENGAGE-F 63
 27 MKPLADRLKLCADQECSHISMAVALQDYPADPCRFPLTHRQGVYVFSKL---KGRGLF 83
 Db 64 WAGSYVGDHDEMGT-VGYPSPNLVKEQRYVQEAATKEIPTTIDPFCE 110
 84 WGSVYVGDYGDLPAARLGTFPSISYVRDQTLKPGKVDVKTIDWDFYCO 131
 QY 64 WAGSYVGDHDEMGT-VGYPSPNLVKEQRYVQEAATKEIPTTIDPFCE 110
 84 WGSVYVGDYGDLPAARLGTFPSISYVRDQTLKPGKVDVKTIDWDFYCO 131
 Db 84 WGSVYVGDYGDLPAARLGTFPSISYVRDQTLKPGKVDVKTIDWDFYCO 131
 RESULT 6
 ID MIA_RAT STANDARD; PRT; 130 AA.
 AC 062346; P97591;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Melanoma derived growth regulatory protein precursor (Melanoma
 DE inhibitory activity) (Cartilage-derived retinoic acid-sensitive
 DE protein) (CD-RAP).
 OS MIA OR CD-RAP.
 OS Rattus norvegicus (Rat).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Mammary gland;
 RA Lu J.X.;
 RT "Gene expression changes associated with chemically-induced rat
 RT mammary carcinogenesis.";
 RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 34-124 FROM N.A.
 RC TISSUE=Cartilage;
 RX MEDLINE=96216414; PubMed=8621736;
 RA Dietz U.H., Sandell L.J.;
 RT "Cloning of a retinoic acid-sensitive mRNA expressed in cartilage and
 RT during chondrogenesis.";
 RL J. Biol. Chem. 271:3311-3316(1996).
 CC -1- FUNCTION: MAY FUNCTION DURING CARTILAGE DEVELOPMENT AND
 CC MAINTENANCE.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: CARTILAGE PRIMORDIA AND CARTILAGE.
 CC -1- INDUCTION: Repressed by retinoic acid.
 CC -1- PTM: MAY POSSESS TWO INTRAMOLECULAR DISULFIDE BONDS.
 CC -1- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
 CC -1- SIMILARITY: Contains 1 SH3 domain.
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CC -----  
DR EMBL; U51438; AAC62481.1; -  
DR EMBL; U67884; AAB40659.1; -.  
DR HSSP; Q16674; 11U.  
DR InterPro; IPR001452; SH3.  
DR Pfam; PF00018; SH3; 1.  
DR SMART; SM00326; SH3; 1.  
DR ProSite; PS50002; SH3; FALSE_NEG.  
DR Growth factor; Signal; SH3 domain.  
FT SIGNAL 1 22 POTENTIAL.  
FT CHAIN 23 130 MELANOMA DERIVED GROWTH REGULATORY  
FT DOMAIN 42 112 PROTEIN.  
FT DISULFID 35 40 BY SIMILARITY.  
FT DISULFID 58 129 BY SIMILARITY.  
FT CONFLECT 46 47 MA -> VT (IN REF. 2).  
SQ SEQUENCE 130 AA; 14536 MW; 5f99149AECF74501 CRC64;  
  
Query Match 44.1%; Score 260.5; DE 1; Length 130;  
Best local Similarity 46.3%; Pred. No. 9,7e-20;  
Matches 50; Conservative 23; Mismatches 30; Indels 5; Gaps 3;  
  
QY MDKLSKKLCADDECVTTISLARAGDENYPNAPDGRFDVKGQOIYYSKLVTENGAGE-F 63  
DB 26 MPKLAADRKLCADECSHPISMAVALQYVAPDDRFLITRGQVYVFSLT---KSGRLF 82  
QY 64 WAGSVGDHODEMGI-VGFEPSPNVKEQRVYOATKEIPTTDIDPFCE 110  
DB 83 WGGSVGDGYGDDLAAHLGLFPSSIVREDLLTKRQGVDMKTDEMDFYCQ 130  
  
RESULT 7  
MIA_BOVIN STANDARD; FRT; 130 AA.  
ID_MIA_BOVIN  
AC Q28038;  
DDT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Melanoma derived growth regulatory protein precursor (Melanoma  
inhibitory activity) (Cartilage-derived retinoic acid-sensitive  
protein) (CD-RAP).  
GN MIA OR CDRAP.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI_TaxId=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96216414; PubMed=8621736;  
RA Dietz U.H., Sandell L.J.;  
RT "Cloning of a retinoic acid-sensitive mRNA expressed in cartilage and  
during chondrogenesis.";  
RU J. Biol. Chem. 271:3311-3316 (1996).  
FU FUNCTION: MAY FUNCTION DURING CARTILAGE DEVELOPMENT AND  
MAINTENANCE.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: CARTILAGE PRIMORDIA AND CARTILAGE.  
CC -1- INDUCTION: Repressed by retinoic acid.  
CC -1- PTM: MAY POSSESS TWO INTRAMOLECULAR DISULFIDE BONDS.  
CC -1- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.  
CC -1- SIMILARITY: Contains 1 SH3 domain.  
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CC EMBL; U51437; AAC48523.1; -  
DR HSSP; Q16674; 11U.
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DR InterPro:IPR001452; SH3.
DR Pfam: PF00018; SH3; 1.
DR SMART: SM00326; SH3; 1.
DR PROSITE: PS50002; SH3; 1.
KM Growth factor; Signal; SH3 domain.
FT SIGNAL 1 22 BY SIMILARITY.
FT CHAIN 23 130 MELANOMA DERIVED GROWTH REGULATORY
FT DOMAIN 42 112 SH3.
FT FT 35 40 BY SIMILARITY.
FT DISULFID 58 129 BY SIMILARITY.
SQ SEQUENCE 130 AA; 14353 MW; 95D153161C7B502A CRC64;

Query Match 43.9%; Score 259.5; DB 1; Length 130;
Best Local Similarity 46.3%; Pred. No. 1.2e-19;
Matches 50; Conservative 23; Mismatches 30; Indels 5; Gaps 3;

QY 5 MDKLSKKLCADEECVYITISLARQEDYNAPPCRFIDVKKGCQIVYKSLTENGAGS-F 63
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 26 MPKLRADKMCADCECHSPISVAVALQDVAAPOCRFLTHGQGVVIFSL--KGRGLF 82
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 64 WAGSVYGDHQ-DENGIVGFPPSLVYEGKRVQGEATEPIPTIDFCE 110
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 83 WGSVGVDDYVGDGAARLGYFPSPSIVSEDQTLKPAKTVDITMDYFCQ 130
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 8
MIA_MOUSE STANDARD; PRT; 130 AA.
ID MIA_MOUSE
AC 061865; 009086; P97495;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Melanoma derived growth regulatory protein precursor (Melanoma
DE inhibitory activity) (Cartilage-derived retinoic acid-sensitive
DE protein) (CD-RAP).
DE
GN MIA OR CD-RAP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c.
RA MEDLINE=95007612; PubMed=7923218;
RA Blesch A., Bosserhoff A.-K., Apfel R., Behl C., Hesseoefter B.,
RA Schmitt A., Jaschkeczak P., Lotzspeich F., Buettner R., Bogdahn U.;
RT "Cloning of a novel malignant melanoma-derived growth-regulatory
RT protein, MIA.",
RL Cancer Res. 54:5695-5701 (1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Sv;
RX MEDLINE=97251311; PubMed=9097023;
RA Bosserhoff A.K., Kondo S., Moser M., Dietz U., Copeland N.G.,
RA Gilbert D.U., Jenkins N.A., Buettner R., Sandell L.J.;
RT "Mouse CD-RAP/MIA gene: structure, chromosomal localization, and
RT expression in cartilage and chondrosarcoma.";
RL Dev. Dyn. 208:516-525 (1997).
CC -1- FUNCTION: ELICITS GROWTH INHIBITION ON MELANOMA CELLS IN VITRO AS
CC WELL AS SOME OTHER NEUROECTODERMAL TUMORS, INCLUDING GLIOMAS (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: ALL MALIGNANT MELANOMA CELL LINES TESTED AND
CC INFREQUENTLY IN GLIOMA CELL LINES.
CC -1- PFM: MAY POSSESS TWO INTRAOLBECULAR DISULFIDE BONDS.
CC -1- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
CC -1- SIMILARITY: Contains 1 SH3 domain.
CC -----
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CC EMBL: X94322; CAA63983.1; -
 CC EMBL: U85612; AAB42082.1; -
 CC EMBL: X97865; CAA66608.1; -
 DR HSSP: Q16674; 1117
 DR MGD; MGI:109615; MIA
 DR GO; GO:0007160; P:cell-matrix adhesion; IMP.
 DR GO; GO:003198; P:extracellular matrix organization and bioge. . . ; IMP.
 DR InterPro: IPR001452; SH3.
 DR Pfam: PF00018; SH3; 1.
 DR SMART; SM00326; SH3; 1; FALSE_NEG.
 DR PROSITE; PS50002; SH3; FALSE_DOMAIN.
 DR Growth factor; Signal; SH3 domain.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 130 MELANOMA DERIVED GROWTH REGULATORY
 FT PROTEIN.
 FT DOMAIN 42 112 BY SIMILARITY.
 FT DISULFID 35 40 BY SIMILARITY.
 FT DISULFID 58 129 BY SIMILARITY.
 FT CONFLICT 112 113 TL -> NS (IN REF. 1).
 FT SEQUENCE 130 AA; 14593 MW; 16C957459C5B85F9 CRC64;

Query Match 41.5%; Score 245.5; DB 1; Length 130;
 Best Local Similarity 45.4%; Pred. No. 3; 3e-18;
 Matches 49; Conservative 21; Mismatches 33; Indels 5; Gaps 3;

QY 5 MDKLSKLCADCECVTISLARQEDYNAIDCRFDVKKGGQIYYSKLVTEENGAGE-F 63
 DB 26 MPKLADMKCADCECHPISMAVALQDYVADCRFLTYRGQVYVFSKL---KGRGLF 82
 QY 64 WAGSVYGDHDEMGV-VGYRPSNUVKEQRYQCATKEIPTDIDFCEC 110
 DB 83 WGSVGGYGGDLARLGYFPSSIVREDTLTKGKIDMKTDQWDFYQ 130

RESULT 9
 ID -VAV RAT STANDARD; PRT; 843 AA.
 AC PS4100;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Vav proto-oncogene (p95).
 GN VAV; OR VAV.
 OS Rattus norvegicus (Rat).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:9923974; PubMed:10395673;
 RA Song J.S., Hallett-Smith H., Arundhantaran R., Gomez J., Scott P.M.,
 RA Mill J.F., Tan T.-H., Rivera U., et al. stimulates IL-6 production in mast
 RA "tyrosine phosphorylation of Vav stimulates IL-6 production in mast
 RA cells by a Rac/C-Jun N-terminal kinase-dependent pathway.";
 RT J. Immunol. 163:802-810(1999).
 RL J. Immunol. 163:802-810(1999).
 CC -1- FUNCTION: Couples tyrosine kinase signals with the activation of
 CC the Rho/Rac GTPases, thus leading to cell differentiation and/or
 CC proliferation.
 CC -1- SUBUNIT: Interacts with SLA (By similarity).
 CC -1- PTM: Phosphorylated on tyrosine residues. (CH) domain.
 CC -1- SIMILARITY: Contains 1 calponin-homology (CH) domain.
 CC -1- SIMILARITY: Contains 1 DBL-homology (DH) domain.
 CC -1- SIMILARITY: Contains 1 zinc-dependent phospho-ester and DAG
 CC binding domain.
 CC -1- SIMILARITY: Contains 1 SH2 domain.
 CC -1- SIMILARITY: Contains 2 SH3 domains.
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CC EMBL: U39476; AAB8606.1; -
 CC HSSP: P29354; IGR1.
 DR InterPro: IPR001715; Calponin-like.
 DR InterPro: IPR003247; CH type.
 DR InterPro: IPR002219; DAG_Pe-bind.
 DR InterPro: IPR001331; GDS_CDC24.
 DR InterPro: IPR001849; PH.
 DR InterPro: IPR000219; RhogEF.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR003096; SM22-calponin.
 DR Pfam: PF00130; CH; 1.
 DR Pfam: PF00130; DAG_Pe-bind; 1.
 DR Pfam: PF00169; PH; 1.
 DR Pfam: PF00621; RhogEF; 1.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 2.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SM22CALPONIN.
 DR PRINTS; PR00888; SM22CALPONIN.
 DR ProDom; PD000093; SH2; 1.
 DR ProDom; PD000066; SH3; 1.
 DR SMART; SM00109; C1; 1.
 DR SMART; SM00033; CH; 1.
 DR SMART; SM00233; PH; 1.
 DR SMART; SM00325; RhogEF; 1.
 DR SMART; SM00326; SH2; 1.
 DR SMART; SM00326; SH3; 2.
 DR PROSITE; PS50021; CH; 1.
 DR PROSITE; PS500479; DAG_Pe_BIND_DOM_1; 1.
 DR PROSITE; PS50081; DAG_Pe_BIND_DOM_2; 1.
 DR PROSITE; PS50010; DH_2; 1.
 DR PROSITE; PS50010; DH_1; 1.
 DR PROSITE; PS00741; DH_1; 1.
 DR PROSITE; PS50003; PH_DOMAIN; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 2.
 KW Proto-oncogene; Phospho-ester binding; Zinc; SH2 domain; SH3 domain;
 KW Guanine-nucleotide releasing factor; Repeat; Phosphorylation.
 FT DOMAIN 1 119 CH.
 FT DOMAIN 194 373 DH.
 FT DOMAIN 402 504 PH.
 FT DOMAIN 516 564 PHORBOL-ESTER AND DAG BINDING.
 FT DOMAIN 615 658 SH3 1.
 FT DOMAIN 669 763 SH2.
 FT DOMAIN 780 840 SH3 2.
 FT SEQUENCE 843 AA; 97953 MW; C4A5CADC45FCB80E CRC64;

Query Match 15.5%; Score 91.5; DB 1; Length 843;
 Best Local Similarity 32.9%; Pred. No. 0.12;
 Matches 23; Conservative 14; Mismatches 20; Indels 13; Gaps 3;

QY 26 ARAQEDYNAPDCRFIDYKKGQIYYSKLVTEENGAGEFVAGSYGCHQDDEMGVGYGPPSN 85
 DB 785 AKARYDCARDRSLSLKEGDII---KLNKKGGQGGWNGEIIYGR-----IGMFPSP 833
 QY 86 LVKEQRYQOE 95
 DB 834 YVEED--YSE 841

RESULT 10
 ID -VAV MOUSE STANDARD; PRT; 845 AA.
 AC P27570;
 DT 01-AUG-1992 (Rel. 23, Created)

01-AUG-1992 (Rel. 23, Last sequence update)
 15-SEP-2003 (Rel. 42, Last annotation update)
 Vav proto-oncogene.
 VAV1 OR VAV.
 Mus musculus (Mouse).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 SEQUENCE FROM N.A.
 MEDLINE=92228488; PubMed=1565462;
 Adams J.A., Houston H., Allen J., Lints T., Harvey R.;
 "The hematopoietically expressed vav proto-oncogene shares homology
 with the db1 GDP-GTP exchange factor, the bcr gene and a yeast gene
 (CDC24) involved in cytoskeletal organization.";
 Oncogene 7:611-618(1992).
 [2]
 SEQUENCE OF 1-93 FROM N.A.
 MEDLINE=91172176; PubMed=2005887;
 Katav S., Cleveland J.L., Heslop H.E., Pulido D.;
 "Loss of the amino-terminal helix-loop-helix domain of the vav proto-
 oncogene activates its transforming potential.";
 Mol. Cell. Biol. 11:1912-1920(1991).
 [3]
 INTERACTION WITH SLA.
 MEDLINE=20130290; PubMed=10662792;
 Sosinowski T., Pandey A., Dixit V.M., Weiss A.;
 "Src-like adaptor protein (SLAP) is a negative regulator of T cell
 receptor signaling.";
 J. Exp. Med. 191:463-474(2000).
 - FUNCTION: Couples tyrosine kinase signals with the activation of
 the Rho/Rac GTPases, thus leading to cell differentiation and/or
 proliferation.
 - SUBUNIT: Interacts with SLA.
 - TISSUE SPECIFICITY: Widely expressed in hematopoietic cells but
 not in other cell types.
 - PTM: Phosphorylated on tyrosine residues (By similarity).
 - SIMILARITY: Contains 1 calponin-homology (CH) domain.
 - SIMILARITY: Contains 1 DBL-homology (DH) domain.
 - SIMILARITY: Contains 1 PH domain.
 - SIMILARITY: Contains 1 zinc-dependent phospho-ester and DAG
 binding domain.
 - SIMILARITY: Contains 1 SH2 domain.
 - SIMILARITY: Contains 2 SH3 domains.

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 or send an email to license@ebi.ac.uk).

DR Pfam: PF00169; PH: 1.
 DR Pfam: PF00621; RHOGEF: 1.
 DR Pfam: PF00017; SH2: 1.
 DR Pfam: PF00018; SH3: 2.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR PRINTS: PR00888; SM22CALPONIN.
 DR ProDom: PD001527; CH type: 1.
 DR ProDom: PD000093; SH2: 1.
 DR ProDom: PD000066; SH3: 1.
 DR SMART: SM00109; CL: 1.
 DR SMART: SM00033; CH: 1.
 DR SMART: SM00233; PH: 1.
 DR SMART: SM00325; RHOGEF: 1.
 DR SMART: SM00252; SH2: 1.
 DR SMART: SM00326; SH3: 2.
 DR PROSITE: PS50021; CH: 1.
 DR PROSITE: PS00479; DAG_PE_BIND_DOM_1; 1.
 DR PROSITE: PS50081; DAG_PE_BIND_DOM_2; 1.
 DR PROSITE: PS50010; DH_2; 1.
 DR PROSITE: PS00741; DH_1; 1.
 DR PROSITE: PS50003; PH DOMAIN; 1.
 DR PROSITE: PS50001; SH2: 1.
 DR PROSITE: PS50002; SH3: 2.
 DR PROSITE: PS50003; PH DOMAIN; 1.
 KW Guanine-nucleotide releasing factor; Repeat; Phosphorylation;
 KW 3D-structure.
 KM DOMAIN 1 119 CH.
 FT DOMAIN 194 373 DH.
 FT DOMAIN 402 504 PH.
 FT DOMAIN 516 564 PHORBOL-ESTER AND DAG BINDING.
 FT DOMAIN 617 660 SH3 1.
 FT DOMAIN 671 765 SH2.
 FT DOMAIN 782 842 SH3 2.
 FT CONFLICT 29 Q -> E (IN REF. 2).
 SQ SEQUENCE 845 AA; 98136 MW; 3666DCCD1C5229DA CRC64;
 Query Match 15.5%; Score 91.5; DB 1; Length 845;
 Best Local Similarity 32.9%; Pred. No. 0.12;
 Matches 23; Conservative 14; Mismatches 20; Indels 13; Gaps 3;
 QY 26 AFAQEDYNAPDFCRFDVKKGGQIIVYSKLVTEENGEGFWMAGSYVDHDEMGIYGFPSN 85
 DB 787 AKARDFCARSRSELSLKEDII---KLNKKGGQGGWRRGRTYGR-----IGKFPN 835
 QY 86 LVKEQRYOE 95
 DB 836 YVEED--YSE 843
 RESULT 11
 VAV3 MOUSE STANDARD; PRT; 847 AA.
 AC G9R0C8;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Vav-3 protein.
 GN VAV3.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC MEDLINE=20179693; PubMed=10713454;
 CC Tienkle T., McClelland M., Adlkofer K., Welsh J.;
 CC "Major transcript variants of VAV3, a new member of the VAV family of
 CC guanine nucleotide exchange factors.";
 CC RT Gene 245:139-149(2000).
 CC - FUNCTION: EXCHANGE FACTOR FOR GTP-BINDING PROTEINS RHOA, RHOG AND,
 CC TO A LESSER EXTENT, RAC-1. BINDS PHYSICALLY TO THE NUCLEOTIDE-FREE
 CC STATES OF THOSE GTPASES (BY SIMILARITY).

```

CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Alpha;
CC IsoId=Q9R0C8-1; Sequence=Displayed;
CC Name=beta;
CC IsoId=Q9R0C8-2; Sequence=Not described;
CC -1- SIMILARITY: Contains 1 calponin-homology (CH) domain.
CC -1- SIMILARITY: Contains 1 DBU-homology (DH) domain.
CC -1- SIMILARITY: Contains 1 PH domain.
CC -1- SIMILARITY: Contains 1 zinc-dependent phospho-ester and DAG
CC binding domain.
CC -1- SIMILARITY: Contains 2 SH3 domains.
CC -----
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF067816; AAF09171.1; -
CC HSSP; P29355; ISEM.
CC MGD; MGI:1888518; Vav3.
CC InterPro; IPR001715; Calponin-like.
CC InterPro; IPR002247; CH type.
CC InterPro; IPR002219; DAG_PE-bind.
CC InterPro; IPR001331; GDS_CDCC4.
CC InterPro; IPR001849; PH.
CC InterPro; IPR000219; RhogEF.
CC InterPro; IPR000980; SH2.
CC InterPro; IPR001452; SH3.
CC InterPro; IPR001096; SM22_calponin.
CC Pfam; PF00307; CH; 1.
CC Pfam; PF00130; DAG_PE-bind; 1.
CC Pfam; PF00169; PH; 1.
CC Pfam; PF00017; RhogEF; 1.
CC Pfam; PF00018; SH3; 1.
CC PRINTS; PR00401; SH2DOMAIN.
CC PRINTS; PR00452; SH3DOMAIN.
CC PRINTS; PR00888; SM22CALPONIN.
CC ProDom; PD0001527; CH type; 1.
CC ProDom; PD000093; SH2; 1.
CC ProDom; PD000066; SH3; 1.
CC SMART; SM00109; C1; 1.
CC SMART; SM00033; CH; 1.
CC SMART; SM00233; PH; 1.
CC SMART; SM00325; RhogEF; 1.
CC SMART; SM00252; SH2; 1.
CC SMART; SM00326; SH3; 2.
CC PROSITE; PS50021; CH; 1.
CC PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
CC PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
CC PROSITE; PS50010; DH_2; 1.
CC PROSITE; PS00741; DH_1; 1.
CC PROSITE; PS50003; PH_DOMAIN; 1.
CC PROSITE; PS50001; SH2; 1.
CC PROSITE; PS50002; SH3; 2.
CC K0M Phospho-ester binding; Zinc; SH2 domain; SH3 domain; Repeat;
CC Guanine-nucleotide releasing factor; Alternative splicing.
CC K0M
CC DOMAIN 1
CC 192 371 DH.
CC FT DOMAIN 192 371 DH.
CC FT DOMAIN 400 502 PH.
CC FT DOMAIN 514 562 PHORBOL-ESTER AND DAG BINDING.
CC FT DOMAIN 592 660 SH3 1.
CC FT DOMAIN 672 766 SH2.
CC FT DOMAIN 788 847 SH3 2.
CC SEQUENCE 847 AA; 97946 MW; 9A6B63F0D3E60F8F CRC64;

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Query Match 15.5%; Score 91.5; DB 1; Length 847;
Best Local Similarity 32.8%; Pred. No. 0.12;

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Matches 22; Conservative 13; Mismatches 21; Indels 11; Gaps 2;
QY 23 ISLARAQEDYNA PDRCFIDYKGGQOIYVSKVTENGAEFWAGSVYGDHDEMGIYGF 82
Db 790 LGIARYPDFCARDMRELSLKGDMVKYITNM-----SANGMRGKVNGR-----VGMF 838
QY 83 PSNLVKE 89
Db 839 PSTYVEE 845
RESULT 12
VAV_HUMAN STANDARD; PRT; 845 AA.
ID VAV_HUMAN
AC P15498; Q15860;
DT 01-APR-1990 (Rel. 14, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE VAV proto-oncogene.
GN VAV1 OR VAV.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxId=9606;
OX NCBI
RN [1]
RP SEQUENCE FROM N.A.
RA Denlinger D.J., Borges C.R., Shaw C.L., Cushman A.M., Kawahara R.S.;
RT "Transcriptional regulation of the vav proto-oncogene."
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 62-845 FROM N.A.
RA MEDLINE=90005432; PubMed=2477241;
RA Katrav S., Martin-Zanca D., Barbacid M.;
RT "vav, a novel human oncogene derived from a locus ubiquitously
RT expressed in hematopoietic cells."
RL EMBO J. 8:2283-2290(1989).
RN [3]
RP SEQUENCE OF 1-61 FROM N.A.
RA MEDLINE=91172176; PubMed=2005887;
RA Katrav S., Cleveland J.L., Heslop H.E., Pulido D.;
RT "Loss of the amino-terminal helix-loop-helix domain of the vav proto-
RT oncogene activates its transforming potential."
RL Mol. Cell. Biol. 11:1912-1920(1991).
RN [4]
RP SEQUENCE OF 299-837 FROM N.A.
RA Romero F.;
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 299-334 FROM N.A.
RA MEDLINE=96038895; PubMed=7478592;
RA Ramos-Morales F., Romero F., Schweighoffer F., Bismuth G., Camonis J.,
RA Tortolero M., Fischer S.;
RT "The proline-rich region of vav binds to Grb2 and Grb3-3."
RL Oncogene 11:1665-1669(1995).
RN [6]
RP SIMILARITY TO CDC24 FAMILY.
RX MEDLINE=92228488; PubMed=1565462;
RX Adams J.M., Houston H., Allen J., Linta T., Harvey R.;
RT "The hematopoietically expressed vav proto-oncogene shares homology
RT with the db1 GDP-GTP exchange factor, the bcr gene and a yeast gene
RT (CDC24) involved in cytoskeletal organization."
RL Oncogene 7:611-618(1992).
CC -1- FUNCTION: Couples tyrosine kinase signals with the activation of
CC the Rho/Rac GTPases, thus leading to cell differentiation and/or
CC proliferation.
CC -1- SUBUNIT: Interacts with SLA (By similarity). Interacts with Grb2
CC and Grb3.
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED IN HEMATOPOIETIC CELLS BUT
CC NOT IN OTHER CELL TYPES.
CC -1- PTM: Phosphorylated on tyrosine residues.
CC -1- MISCELLANEOUS: 'vav' stands for the sixth letter of the Hebrew
CC alphabet.
CC -1- SIMILARITY: Contains 1 calponin-homology (CH) domain.

```

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DR EMBL, AF030201, AAC25011.1, JOINED.
DR EMBL, AF030202, AAC25011.1, JOINED.
DR EMBL, AF030203, AAC25011.1, JOINED.
DR EMBL, AF030204, AAC25011.1, JOINED.
DR EMBL, AF030205, AAC25011.1, JOINED.
DR EMBL, AF030206, AAC25011.1, JOINED.
DR EMBL, AF030207, AAC25011.1, JOINED.
DR EMBL, AF030208, AAC25011.1, JOINED.
DR EMBL, AF030209, AAC25011.1, JOINED.
DR EMBL, AF030210, AAC25011.1, JOINED.
DR EMBL, AF030212, AAC25011.1, JOINED.
DR EMBL, AF030213, AAC25011.1, JOINED.
DR EMBL, AF030214, AAC25011.1, JOINED.
DR EMBL, AF030215, AAC25011.1, JOINED.
DR EMBL, AF030216, AAC25011.1, JOINED.
DR EMBL, AF030217, AAC25011.1, JOINED.
DR EMBL, AF030218, AAC25011.1, JOINED.
DR EMBL, AF030219, AAC25011.1, JOINED.
DR EMBL, AF030220, AAC25011.1, JOINED.
DR EMBL, AF030221, AAC25011.1, JOINED.
DR EMBL, AF030222, AAC25011.1, JOINED.
DR EMBL, AF030223, AAC25011.1, JOINED.
DR EMBL, AF030224, AAC25011.1, JOINED.
DR EMBL, AF030225, AAC25011.1, JOINED.
DR EMBL, AF030226, AAC25011.1, JOINED.
DR EMBL, X16316, CAA34383.1, ALT_FRAME.
DR EMBL, M59834, AA6387.1, -.
DR EMBL, X83931, CAA58783.1, -.
DR PIR, B39576, TVHUV.
DR HSSP, P29354, IGRI.
DR TRANSFAC, T006880, -.
DR Genew, HGNC:12657, VAV1.
DR MIM, 144875, -.
DR GO, GO:0003700, F:transcription factor activity, TAS.
DR GO, GO:0007048, P:oncogenesis, TAS.
DR InterPro, IPR001715, Calponin-like.
DR InterPro, IPR003247, CH type.
DR InterPro, IPR002219, DAG_PE-bind.
DR InterPro, IPR001331, GDS_CDC24.
DR InterPro, IPR001849, PH.
DR InterPro, IPR000219, RhogEF.
DR InterPro, IPR000980, SH2.
DR InterPro, IPR001452, SH3.
DR InterPro, IPR003096, SM22_calponin.
DR Pfam, PF00307, CH, 1.
DR Pfam, PF00130, DAG_PE-bind, 1.
DR Pfam, PF00169, PH, 1.
DR Pfam, PF00621, RhogEF, 1.
DR Pfam, PF00017, SH2, 1.
DR Pfam, PF00018, SH3, 2.
DR PRINTS, PRO0401, SH2DOMAIN.
DR PRINTS, PRO0452, SH3DOMAIN.
DR PRINTS, PRO0888, SM22CALPONIN.
DR ProDom, PD001527, CH_type, 1.

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[illegible]

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CC Event=Alternative splicing; Named isoforms=2;
CC Name=Alpha;
CC IsoId=Q9UKM4-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=Q9UKM4-2; Sequence=VSP_001820;
CC -1 SIMILARITY: Contains 1 calponin-homology (CH) domain.
CC -1 SIMILARITY: Contains 1 DBL-homology (DH) domain.
CC -1 SIMILARITY: Contains 1 PH domain.
CC -1 SIMILARITY: Contains 1 zinc-dependent phorbol-ester and DAG
CC binding domain.
CC -1 SIMILARITY: Contains 1 SH2 domain.
CC -1 SIMILARITY: Contains 2 SH3 domains.
-----
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CC or send an email to license@isb-sib.ch).
-----
DR EMBL: AF118887; AAD20349.1; -
DR EMBL: AF118886; AAD20348.1; -
DR EMBL: AF067817; AAC79695.1; -
DR HSSP: P29355; 1SEM.
DR GeneW: HGNC:12659; VAV3.
DR MIM: 605541; -
DR GO: GO:0005096; F:GTPase activator activity; TAS.
DR GO: GO:0005076; F:SH3/SH2 adaptor protein activity; TAS.
DR GO: GO:0007264; P:small GTPase mediated signal transduction; TAS.
DR InterPro: IPR001715; Calponin-like.
DR InterPro: IPR003247; CH_type.
DR InterPro: IPR002219; DAG_PE-bind.
DR InterPro: IPR001331; GDS_CDC24.
DR InterPro: IPR001849; PH.
DR InterPro: IPR000219; RhoGEF.
DR InterPro: IPR000980; SH2.
DR InterPro: IPR001452; SH3.
DR InterPro: IPR003096; SM22-calponin.
DR Pfam: PF00307; CH_1.
DR Pfam: PF00130; DAG_PE-bind; 1.
DR Pfam: PF00169; PH_1.
DR Pfam: PF00621; RhoGEF; 1.
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF00018; SH3; 1.
DR PRINTS: PR00401; SH2DOMAIN.
DR PRINTS: PR00452; SH3DOMAIN.
DR PRINTS: PR00888; SM22CALPONIN.
DR PRODOM: PD001527; CH_type; 1.
DR PRODOM: PD000093; SH2; 1.
DR PRODOM: PD000066; SH3; 1.
DR SMART: SM00109; C1; 1.
DR SMART: SM00033; C1; 1.
DR SMART: SM00223; PH; 1.
DR SMART: SM00125; RhoGEF; 1.
DR SMART: SM00252; SH2; 1.
DR SMART: SM00326; SH3; 2.
DR PROSITE: PS00821; CH_1.
DR PROSITE: PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE: PS00861; DAG_PE_BIND_DOM_2; 1.
DR PROSITE: PS00010; DH_2; 1.
DR PROSITE: PS00741; DH_1; 1.
DR PROSITE: PS00003; PH_DOMAIN; 1.
DR PROSITE: PS00001; SH2; 1.
DR PROSITE: PS00002; SH3; 2.
DR PROSITE: PS00002; SH3; 2.
KW Phorbol-ester binding; Zinc; SH2 domain; SH3 domain; Repeat;
KW Guanine-nucleotide releasing factor; Alternative splicing.
FT DOMAIN 1 119 CH.
FT DOMAIN 192 371 DH.
FT DOMAIN 400 502 PH.
FT DOMAIN 514 562 PHORBOL-ESTER AND DAG BINDING.
FT DOMAIN 592 660 SH3 1.
FT DOMAIN 672 766 SH2.

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FT DOMAIN 788 847 SH3 2.
FT VARSPIC 1 107 MEMPKOQAQMLTHCKVLPPTNHRVTVDSAGVFDLAQTLRGV
FT FT LCOLLNLRAHSINKLEINRPSMSQFLCKNIRFLTRAC
FT FT CEFKGRKSELFEAFDLFVRDPSGK -> MOLPDCPCRAHL
FT FT P (in isoform Beta).
FT FT /FTID=VSP_001820.
FT FT K -> E (IN REF. 2).
FT FT Y -> H (IN REF. 1; AAD20348).
FT FT T -> S (IN REF. 2).
FT FT V -> A (IN REF. 1; AAD20348).
FT FT 429 429 C
FT FT 97775 MW; C1E29F0B094CB721 CRC64;
SQ SEQUENCE 847 AA; 97775 MW; C1E29F0B094CB721 CRC64;

Query Match 15.1%; Score 89.5; DB 1; Length 847;
Best Local Similarity 32.8%; Pred. No. 0.2;
Matches 22; Conservative 13; Mismatches 21; Indels 11; Gaps 2;

QY 23 ISLRACEDYNAPRCFRIDVKKGOIIVYSKLTENGAGEFPMASVYGDHDEMGVGYF 82
DB 790 LGIATARDYFCARDMRELTLKGVVXYTKM-----SANGMWRGEVNGR-----VGMF 838
QY 83 PENLYKE 89
DB 839 PSTYVEE 845

RESULT 14
VAV2_MOUSE STANDARD; PRT; 868 AA.
ID VAV2_MOUSE
AC Q60952;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vav-2 protein.
GN VAV2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=96313271; PubMed=8710375;
RA Schuebel K.E., Bustelo X.R., Nielsen D.A., Song B.J., Barbacid M.,
RT Goldman D., Lee I.J.;
RT "Isolation and characterization of murine vav2, a member of the vav
RT family of proto-oncogenes.";
RL Oncogene 13:363-371(1996).
CC -1 FUNCTION: Guanine nucleotide exchange factor for the Rho family
CC of Ras-related GTPases (By similarity).
CC -1 SIMILARITY: Contains 1 calponin-homology (CH) domain.
CC -1 SIMILARITY: Contains 1 DBL-homology (DH) domain.
CC -1 SIMILARITY: Contains 1 PH domain.
CC -1 SIMILARITY: Contains 1 zinc-dependent phorbol-ester and DAG
CC binding domain.
CC -1 SIMILARITY: Contains 1 SH2 domain.
CC -1 SIMILARITY: Contains 2 SH3 domains.
-----
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-----
DR EMBL: U37017; AAC52761.1; -
DR HSSP: Q60631; 1GBQ.
DR MGD: MGI:103718; Vav2.
DR InterPro: IPR001715; Calponin-like.
DR InterPro: IPR003247; CH_type.
DR InterPro: IPR002219; DAG_PE-bind.
DR InterPro: IPR001331; GDS_CDC24.
DR InterPro: IPR001849; PH.

```


CC TISSUE=Brain;
RX MEDLINE=95293325; PubMed=7762992;
RA Hanske E.P., Short M.P., Jozwiak S., Bovey C.M., Ramakhan S.,
RT Haines J.L., Kwiatkowski D.J.,
RL "Identification of VAV2 on 9q34 and its exclusion as the tuberous
sclerosis gene TSC1."
Ann. Hum. Genet. 59:25-37(1995).
[2]
RP PHOSPHORYLATION OF TYR-142; TYR-159 AND TYR-172.
EX MEDLINE=22464432; PubMed=12454019;
RA Tamas P., Soltau Z., Bauer P., Illes A., Sipkei S., Bauer A.,
RT Fargao A., Downard J., Buday L.,
RL "Mechanism of epidermal growth factor regulation of Vav2, a guanine
nucleotide exchange factor for Rac."
J. Biol. Chem. 278:5163-5171(2003).
CC - FUNCTION: Guanine nucleotide exchange factor for the Rho family
of Ras-related GTPases.
CC - TISSUE SPECIFICITY: Widely expressed.
CC - SIMILARITY: Contains 1 calponin-homology (CH) domain.
CC - SIMILARITY: Contains 1 DBL-homology (DH) domain.
CC - SIMILARITY: Contains 1 PH domain.
CC - SIMILARITY: Contains 1 zinc-dependent phospho-ester and DAG
binding domain.
CC - SIMILARITY: Contains 1 SH2 domain.
CC - SIMILARITY: Contains 2 SH3 domains.

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CC or send an email to license@isb-sib.ch).

DR EMBL, S76992; AAC34377.1; -
DR PIR, I51940; I51940.
DR HSSP, P08631; 1BU1.
DR GeneW, HGNC:12658; VAV2.
DR MIM, 600428; -
DR InterPro, IPR007145; Calponin-like.
DR InterPro, IPR003247; CH type.
DR InterPro, IPR002219; DAG_PE_bind.
DR InterPro, IPR001331; GDS_CDC24.
DR InterPro, IPR001848; PH.
DR InterPro, IPR000219; RhGEF.
DR InterPro, IPR000980; SH2.
DR InterPro, IPR01452; SH3.
DR Pfam, PF00307; CH; 1.
DR Pfam, PF00130; DAG_PE_bind; 1.
DR Pfam, PF00169; PH_1.
DR Pfam, PF00621; RhGEF; 1.
DR Pfam, PF00017; SH2; 1.
DR Pfam, PF00018; SH3; 2.
DR PRINTS, PR00401; SH3DOMAIN.
DR PRINTS, PR00452; SH3DOMAIN.
DR ProDom, PD001527; CH_type; 1.
DR ProDom, PD000093; SH2; 1.
DR ProDom, PD000066; SH3; 2.
DR SMART, SM00109; C1; 1.
DR SMART, SM00033; CH; 1.
DR SMART, SM00233; PH; 1.
DR SMART, SM00325; RhGEF; 1.
DR SMART, SM00252; SH2; 1.
DR SMART, SM00326; SH3; 2.
DR PROSITE, PS00021; CH; 1.
DR PROSITE, PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE, PS00081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE, PS00010; DH_2; 1.
DR PROSITE, PS00741; DH_1; 1.
DR PROSITE, PS00003; PH_DOMAIN; 1.
DR PROSITE, PS00001; SH2; 1.
DR PROSITE, PS00002; SH3; 2.
DR ProDom, ester binding; Zinc; SH2 domain; SH3 domain;
KW Phospho-ester binding; Zinc; SH2 domain; SH3 domain;

GenCore version 5.1.6
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OW protein - protein search, using SW model

Run on: December 29, 2003, 16:03:18 ; Search time 16.9468 seconds
(without alignments)
1674.996 Million cell updates/sec

Title: US-10-019-455a-26
Perfect score: 591
Sequence: 1 HGVMFKLSSKLCADCECV.....RVYQATKEIPTDIDFCE 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP viirus:*
16: SP bacteriaph:*
17: SP archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 231.5 | 39.2 | 96 | 11 | Q9J109 mesocricetu |
| 2 | 218 | 36.9 | 268 | 11 | Q8BJE9 mus musculu |
| 3 | 218 | 36.9 | 1239 | 11 | Q8BI84 mus musculu |
| 4 | 182 | 30.8 | 137 | 11 | Q9J1X3 mus musculu |
| 5 | 179.5 | 30.4 | 88 | 13 | Q9GXF1 tetraodon n |
| 6 | 164.5 | 27.8 | 119 | 4 | Q96PCS homo sapien |
| 7 | 155.5 | 26.3 | 119 | 11 | Q9J1V0 mus musculu |
| 8 | 111 | 18.8 | 68 | 11 | Q8C899 mus musculu |
| 9 | 91.5 | 15.5 | 166 | 11 | Q8C899 mus musculu |
| 10 | 91.5 | 15.5 | 287 | 11 | Q8R076 mus musculu |
| 11 | 91.5 | 15.5 | 806 | 11 | Q8R076 mus musculu |
| 12 | 91.5 | 15.5 | 845 | 11 | Q8BTU7 mus musculu |
| 13 | 91.5 | 15.5 | 846 | 13 | Q8BUX6 gallus galli |
| 14 | 89.5 | 15.1 | 719 | 4 | Q96D37 homo sapien |
| 15 | 86.5 | 14.6 | 839 | 13 | Q8BUX5 gallus galli |
| 16 | 82.5 | 14.0 | 259 | 10 | Q8RZ28 oryza sativ |

| | | | | | |
|----|------|------|------|----|--------------------|
| 17 | 82 | 13.9 | 827 | 13 | Q8UW56 tetraodon n |
| 18 | 81.5 | 13.8 | 1196 | 4 | Q9J0H2 homo sapien |
| 19 | 81.5 | 13.8 | 1196 | 4 | Q8N157 homo sapien |
| 20 | 81.5 | 13.8 | 1215 | 5 | Q77202 acanthamoeb |
| 21 | 81 | 13.7 | 615 | 10 | Q94330 oryza sativ |
| 22 | 80.5 | 13.6 | 636 | 10 | Q9FT28 oryza sativ |
| 23 | 80 | 13.5 | 344 | 10 | Q9FU07 oryza sativ |
| 24 | 80 | 13.5 | 643 | 10 | Q9FU04 oryza sativ |
| 25 | 79 | 13.4 | 638 | 10 | Q9AT05 oryza sativ |
| 26 | 78 | 13.2 | 637 | 10 | Q9ARW8 oryza sativ |
| 27 | 78 | 13.2 | 1257 | 5 | Q9YMA8 drosophila |
| 28 | 78 | 13.2 | 1430 | 5 | Q9YMA7 drosophila |
| 29 | 77.5 | 13.1 | 635 | 10 | Q9FU01 oryza sativ |
| 30 | 76 | 12.9 | 352 | 10 | Q94EK2 allium asca |
| 31 | 76 | 12.9 | 352 | 10 | Q94EK5 allium wake |
| 32 | 76 | 12.9 | 479 | 10 | Q43366 allium cepa |
| 33 | 76 | 12.9 | 479 | 10 | Q9SYV1 allium cepa |
| 34 | 76 | 12.9 | 479 | 10 | Q9AT06 oryza sativ |
| 35 | 75.5 | 12.8 | 498 | 4 | Q9H803 oryza sativ |
| 36 | 75.5 | 12.8 | 514 | 10 | Q8S003 oryza sativ |
| 37 | 74.5 | 12.6 | 839 | 10 | Q94F88 oryza sativ |
| 38 | 74.5 | 12.6 | 1097 | 5 | Q9U2T9 caenorhabdi |
| 39 | 74 | 12.5 | 355 | 10 | Q94EK0 allium sati |
| 40 | 74 | 12.5 | 621 | 10 | Q9FTF3 oryza sativ |
| 41 | 73.5 | 12.4 | 533 | 5 | Q8MY10 dictyosteli |
| 42 | 73 | 12.4 | 994 | 5 | Q93575 caenorhabdi |
| 43 | 72.5 | 12.3 | 304 | 10 | Q9FTG1 oryza sativ |
| 44 | 72.5 | 12.3 | 650 | 10 | Q9JL57 oryza sativ |
| 45 | 72.5 | 12.3 | 663 | 10 | Q9FE96 oryza sativ |

ALIGNMENTS

| | |
|---|---|
| RESULT 1 | |
| ID Q9J109 | PRELIMINARY; PRT; 96 AA. |
| AC Q9J109 | |
| DT 01-OCT-2000 (TRENBLrel. 15, Created) | |
| DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update) | |
| DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update) | |
| DE Melanoma inhibitory activitly protein (Fragment). | |
| OS Mesocricetus auratus (Golden hamster). | |
| OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | |
| OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; | |
| OC Mesocricetus. | |
| OX NCBI_TaxId=10036; | |
| RN [1] | |
| RP SEQUENCE FROM N.A. | |
| RA Guba W., Bosserhoff A.K., Steinbauer M., Anthuber M., Buettner R., | |
| RA Janch K.W.; | |
| RT "Overexpression of MIA enhances extravasation and metastasis of A-mel3 | |
| RT melanoma cells."; | |
| RL Submitted (May-2000) to the EMBL/GenBank/DBJ databases. | |
| CC -1. SIMILARITY: CONTAINS 1 SH3 DOMAIN. | |
| DR EMBL; AF271694; AAF76220.1; . | |
| DR HSPF; Q16674; 111J. | |
| DR InterPro; IPR001452; SH3. | |
| DR Pfam; PF00018; SH3; 1. | |
| DR SMART; SMO0326; SH3; 1. | |
| DR PROSITE; PS50002; SH3; 1. | |
| KW SH3 domain. | |
| FT NON TER | 1 |
| FT NON TER | 96 |
| SO SEQUENCE | 96 AA; 10756 MW; E7B466C3B5505BFB CRC64; |
| Query Match | 39.2%; Score 231.5; DB 11; Length 96; |
| Best Local Similarity | 45.4%; Pred. No. 1.6e-17; |
| Matches | 44; Conservative 22; Mismatches 26; Indels 5; Gaps 3; |
| QY | 8 LSSKLCADCECVTISLAAQEDRYNAPDRCFIDVKKGGQIYVSKVTEVNGAGE-FWAG 66 |
| DB | 1 LADRLKLCADCECVHPISMVAVALQDYMADRCFIFTHRGQVYVFSKL---KGRGRLEWGG 57 |

QY 67 SVYGDHQDEMKI-VGTFPSNLVKEQGVYQETKTEIPT 102
|||:::|||||:::|
Db 58 SVQGDYGGDLARLGYFPSSTVREDQTLKPGKDVKT 94

RESULT 2

| ID | Q8BJE9 | PRELIMINARY: | PRT; | 268 AA. |
|----|---|------------------------|------|---------|
| AC | Q8BJE9; | | | |
| DT | 01-MAR-2003 (TrEMBLrel. 23) | Created | | |
| DT | 01-MAR-2003 (TrEMBLrel. 23) | Last sequence update | | |
| DT | 01-MAR-2003 (TrEMBLrel. 23) | Last annotation update | | |
| DE | Weakly similar to NPIP-like protein (Fragment). | | | |
| OS | Mus musculus (Mouse). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus | | | |
| OX | NCBI_Taxid=10090; | | | |

| | | | | | | |
|----|----------|-----|-----|-------|-----------------|--------|
| FT | NON_TER | 268 | 268 | MM; | 67339C62D684402 | CRC64; |
| QO | SEQUENCE | 268 | AA; | 29722 | | |

| | | | | |
|-----------------------|-------|--------------------|--------|----------------|
| Query Match | 36.9% | Score 218; | DB 11; | Length 268; |
| Best Local Similarity | 42.2% | Pred. No. 1.6e-15; | | |
| Matches | 46; | Conservative | 13; | Mismatches 38; |
| | | | Indels | 12; |
| | | | Gaps | 4 |

Qy 1 HGVFMDLSSKKLCADEECVYITISLAAGQEDINAPDCRFIDYKKGGQIYVYSKLVLENGA 600
Db 28 HG--RRFSDLVKCGDEECSMIMYRGALAEPTGPDGRFVNFKKGGDQVYVYKLA--GGS 822

Qy 61 GEFNAGSVYGDHDEMGIVGYFENLVKEQRYVEATKEIPTTDIDFFC 109
Db 83 LELWAGSV--EHS-----FGYFPDLIKVLHKTEELHIIPADETFVC 124

RESULT 3

| | | | | | |
|----|--------|--------------|------|------|----|
| ID | Q8BI84 | PRELIMINARY; | PRT; | 1239 | AA |
|----|--------|--------------|------|------|----|

| |
|--|
| NCBI_TaxID=10990; |
| Mammalia; Euteheria; Rodentia; Sciuromorphi; Muridae; Murinae; Mus |
| OOC |
| Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| OS |
| Mus musculus (Mouse). |
| DE |
| Weakly similar to NIP-1-like protein. |
| DT |
| 01-VAR-2003 (TREMBLrel_23, last annotation update) |
| DT |
| 01-VAR-2003 (TREMBLrel_23, last annotation update) |
| DT |
| 01-VAR-2003 (TREMBLrel_23, last sequence update) |
| DT |
| Created) |

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Retina;
RC MEDLINE=22354683; PubMed=12466651;
RX The FANTOM Consortium,
RA the RIKEN Genome Exploration
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RT Nature 420:563-573 (2002).
RL EMBL: AK044748; BAC32064.1; -;
DR EMBL: AK044748; BAC32064.1; -;
SQ SEQUENCE 1239 AA; 136350 MW; 6E1EF9D42EEFF05 CRC64;

| | | | | |
|-----------------------|--------|------------------|--------|----------------|
| Query Match | 36.9%; | Score 218; | DB 11; | Length 1239; |
| Best Local Similarity | 42.2%; | Pred. No. 1e-14; | | |
| Matches | 46; | Conservative | 13; | Mismatches 38; |
| | | | Indels | 12; |
| | | | Gaps | 4; |

1 HGVFMDKLSKCLCADEECVYTI SLARAQEDYNAPDCRFIDVKKGOIYVYSKLV TENGA 60

Db 28 HG---RRFDLAKTCGGEECSMLRYRKALEDFTGPPRCRRVNNRKGDDVYVYKLA--GSS 82

QY 61 GEFWAGSVYGDHODENGIVGYFPNSMLVKEQRVYQATKEIPTTDIDFC 109

Db 83 LELMAASV---EHS-----FGYFPKDLIKLHNYTEBELIIPADEDTFVC 124

RESULT 4

| ID | PRELIMINARY; | PRT; | 137 AA. |
|----|---|---|---------|
| AC | Q921X3; | | |
| DT | 01-DEC-2001 | (TrEMBLrel. 19, Created) | |
| DT | 01-DEC-2001 | (TrEMBLrel. 19, Last sequence update) | |
| DT | 01-MAR-2003 | (TrEMBLrel. 23, Last annotation update) | |
| DE | Similar to cartilage derived retinoic acid sensitive protein. | | |
| DN | CDRAP. den | | |

OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
OC NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC009815; AA09815.1; -
DR MGD; MGI:109615; Cdkap.
DR InterPro: IPR001452; SH3.
DR Pfam; PF00018; SH3.1.
DR SMART; SMO0326; SH3.1.
DR Q6
SEQUENCE 137 AA; 15441 MW; 9741555266FD536 CRC64;

| | | | | |
|--------------------------|--------|--------------------|-----------|-------------|
| Query Match | 30.8%; | Score 182; | DB 11; | Length 137; |
| Best Local Similarity | 56.9%; | Pred. No. 5.8e-12; | | |
| Matches 37; Conservative | 9; | Mismatches 15; | Indels 4; | Gaps 2 |

QY 5 MDKLSKKLCADDECVYTISLRAGEDYNAPDCRFIDYKKGGQQLIVYSKLVTENGAGE-F 63
Dd 26 MPTLADWKLCADDECSHPISMAVALQDYVAPDCRFLTYIRGQVVVFYSKL---KGGRLF 82

| | | | |
|----|----|-------|----|
| Qy | 64 | WAGSV | 68 |
| | | | |
| Ph | 83 | WGSV | 87 |

RESULT 5

| | | | | | |
|----|--------|--------------|------|----|-----|
| ID | Q90XF1 | PRELIMINARY; | PRT; | 88 | AA. |
|----|--------|--------------|------|----|-----|

DT 01-DEC-2001 (TREMblrel, 19, Created)
 DT 01-DEC-2001 (TREMblrel, 19, Last sequence update)
 DT 01-MAR-2003 (TREMblrel, 23, Last annotation update)
 DE Melanoma inhibitory activity protein (Fragment).
 OS Tetradon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorphi; Acanthopterygii; Percomorphi; Tetradontiformes;
 OC Tetradontoidea; Tetradontidae; Tetradon.
 NCBI_TaxID=99883;

RP SEQUENCE FROM N.A.
RA Bossert A.K., Buetner R.;
RT "Characterization of the MA gene family."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases
EMBL: AF390176; AAL26991.1; -
DR InterPro: IPR001452; SH3.
DR Pfam: PF00018; SH3; 1.
DR SMART: SM00326; SH3; 1.
FT NON_TER 1
SQ SEQUENCE 98 AA; 10080 MW; C355C1FE04D42A22EA CEC64;

| Query Match | Score | DB | Length |
|-----------------------|-----------|----------|--------|
| 30.4%; | 179.5; | 13; | 88; |
| Best Local Similarity | Pred. No. | 6.3e-12; | |

Matches 39; Conservative 17; Mismatches 25; Indels 11; Gaps 4;

QY 23 ISAPADENYADPCRFIDVKKGOIYVSKLVTENGAG--EFWAGSY---YGDHODENG 77

Db 3 IMARACQDYPPDCXPIPIROGLIYVYAML---KORSGFVAGSVQDSYQOQEAR-- 57

QY 78 IVGYFPSNLVKEORVYQEAATKEIPTDIDFFC 109

Db 58 -IGHFSSIVEETHPLMAQTEVXTSMWDFYC 88

RESULT 6

Q96PCS PRELIMINARY; PRT; 119 AA.

AC Q96PCS; 01-DEC-2001 (TReMBLrel. 19, Created)

DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)

DE Melanoma inhibitory activity protein 2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.

RC TISSUE=Embryo;

RA Roserhoff A.K.; Buettner R.;

RT "Characterization of the MIA gene family.";

RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF390175; AA26990.1; -

DR InterPro: IPR001452; SH3.

DR SMART; SM00326; SH3; 1.

SEQUENCE 119 AA; 1353 MW; AEF529762D860A5 CRC64;

Query Match 27.8%; Score 164.5; DB 4; Length 119;

Best Local Similarity 35.3%; Pred. No. 3.9e-10;

Matches 36; Conservative 16; Mismatches 41; Indels 9; Gaps 2;

QY 8 LSKKLCADDEECVYTTSLAPQEDYNAPDRCFIDVKKGOIYVSKLVTENGAGEFWAGS 67

Db 26 LAHLKKCGDLBCEETLSKVLALRDYTGDPDCRYLNTTBEISVYKLGDDR--EDLMAGS 83

QY 68 VYGDHODENGIVGYFPSNLVKEORVYQEAATKEIPTDIDFFC 109

Db 84 KGE-----FGYPRDAVQIEVFISEIOMSTKESDFLC 118

RESULT 7

Q91ZVO PRELIMINARY; PRT; 119 AA.

AC Q91ZVO; 01-DEC-2001 (TReMBLrel. 19, Created)

DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)

DE Melanoma inhibitory activity protein 2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

RP SEQUENCE FROM N.A.

RC TISSUE=Embryo;

RA Roserhoff A.K.; Buettner R.;

RT "Characterization of the MIA gene family.";

RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF390177; AA26992.1; -

DR InterPro: IPR001452; SH3.

DR SMART; SM00326; SH3; 1.

SEQUENCE 119 AA; 1339 MW; 589F390C0B49D1C7 CRC64;

Query Match 26.3%; Score 155.5; DB 11; Length 119;

Best Local Similarity 35.3%; Pred. No. 3.7e-09;

Matches 36; Conservative 15; Mismatches 42; Indels 9; Gaps 2;

QY 8 LSKKLCADDEECVYTTSLAPQEDYNAPDRCFIDVKKGOIYVSKLVTENGAGEFWAGS 67

Db 26 LAHLKKCGDLBCEETLSKVLALRDYTGDPDCRYLNTTBEISVYKLGDDR--EDLMAGS 83

QY 68 VYGDHODENGIVGYFPSNLVKEORVYQEAATKEIPTDIDFFC 109

Db 84 KGE-----FGYPRDAVQIEVFISEIOMSTKESDFLC 118

RESULT 8

Q8C899 PRELIMINARY; PRT; 68 AA.

AC Q8C899; 01-MAR-2003 (TReMBLrel. 23, Created)

DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)

DE Otoraplin.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Head;

RA The FANTOM Consortium;

RT "Analysis of the mouse transcriptome based on functional annotation of

60,770 full-length cDNAs.";

DR EMBL; AK047965; BAC33202.1; -

SEQUENCE 68 AA; 7431 MW; 3CBE75527D3CB7F CRC64;

Query Match 18.8%; Score 111; DB 11; Length 68;

Best Local Similarity 51.1%; Pred. No. 0.00013;

Matches 24; Conservative 5; Mismatches 8; Indels 10; Gaps 2;

QY 1 HGVFMDKLSKXKLCADDEECV-----YTTSLAPQEDYNA--PDC 37

Db 19 HGVFMDKLSKXKLCADDEECVKKALLTWFSLSFYHIMGNLSGKQPDG 65

RESULT 9

Q08526 PRELIMINARY; PRT; 166 AA.

AC Q08526; 01-JUN-1997 (TReMBLrel. 04, Created)

DT 01-JUN-1997 (TReMBLrel. 04, Last sequence update)

DE Vav-T.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

RP SEQUENCE FROM N.A.

RC STRAIN=ddY; TISSUE=Testis;

RA Okumura K.; Kaneko Y.; Nonoguchi K.; Nishiyama H.; Yokoi H.;

Higuchi T.; Itoh K.; Yoshida O.; Miki T.; Fujita J.;

"Expression of a novel isoform of Vav, Vav-T, containing a single

Src homology 3 domain in murine testicular germ cells.";

DR Oncogene 14:713-720(1997).

CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.

DR EMBL; D83266; BAA18950.1; -

DR HSSP; Q6631; IGBO.

DR MGD; MGI:98923; Vav.

DR InterPro: IPR000980; SH2.

DR InterPro: IPR001452; SH3.

DR Pfam; PF00017; SH2; 1.

DR Pfam; PF00018; SH3; 1.

DR PRINTS; PR00452; SH3DOMAIN.
 DR ProdDom; PD000093; SH2; 1.
 DR ProdDom; PD000066; SH3; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR PRODITE; PS50001; SH2; 1.
 DR PRODITE; PS50002; SH3; 1.
 DR SH3 domain.
 SQ SEQUENCE 166 AA; 19434 MW; 2C3AF1FF07A5018F CRC64;

Query Match 15.5%; Score 91.5; DB 11; Length 166;
 Best Local Similarity 32.9%; Pred. No. 0.05;
 Matches 23; Conservative 14; Mismatches 20; Indels 13; Gaps 3;

QY 26 ARAQEDYNAPDCRFIDVKKGOQIYYYSKLVTEENGAFEFNAGSVYGDHODEMGIYGFPSN 85
 DB 108 AKARYDFCARDSRLSLKEGDII---KILNKKGGQGMWRGEIYGR-----IGWFPSPN 156

QY 86 LYKEQRYOE 95
 DB 157 YVEED--YSE 164

RESULT 10
 Q8R076 PRELIMINARY; PRT; 287 AA.

AC 28R076;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Hypothetical 32.7 kDa protein.
 GN VAV3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC027242; AAH27242.1; -
 DR MGI; MGI:188518; Vav3.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF00017; SH2; 1.
 DR ProdDom; PD000093; SH2; 1.
 DR ProdDom; PD000066; SH3; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 2.
 DR PRODITE; PS50001; SH2; 1.
 DR PRODITE; PS50002; SH3; 2.
 DR Hypothetical protein.
 SQ SEQUENCE 287 AA; 32662 MW; BF2850B8F921F048 CRC64;

Query Match 15.5%; Score 91.5; DB 11; Length 287;
 Best Local Similarity 32.8%; Pred. No. 0.097;
 Matches 22; Conservative 13; Mismatches 21; Indels 11; Gaps 2;

QY 23 ISLARACEDYNAPDCRFIDVKKGOQIYYYSKLVTEENGAFEFNAGSVYGDHODEMGIYGF 82
 DB 230 LGIATARYDFCARDSRLSLKEGDII---KILNKKGGQGMWRGEIYGR-----YGMF 278

QY 83 PSNLVKE 89
 DB 279 PSTYVEE 285

RESULT 11
 Q8VDU4 PRELIMINARY; PRT; 806 AA.
 AC Q8VDU4;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Similar to vav oncogene.
 GN VAV.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Strausberg R.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
 DR EMBL; BC020487; AAH20487.1; -
 DR MGI; MGI:98923; Vav.

DR InterPro; IPR005613; AIP3.
 DR InterPro; IPR001715; Calponin-like.
 DR InterPro; IPR003247; CH_type.
 DR InterPro; IPR002219; DAG_PE-bind.
 DR InterPro; IPR001331; GDS_CDC24.
 DR InterPro; IPR001849; PH_CDC24.
 DR InterPro; IPR000219; RhogEF.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR InterPro; IPR003096; SM22_calponin.
 DR Pfam; PF03915; AIP3; 1.
 DR Pfam; PF00307; CH; 1.
 DR Pfam; PF00150; DAG_PE-bind; 1.
 DR Pfam; PF00169; PH; 1.
 DR Pfam; PF00621; RhogEF; 1.
 DR Pfam; PF00017; SH2; 1.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00886; SM22CALPONIN.
 DR ProdDom; PD001527; CH_type; 1.
 DR ProdDom; PD000093; SH2; 1.
 DR ProdDom; PD000066; SH3; 1.
 DR SMART; SM00109; C1; 1.
 DR SMART; SM00033; CH; 1.
 DR SMART; SM00233; PH; 1.
 DR SMART; SM00325; RhogEF; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 2.
 DR PRODITE; PS50021; CH; 1.
 DR PRODITE; PS00479; DAG_PE_BIND_DOM_1; 1.
 DR PRODITE; PS50081; DAG_PE_BIND_DOM_2; 1.
 DR PRODITE; PS00741; DH_1; 1.
 DR PRODITE; PS50010; DH_2; 1.
 DR PRODITE; PS50003; PH_DOMAIN; 1.
 DR PRODITE; PS50001; SH2; 1.
 DR PRODITE; PS50002; SH3; 2.
 SQ SEQUENCE 806 AA; 93868 MW; F4368CD13A62D695 CRC64;

Query Match 15.5%; Score 91.5; DB 11; Length 806;
 Best Local Similarity 32.9%; Pred. No. 0.34;
 Matches 23; Conservative 14; Mismatches 20; Indels 13; Gaps 3;

QY 26 ARAQEDYNAPDCRFIDVKKGOQIYYYSKLVTEENGAFEFNAGSVYGDHODEMGIYGFPSN 85
 DB 748 AKARYDFCARDSRLSLKEGDII---KILNKKGGQGMWRGEIYGR-----IGWFPSPN 796

QY 86 LYKEQRYOE 95
 DB 797 YVEED--YSE 804

RESULT 12
 Q8BTU7 PRELIMINARY; PRT; 845 AA.
 AC Q8BTU7;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=MOD; TISSUE=Thymus;
 RX MEDLINE=22354683; PubMed=1466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 DR EMBL: AK088566; BAC40436.1;
 SQ SEQUENCE 845 AA; 98093 MW; 5D0DED0D9311DFB8B CRC64;

Query Match 15.5%; Score 91.5; DB 11; Length 845;
 Best Local Similarity 32.9%; Pred. No. 0.36;
 Matches 23; Conservative 14; Mismatches 20; Indels 13; Gaps 3;

QY 26 ARAGEEDYNAPDCRFIDVKKGGQIYVYSKLVTEHGAGFEFAGSVYGDHDEMGIVGFPN 85
 DB 787 AKARYDFCARDRSELSLKEGDII-----KILNKGQGGWGRGEIVGR-----IGMFPN 835
 QY 86 LKSGQRYQE 95
 DB 836 YVEED--YSE 843

RESULT 13

Q8UX6 PRELIMINARY; PRT; 846 AA.

AC Q8UX6; 01-MAR-2002 (TRENBLREL. 20, Created)
 DT 01-MAR-2002 (TRENBLREL. 20, Last sequence update)
 DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
 DE GDP/GTP exchange factor VAV3.
 GN VAV3.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosaustra; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX PubMed=11805146;
 RA Inabe K., Ishai M., Scharenberg A.M., Freshney N., Downward J.,
 RA Kurosaki T.;
 RT "Vav3 Modulates B Cell Receptor Responses by Regulating
 RT Phosphoinositide 3-Kinase Activation";
 RL J. Exp. Med. 195:189-200(2002).
 CC -1- SIMILARITY: CONTAINS 2 SH3 DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
 DR EMBL: AY046915; AL06249.1;
 DR InterPro: IPR001715; Calponin-like.
 DR InterPro: IPR003247; CH_type.
 DR InterPro: IPR002219; DAG_PE-bind.
 DR InterPro: IPR001331; GDS_CDC24.
 DR InterPro: IPR001849; PH.
 DR InterPro: IPR000219; RhogEF.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR003096; SM22_calponin.
 DR Pfam: PF00307; CH_1.
 DR Pfam: PF00130; DAG_PE-bind; 1.
 DR Pfam: PF00169; PH_1.
 DR Pfam: PF00621; RhogEF; 1.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 2.
 DR PRINTS: PRO0401; SH2DOMAIN.
 DR PRINTS: PRO0452; SH3DOMAIN.
 DR PRINTS: PRO0688; SM22CALPONIN.
 DR ProDom: PD001527; CH_type; 1.
 DR ProDom: PD000093; SH2; 1.

DR ProDom: PD000066; SH3; 1.
 DR SMART: SM00109; C1; 1.
 DR SMART: SM00033; CH; 1.
 DR SMART: SM00233; PH; 1.
 DR SMART: SM00325; RhogEF; 1.
 DR SMART: SM00252; SH2; 1.
 DR SMART: SM00326; SH3; 2.
 DR PROSITE: PS50021; CH; 1.
 DR PROSITE: PS00479; DAG_PE_BIND_DOM_1; 1.
 DR PROSITE: PS50081; DAG_PE_BIND_DOM_2; 1.
 DR PROSITE: PS00741; DH_1; 1.
 DR PROSITE: PS50010; DH_2; 1.
 DR PROSITE: PS50003; PH_DOMAIN; 1.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 2.
 DR SH3 domain.
 SQ SEQUENCE 846 AA; 97815 MW; C47EE949D873821B CRC64;

Query Match 15.5%; Score 91.5; DB 13; Length 846;
 Best Local Similarity 34.3%; Pred. No. 0.36;
 Matches 23; Conservative 12; Mismatches 21; Indels 11; Gaps 2;

QY 23 ISLARAQEDYNAPDCRFIDVKKGGQIYVYSKLVTEHGAGFEFAGSVYGDHDEMGIVGFP 82
 DB 789 IGAIARYDFCARDRSELSLKGVDVYIKM-----SANGWGRGEVNGR-----VGMF 837

QY 83 PSNLYKE 89
 DB 838 PSTYVEE 844

RESULT 14

Q96D37 PRELIMINARY; PRT; 719 AA.

AC Q96D37; 01-DEC-2001 (TRENBLREL. 19, Created)
 DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)
 DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RA Strausberg R.;
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 2 SH3 DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
 DR EMBL: BC013361; AAH13361.1;
 DR InterPro: IPR002219; DAG_PE-bind.
 DR InterPro: IPR001331; GDS_CDC24.
 DR InterPro: IPR001849; PH.
 DR InterPro: IPR000219; RhogEF.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR Pfam: PF00130; DAG_PE-bind; 1.
 DR Pfam: PF00169; PH; 1.
 DR Pfam: PF00621; RhogEF; 1.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 2.
 DR PRINTS: PRO0401; SH2DOMAIN.
 DR PRINTS: PRO0452; SH3DOMAIN.
 DR ProDom: PD000093; SH2; 1.
 DR ProDom: PD000066; SH3; 1.
 DR SMART: SM00109; C1; 1.
 DR SMART: SM00233; PH; 1.
 DR SMART: SM00325; RhogEF; 1.
 DR SMART: SM00252; SH2; 1.
 DR SMART: SM00326; SH3; 2.
 DR PROSITE: PS00479; DAG_PE_BIND_DOM_1; 1.
 DR PROSITE: PS50081; DAG_PE_BIND_DOM_2; 1.

DR PROSITE; PS00741; DH 1; 1.
 DR PROSITE; PS50010; DH 2; 1.
 DR PROSITE; PS50003; PH DOMAIN; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 2.
 DR Hypothetical protein; SH3 domain.
 KW SEQUENCE 719 AA; 83727 MW; A51B757DA543BA6C CRC64;

Query Match 15.1%; Score 89.5; DB 4; Length 719;
 Best Local Similarity 32.9%; Pred. No. 0.49; Mismatches 20; Indels 13; Gaps 3;
 Matches 23; Conservative 14; Mismatches 14; Indels 13; Gaps 3;

QY 26 ARAQEDYNAPDCRFIDVKKGQIYVYSKLVTEAGGEFMAGSVYGDHODEMGIQYPPSN 85
 DB 661 AKARDFPCARDRSELSLKEGDI-----KLNKKGGQGMWRGEIYGR-----VGMFPAN 709
 QY 86 LVKEQRYOE 95
 DB 710 YVEED--YSE 717

RESULT 15
 Q8UX5 PRELIMINARY; PRT; 839 AA.
 AC Q8UX5;
 DT 01-MAR-2002 (TRENBLREL. 20, Created)
 DT 01-MAR-2002 (TRENBLREL. 20, Last sequence update)
 DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
 DE GDP/GTP exchange factor VAV2.
 GN VAV2.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=11805146;
 RA Inaba K., Ishiai M., Scharenberg A.M., Freshney N., Downard J.,
 RA Kurosaki T.;
 RT "Vav3 Modulates B Cell Receptor Responses by Regulating
 RT Phosphoinositide 3-Kinase Activation.";
 RT J. Exp. Med. 195;189-200(2002).
 CC -1- SIMILARITY: CONTAINS 2 SH3 DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
 DR EMBL; AY046916; AAL06250.1; -;
 DR InterPro; IPR001715; Calponin-like.
 DR InterPro; IPR003247; CH type.
 DR InterPro; IPR002219; DAG-pe-bind.
 DR InterPro; IPR001331; GDS_CDC24.
 DR InterPro; IPR001849; PH.
 DR InterPro; IPR000219; RhGEF.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF00307; CH; 1.
 DR Pfam; PF00130; DAG-pe-bind; 1.
 DR Pfam; PF00169; PH; 1.
 DR Pfam; PF00621; RhGEF; 1.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 2.
 DR PRINTS; PR00401; SH3DOMAIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR ProDom; PD001527; CH_type; 1.
 DR ProDom; PD000093; SH2; 1.
 DR ProDom; PD000066; SH3; 2.
 DR SMART; SM00109; C1; 1.
 DR SMART; SM00033; CH; 1.
 DR SMART; SM00233; PH; 1.
 DR SMART; SM00325; RhGEF; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 2.
 DR PROSITE; PS50021; CH; 1.
 DR PROSITE; PS00479; DAG-pe-bind_DOM_1; 1.

DR PROSITE; PS50081; DAG-pe-bind_DOM_2; 1.
 DR PROSITE; PS00741; DH 1; 1.
 DR PROSITE; PS50010; DH 2; 1.
 DR PROSITE; PS50003; PH DOMAIN; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 2.
 DR SH3 domain.
 KW SEQUENCE 839 AA; 97500 MW; 6C1322ABAC23A530 CRC64;

Query Match 14.6%; Score 86.5; DB 13; Length 839;
 Best Local Similarity 30.3%; Pred. No. 1.2; Mismatches 22; Indels 13; Gaps 3;
 Matches 23; Conservative 18; Mismatches 18; Indels 13; Gaps 3;

QY 20 VYT---ISLARAQEDYNAPDCRFIDVKKGQIYVYSKLVTEAGGEFMAGSVYGDHODEM 76
 DB 773 VFTPRVIGTAVARYNFAARMRELSLRGDEVVYKIRSGDQ---WNRG-----ETN 822
 QY 77 GIVGYPPSNLVKEQRY 92
 DB 823 GRVGMFPSTYVEEGV 838

Search completed: December 29, 2003, 16:06:26
 Job time : 17.9468 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 29, 2003, 16:03:18 ; Search time 21.5686 Seconds

(without alignments)
809.506 Million cell updates/sec

Title: US-10-019-455A-26

Perfect score: 591
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 591 | 100.0 | 110 | 22 | Mouse MLP protein |
| 2 | 591 | 100.0 | 128 | 22 | Mouse MLP protein |
| 3 | 574 | 97.1 | 110 | 22 | Rat MLP protein se |
| 4 | 574 | 97.1 | 128 | 22 | Rat MLP protein se |
| 5 | 547 | 92.6 | 110 | 22 | Human MLP protein |
| 6 | 547 | 92.6 | 128 | 22 | Human growth regul |
| 7 | 547 | 92.6 | 128 | 22 | Human MLP protein |
| 8 | 547 | 92.6 | 128 | 23 | Human angiogenesis |
| 9 | 547 | 92.6 | 128 | 23 | Human PRO873 prot |

| | | | | | | |
|----|-------|------|------|----|----------|--------------------|
| 10 | 547 | 92.6 | 128 | 23 | AAU83627 | Human PRO protein, |
| 11 | 547 | 92.6 | 128 | 23 | AAU09871 | Novel human secret |
| 12 | 519 | 87.8 | 105 | 22 | AA882672 | Human growth regul |
| 13 | 449 | 76.0 | 87 | 22 | AA869129 | Rat MLP protein se |
| 14 | 261.5 | 44.2 | 131 | 16 | AA869811 | Melanoma inhibiti |
| 15 | 261.5 | 44.2 | 131 | 22 | AA865614 | Human MIA protein |
| 16 | 259.5 | 43.9 | 137 | 22 | AA865615 | Recombinant human |
| 17 | 241.5 | 40.9 | 130 | 16 | AA869812 | Melanoma inhibiti |
| 18 | 218 | 36.9 | 125 | 23 | AA882119 | Mouse TANGO 130 MI |
| 19 | 218 | 36.9 | 130 | 22 | AA829304 | Human PRO polypept |
| 20 | 218 | 36.9 | 130 | 22 | AA887608 | Human PRO polypept |
| 21 | 218 | 36.9 | 130 | 23 | ABG95933 | Human secreted/tra |
| 22 | 218 | 36.9 | 130 | 23 | AB895600 | Human angiogenesis |
| 23 | 218 | 36.9 | 130 | 23 | AB884994 | Human PRO19670 pro |
| 24 | 218 | 36.9 | 130 | 24 | ABU71392 | Human PRO19670 pro |
| 25 | 218 | 36.9 | 130 | 24 | ABU71588 | Human secreted pol |
| 26 | 218 | 36.9 | 130 | 24 | ABU72034 | Novel human secret |
| 27 | 218 | 36.9 | 130 | 24 | ABU72191 | Human PRO polypept |
| 28 | 218 | 36.9 | 130 | 24 | ABU65849 | Human secreted/tra |
| 29 | 218 | 36.9 | 130 | 24 | ABU66182 | Novel human secret |
| 30 | 218 | 36.9 | 130 | 24 | ABU67586 | Human secreted/tra |
| 31 | 218 | 36.9 | 130 | 24 | ABU65544 | Human PRO polypept |
| 32 | 218 | 36.9 | 130 | 24 | ABU58680 | Human PRO polypept |
| 33 | 218 | 36.9 | 130 | 24 | ABU56216 | Human secreted/tra |
| 34 | 218 | 36.9 | 130 | 24 | ABU57211 | Human PRO polypept |
| 35 | 218 | 36.9 | 130 | 24 | ABU10790 | Human secreted/tra |
| 36 | 218 | 36.9 | 130 | 24 | AAU70209 | Murine TANGO 130 P |
| 37 | 218 | 36.9 | 130 | 23 | AB882117 | Human TANGO 130 po |
| 38 | 209.5 | 35.4 | 138 | 22 | AAU25834 | Human protein sequ |
| 39 | 208.5 | 35.3 | 125 | 23 | AB882120 | Human TANGO 130 MI |
| 40 | 208.5 | 35.3 | 410 | 21 | AAU70210 | Human TANGO 130 pr |
| 41 | 208.5 | 35.3 | 410 | 23 | AB882118 | Human TANGO 130 pa |
| 42 | 208.5 | 35.3 | 1907 | 23 | AB882127 | Human TANGO 130 po |
| 43 | 200 | 33.8 | 499 | 22 | AAU29319 | Human PRO polypept |
| 44 | 200 | 33.8 | 499 | 24 | ABU71407 | Human PRO20088 pro |
| 45 | 200 | 33.8 | 499 | 24 | ABU65864 | Human secreted/tra |

ALIGNMENTS

```

RESULT 1
AAB69127 standard; Protein; 110 AA.
..U
AC AAB69127;
AC
XX
DT 23-APR-2001 (first entry)
XX
DE Mouse MLP protein sequence SEQ ID NO:26.
XX
XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
XX joint disease; pathologic angiogenesis; diagnosis; antitumour;
XX cardiac; gene therapy; secretory cell function regulator; promoter;
XX inhibitor.
XX
XX Mus musculus.
XX
XX WO200102564-A1.
XX
XX 11-JAN-2001.
XX
XX 29-JUN-2000; 2000WO-0P04278.
XX
XX 30-JUN-1999; 99JP-0186718.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Itch Y, Nishi K, Ogi K, Okubo S, Mogi S, Noguchi Y, Yoshimura K;
XX Tanaka H;
XX
XX MPI: 2001-159271/16.
XX
XX N-PSDB: AAF59080.

```

XX Safe, low-toxicity secretory cell function-regulatory protein and
 PT encoded DNA, applicable as drugs, in diagnosis and development of
 PT promoters and inhibitors for preventing or treating e.g. bone and joint
 PT diseases -
 XX
 PS Claim 3; Page 98-99; 111pp; Japanese.
 XX
 CC The present invention describes novel MLP proteins and their encoding
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
 CC activities, and can be used in gene therapy and as secretory cell
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in
 CC the diagnosis and development of promoters and inhibitors for preventing
 CC or treating bone and joint diseases as well as pathologic angiogenesis.
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
 CC in the exemplification of the present invention.
 CC
 XX
 SQ Sequence 110 AA;
 Query Match 100.0%; Score 591; DB 22; Length 110;
 Best Local Similarity 100.0%; Pred. No. 2,7e-68;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HGVMFMDKLSKKLCADEECVYTTISLARAQEDYNAPDCRFIDVKKGOQIYVSKLVTENGA 60
 DB 1 HGVMFMDKLSKKLCADEECVYTTISLARAQEDYNAPDCRFIDVKKGOQIYVSKLVTENGA 60
 QY 61 GEFWAGSVYGDHDEMGIYGFPSNLVKEQRYOATKEIPTDIDFCE 110
 DB 61 GEFWAGSVYGDHDEMGIYGFPSNLVKEQRYOATKEIPTDIDFCE 110
 RESULT 2
 AAB69125
 ID AAB69125 standard; Protein; 128 AA.
 XX
 AC AAB69125;
 XX
 DT 23-APR-2001 (first entry)
 XX
 DE Mouse MLP protein sequence SEQ ID NO:12.
 XX
 KM MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
 KM joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
 KM cardiant; gene therapy; secretory cell function regulator; promoter;
 KM inhibitor.
 XX
 OS Mus musculus.
 XX
 PN WO200102564-A1.
 XX
 PD 11-JAN-2001.
 XX
 PF 29-JUN-2000; 2000WO-JP04278.
 XX
 PR 30-JUN-1999; 99JP-0186718.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Itch Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
 PI Tanaka H;
 XX
 DR WPI; 2001-159271/16.
 DR N-PSDB; AAF59068.
 XX
 CC Safe, low-toxicity secretory cell function-regulatory protein and
 PT encoded DNA, applicable as drugs, in diagnosis and development of
 PT promoters and inhibitors for preventing or treating e.g. bone and joint
 PT diseases -
 XX
 PS Claim 4; Page 93-94; 111pp; Japanese.
 PS
 CC The present invention describes novel MLP proteins and their encoding

CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
 CC activities, and can be used in gene therapy and as secretory cell
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in
 CC the diagnosis and development of promoters and inhibitors for preventing
 CC or treating bone and joint diseases as well as pathologic angiogenesis.
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
 CC in the exemplification of the present invention.
 CC
 XX
 SQ Sequence 128 AA;
 Query Match 100.0%; Score 591; DB 22; Length 128;
 Best Local Similarity 100.0%; Pred. No. 3.3e-68;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HGVMFMDKLSKKLCADEECVYTTISLARAQEDYNAPDCRFIDVKKGOQIYVSKLVTENGA 60
 DB 19 HGVMFMDKLSKKLCADEECVYTTISLARAQEDYNAPDCRFIDVKKGOQIYVSKLVTENGA 78
 QY 61 GEFWAGSVYGDHDEMGIYGFPSNLVKEQRYOATKEIPTDIDFCE 110
 DB 79 GEFWAGSVYGDHDEMGIYGFPSNLVKEQRYOATKEIPTDIDFCE 128
 RESULT 3
 AAB69131
 ID AAB69131 standard; Protein; 110 AA.
 XX
 AC AAB69131;
 XX
 DT 23-APR-2001 (first entry)
 XX
 DE Rat MLP protein sequence SEQ ID NO:49.
 XX
 KM MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
 KM joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
 KM cardiant; gene therapy; secretory cell function regulator; promoter;
 KM inhibitor.
 XX
 OS Rattus sp.
 XX
 PN WO200102564-A1.
 XX
 PD 11-JAN-2001.
 XX
 PF 29-JUN-2000; 2000WO-JP04278.
 XX
 PR 30-JUN-1999; 99JP-0186718.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Itch Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
 PI Tanaka H;
 XX
 DR WPI; 2001-159271/16.
 DR N-PSDB; AAF59099.
 XX
 CC Safe, low-toxicity secretory cell function-regulatory protein and
 PT encoded DNA, applicable as drugs, in diagnosis and development of
 PT promoters and inhibitors for preventing or treating e.g. bone and joint
 PT diseases -
 XX
 PS Claim 5; Page 107; 111pp; Japanese.
 PS
 CC The present invention describes novel MLP proteins and their encoding
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
 CC activities, and can be used in gene therapy and as secretory cell
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in
 CC the diagnosis and development of promoters and inhibitors for preventing
 CC or treating bone and joint diseases as well as pathologic angiogenesis.
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
 CC in the exemplification of the present invention.
 CC
 XX
 SQ Sequence 110 AA;

Query Match 97.1%; Score 574; DB 22; Length 110;
 Best Local Similarity 96.4%; Pred. No. 4.3e-66;
 Matches 106; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 HGVFMDLSSKRLCADEECVYTTISLARAQEDYNAPDCRFIDVKKGGQIYVYSKLVTENGA 60
 DB 1 HGVFMDLSSKRLCADEECVYTTISLARAQEDYNAPDCRFIDVKKGGQIYVYSKLVTENGA 60

QY 61 GEFWAGSVYGDHODEMGIVGFPPSNLVKEQRYVQEAATKEIPTTIDIFPCE 110
 DB 61 GEFWAGSVYGDHODEMGIVGFPPSNLVKEQRYVQEAATKEIPTTIDIFPCE 110

RESULT 4
 AAB69130
 ID AAB69130 standard; Protein; 128 AA.

XX AAB69130;

XX 23-APR-2001 (first entry)

DE Rat MLP protein sequence SEQ ID NO:47.

KM MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
 KM joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
 KM cardiant; gene therapy; secretory cell function regulator; promoter;
 KM inhibitor.

XX Rattus sp.

XX WO200102564-A1.

XX 11-JAN-2001.

XX 23-JUN-2000; 2000WO-JP04278.

XX 30-JUN-1999; 99JP-0186718.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
 XX Tanaka H;

XX WPI; 2001-159271/16.

XX N-PSDB; AAF59098.

PT Safe, low-toxicity secretory cell function-regulatory protein and
 PT encoded DNA, applicable as drugs, in diagnosis and development of
 PT promoters and inhibitors for preventing or treating e.g. bone and joint
 PT diseases -

PS Claim 6; Page 106; 111pp; Japanese.

XX The present invention describes novel MLP proteins and their encoding
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
 CC activities, and can be used in gene therapy and as secretory cell
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in
 CC the diagnosis and development of promoters and inhibitors for preventing
 CC or treating bone and joint diseases as well as pathologic angiogenesis.
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
 CC in the exemplification of the present invention.

XX Sequence 128 AA;

Query Match 97.1%; Score 574; DB 22; Length 128;
 Best Local Similarity 96.4%; Pred. No. 5.3e-66;
 Matches 106; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 HGVFMDLSSKRLCADEECVYTTISLARAQEDYNAPDCRFIDVKKGGQIYVYSKLVTENGA 60
 DB 1 HGVFMDLSSKRLCADEECVYTTISLARAQEDYNAPDCRFIDVKKGGQIYVYSKLVTENGA 78

QY 61 GEFWAGSVYGDHODEMGIVGFPPSNLVKEQRYVQEAATKEIPTTIDIFPCE 110
 DB 79 GEFWAGSVYGDHODEMGIVGFPPSNLVKEQRYVQEAATKEIPTTIDIFPCE 128

RESULT 5
 AAB69126
 ID AAB69126 standard; Protein; 110 AA.

XX AAB69126;

XX 23-APR-2001 (first entry)

DE Human MLP protein sequence SEQ ID NO:24.

KM MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
 KM joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
 KM cardiant; gene therapy; secretory cell function regulator; promoter;
 KM inhibitor.

XX Homo sapiens.

XX WO200102564-A1.

XX 11-JAN-2001.

XX 29-JUN-2000; 2000WO-JP04278.

XX 30-JUN-1999; 99JP-0186718.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
 XX Tanaka H;

XX WPI; 2001-159271/16.

XX N-PSDB; AAF59079.

PT Safe, low-toxicity secretory cell function-regulatory protein and
 PT encoded DNA, applicable as drugs, in diagnosis and development of
 PT promoters and inhibitors for preventing or treating e.g. bone and joint
 PT diseases -

PS Claim 1; Page 97-98; 111pp; Japanese.

XX The present invention describes novel MLP proteins and their encoding
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
 CC activities, and can be used in gene therapy and as secretory cell
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in
 CC the diagnosis and development of promoters and inhibitors for preventing
 CC or treating bone and joint diseases as well as pathologic angiogenesis.
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
 CC in the exemplification of the present invention.

XX Sequence 110 AA;

Query Match 92.6%; Score 547; DB 22; Length 110;
 Best Local Similarity 90.0%; Pred. No. 1.3e-62;
 Matches 99; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 HGVFMDLSSKRLCADEECVYTTISLARAQEDYNAPDCRFIDVKKGGQIYVYSKLVTENGA 60
 DB 1 HGVFMDLSSKRLCADEECVYTTISLARAQEDYNAPDCRFIDVKKGGQIYVYSKLVTENGA 60

QY 61 GEFWAGSVYGDHODEMGIVGFPPSNLVKEQRYVQEAATKEIPTTIDIFPCE 110
 DB 61 GEFWAGSVYGDHODEMGIVGFPPSNLVKEQRYVQEAATKEIPTTIDIFPCE 110

RESULT 6
 AAB82671
 ID AAB82671 standard; Protein; 128 AA.

AC AAB82671;
 XX 02-OCT-2001 (first entry)
 XX Human growth regulatory-like polypeptide.
 DE Growth regulatory-like polypeptide; human; cartilage; melanoma;
 KM neuroectodermal tumour; glioma; cancer; therapy; diagnosis.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 PH Peptide 1..23
 FT /label= Signal_peptide
 FT Protein 24..128
 FT /label= Mature_protein
 FT /note= "separately claimed in Claim 10"
 XX
 XX W020015332-A2.
 XX
 XX 02-AUG-2001.
 XX
 XX 25-JAN-2001; 2001WO-US02455.
 XX
 XX 25-JAN-2000; 2000US-049,404.
 XX 02-MAY-2000; 2000US-0563786.
 XX
 XX (HYSEQ) HYSEQ INC.
 XX
 XX Mize NK, Boyle BJ, Ford JE, Arterburn MC, Tang YF, Liu C;
 PI Drmanac RT;
 PI WPI: 2001-483233/52.
 DR N-PSDB; AAB6343.
 XX
 XX Isolated human growth regulatory-like polypeptide: useful for treating
 PT e.g. Alzheimer's disease, cancer, autoimmune disorders,
 PT hyperproliferative disorders, coagulation disorders, and nervous system
 PT disorders -
 PT
 PS Claim 10; Page 116-117; 119pp; English.
 XX
 XX The present sequence is that of a novel human growth regulatory-like
 CC polypeptide (GRLP). The amino acid sequence is predicted from a
 CC novel assembled cDNA (see AAB26343) based on Hyseq clone number
 CC 16322272. The protein has a mol.wt. of 14 kDa unglycosylated. GRLP
 CC belongs to the same protein family as growth regulatory proteins,
 CC growth factors, human melanoma derived growth regulatory proteins,
 CC precursor (64% similarity and 45% identity over 111 amino acids)
 CC or melanoma inhibitory activity, cattle cartilage-derived
 CC retinoic acid sensitive protein (CD-RAP, 44% identity and 64%
 CC similarity over 126 amino acids) and other retinoic acid-sensitive
 CC proteins. GRLP polypeptides and polynucleotides of the invention
 CC can be used in the prophylaxis, treatment (including gene therapy)
 CC and diagnosis of disorders and diseases caused by, or involving,
 CC cartilage development and maintenance, inhibition of melanoma cell
 CC growth, and tumours, including neuroectodermal tumours such as
 CC gliomas. The polypeptides, which include the GRLP mature protein,
 CC may also have nutritional uses, cytokine and cell proliferation
 CC or differentiation activity, stem cell growth factor activity,
 CC haematopoiesis regulating activity, tissue growth activity,
 CC immunosuppressive or immunostimulant activity, activin/inhibin
 CC activity, chemotactic/chemokinetic activity, haemostatic and
 CC thrombolytic activity, use in cancer diagnosis and therapy,
 CC drug screening, receptor/ligand activity, antiinflammatory
 CC activity, and treatment of leukaemia, nervous system disorders,
 CC arthritis and inflammation.
 XX
 XX Sequence 128 AA;
 SQ
 Query Match 92.6%; Score 547; DB 22; Length 128;
 Best Local Similarity 90.0%; Pred. No. 1.7e-62;
 Matches 99; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 HGVMFMDKLSKKKLCADDECCTTISLAPAOEDYNAPDCRFIDVKKQGOIYVSKLVTENGA 60
 DB 19 HGIFMDRLASKKLCADDECCTTISLAPAOEDYNAPDCRFINVKKGOIYVSKLVENGA 78
 QY 61 GEFMAGSVYGDHODEMGIVGFPPSNLVKEQRYQATKEIPTTDIDFCE 110
 DB 79 GEFMAGSVYGDGODEMGVGFPPRLVKEQRYQATKEVPTTDIDFCE 128
 RESULT 7
 AAB69123
 ID AAB69123 standard; Protein; 128 AA.
 XX
 XX AAB69123;
 AC
 XX 23-APR-2001 (first entry)
 DT
 XX Human MLP protein sequence SEQ ID NO:6.
 DE
 XX MLP: MIA; melanoma inhibitory activity; cancer; bone disease;
 KM joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
 KM cardiant; gene therapy; secretory cell function regulator; promoter;
 KM inhibitor.
 XX
 XX Homo sapiens.
 OS
 XX W0200102564-A1.
 XX
 XX 11-JAN-2001.
 XX
 XX 23-JUN-2000; 2000WO-JP04278.
 XX
 XX 30-JUN-1999; 99JP-0186718.
 XX
 XX (TAKE) TAKEDA CHEM IND LTD.
 PA
 XX Itoh Y, Nishi K, Ogi K, Okubo S, Mogi S, Noguchi Y, Yoshimura K;
 PI Tanaka H;
 PI WPI: 2001-159271/16.
 DR N-PSDB; AAF59065.
 XX
 XX Safe, low-toxicity secretory cell function-regulatory prorein and
 PT encoded DNA, applicable as drugs, in diagnosis and development of
 PT promoters and inhibitors for preventing or treating e.g. bone and joint
 PT diseases -
 PT
 PS Claim 2; Page 91-92; 111pp; Japanese.
 XX
 XX The present invention describes novel MLP proteins and their encoding
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
 CC activities, and can be used in gene therapy and as secretory cell
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in
 CC the diagnosis and development of promoters and inhibitors for preventing
 CC or treating bone and joint diseases as well as pathologic angiogenesis.
 CC AAF59063 to AAF59059 and AAB69122 to AAB69132 represent sequences used
 CC in the exemplification of the present invention.
 XX
 XX Sequence 128 AA;
 SQ
 Query Match 92.6%; Score 547; DB 22; Length 128;
 Best Local Similarity 90.0%; Pred. No. 1.7e-62;
 Matches 99; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
 QY 1 HGVMFMDKLSKKKLCADDECCTTISLAPAOEDYNAPDCRFIDVKKQGOIYVSKLVTENGA 60
 DB 19 HGIFMDRLASKKLCADDECCTTISLAPAOEDYNAPDCRFINVKKGOIYVSKLVENGA 78
 QY 61 GEFMAGSVYGDHODEMGIVGFPPSNLVKEQRYQATKEIPTTDIDFCE 110
 DB 79 GEFMAGSVYGDGODEMGVGFPPRLVKEQRYQATKEVPTTDIDFCE 128

RESULT 8
ID ABB95602
XX ABB95602 standard; Protein, 128 AA.
XX
AC ABB95602;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human angiogenesis related protein PRO9873 SEQ ID NO: 360.
XX
KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KM atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KM cardiac; cytosolic; antiangiogenic; hypotensive; vlnetary;
XX antiarteriosclerotic.
XX
OS Homo sapiens.
XX
PN MO200208284-A2.
XX
PD 31-JAN-2002.
XX
PE 09-JUL-2001; 2001WO-US21735.
XX
PF 20-JUL-2000; 2000US-219556P.
XX
PR 25-JUL-2000; 2000US-220624P.
PR 25-JUL-2000; 2000US-220624P.
PR 28-JUL-2000; 2000WO-US20710.
PR 02-AUG-2000; 2000US-222695P.
PR 17-AUG-2000; 2000US-064365P.
PR 23-AUG-2000; 2000WO-US2352P.
PR 24-AUG-2000; 2000WO-US2332P.
PR 07-SEP-2000; 2000US-230978P.
PR 15-SEP-2000; 2000US-000000P.
PR 18-SEP-2000; 2000US-0654610.
PR 18-SEP-2000; 2000US-065350.
PR 24-OCT-2000; 2000US-242922P.
PR 08-NOV-2000; 2000US-070923P.
PR 08-NOV-2000; 2000WO-US3095P.
PR 10-NOV-2000; 2000WO-US3087P.
PR 20-DEC-2000; 2000WO-US3267P.
PR 20-DEC-2000; 2000US-074725P.
PR 20-DEC-2000; 2000WO-US3495P.
PR 22-JAN-2001; 2001US-076760P.
PR 28-FEB-2001; 2001US-079649P.
PR 28-FEB-2001; 2001WO-US0652P.
PR 01-MAR-2001; 2001WO-US0666P.
PR 09-MAR-2001; 2001US-080270P.
PR 14-MAR-2001; 2001US-080688P.
PR 22-MAR-2001; 2001US-081674P.
PR 05-APR-2001; 2001US-082836P.
PR 10-MAY-2001; 2001US-085420P.
PR 10-MAY-2001; 2001US-085428P.
PR 25-MAY-2001; 2001US-086602P.
PR 25-MAY-2001; 2001US-086603P.
PR 30-MAY-2001; 2001US-087057P.
PR 30-MAY-2001; 2001WO-US1744P.
PR 01-JUN-2001; 2001WO-US1780P.
PR 20-JUN-2001; 2001WO-US19692P.
PR 28-JUN-2001; 2001WO-US00000P.
XX
PA (GETH) GENENTECH INC.
PA (BAKE) BAKER K P.
PA (FERR) FERRARA N.
PA (GERR) GERBER H.
PA (GERR) GERITSEN M E.
PA (GODD) GODDARD A.
PA (GODD) GODOWSKI P J.
PA (GURN) GURNEY A L.
PA (HILL) HILLAN K J.
PA (MARS) MARSTERS S A.
PA (PANJ) PAN J.

PA (PAON) PAONI N F.
PA (STEP) STEPHAN J F.
PA (WATA) WATANABE C K.
PA (WILL) WILLIAMS P M.
PA (WOOD) WOOD W I.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
DR WPI: 2002-171999/22.
DR N-PSDB; ABL95740.
XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal -
XX
PS Claim 11; Fig 360; 567pp; English.
XX
CC The present invention provides the protein and coding sequences of human
CC PRO proteins. These are useful for treating or diagnosing a
CC cardiovascular, endothelial or angiogenic disorder, including cardiac
CC hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
XX healing. The present sequence is a PRO protein of the invention.
XX
SQ Sequence 128 AA;
XX
Query Match 92.6%; Score 547; DB 23; Length 128;
Best Local Similarity 90.0%; Pred. No. 1,7e-62;
Matches 99; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
XX
QY 1 HGVMFKLSKKKLCADCECVTITSLAQEDYNAPDCRFIDVKKGQIIVYSKLYTNGA 60
DB 19 HGIFMDRLASKKLCADCECVTITSLAQEDYNAPDCRFIDVKKGQIIVYSKLYTNGA 78
XX
QY 61 GEFWAGSYVGDHODEMGIIVGFPNSLVKQRYQOATKIEPTDIDFCE 110
DB 79 GEFWAGSYVGDHODEMGIIVGFPNSLVKQRYQOATKIEPTDIDFCE 128
XX
RESULT 9
ID ABB84996
XX ABB84996 standard; Protein, 128 AA.
XX
AC ABB84996;
XX
DT 16-MAY-2002 (first entry)
XX
DE Human PRO9873 protein sequence SEQ ID NO:360.
XX
DE Human PRO9873 protein sequence SEQ ID NO:360.
XX
KW Human; angiogenesis; cardiac; cytosolic; antiangiogenic; hypotensive;
KM vulnerable; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
KM gene therapy; cardiovascular disorder; endothelial disorder; cancer;
KM angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
KM age-related macular degeneration; arterial restenosis; angina;
KM rheumatoid arthritis; myocardial infarction; thrombophlebitis;
KM lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
KM wound healing; chromosome mapping; gene mapping.
XX
OS Homo sapiens.
XX
PN MO200200690-A2.
XX
PD 03-JAN-2002.
XX
PF 20-JUN-2001; 2001WO-US19692.
XX
PR 23-JUN-2000; 2000US-213637P.
PR 20-JUL-2000; 2000US-219556P.
PR 25-JUL-2000; 2000US-220624P.

PR 25-JUL-2000; 2000US-220664P.
 PR 28-JUL-2000; 2000MO-US20710.
 PR 02-AUG-2000; 2000US-222695P.
 PR 17-AUG-2000; 2000US-0643657.
 PR 23-AUG-2000; 2000MO-US23522.
 PR 24-AUG-2000; 2000MO-US23328.
 PR 07-SEP-2000; 2000US-230978P.
 PR 18-SEP-2000; 2000US-0664610.
 PR 18-SEP-2000; 2000US-0665350.
 PR 24-OCT-2000; 2000US-242922P.
 PR 08-NOV-2000; 2000US-0709238.
 PR 08-NOV-2000; 2000MO-US30952.
 PR 10-NOV-2000; 2000MO-US30873.
 PR 01-DEC-2000; 2000MO-US32678.
 PR 20-DEC-2000; 2000US-0747259.
 PR 20-DEC-2000; 2000MO-US34956.
 PR 22-JAN-2001; 2001US-0767609.
 PR 28-FEB-2001; 2001US-0796498.
 PR 28-FEB-2001; 2001MO-US06520.
 PR 01-MAR-2001; 2001MO-US06566.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0808689.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 25-MAY-2001; 2001MO-US17092.
 PR 30-MAY-2001; 2001US-0870574.
 PR 30-MAY-2001; 2001MO-US17443.
 PR 01-JUN-2001; 2001MO-US17800.

XX (GETH) GENENTECH INC.

XX Baker KP, Ferreira N, Gerber H, Gerritsen ME, Goddard A, Godowski PJ, Godowski PJ, Gurney AL, Hillan KJ, Masters SA, Pan J, Paoni NF, PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W, XX
 DR WPI: 2002-090516/12.
 DR N-PSDB: ABL88251.

PT One hundred and eighty seven nucleic acids encoding PRO polypeptides, PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal -

XX Claim 11; Fig 360; 565pp; English.

XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic, CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic CC activities, and can be used in gene therapy. The PRO polynucleotides, CC proteins, agonists and antagonists are useful for treating or diagnosing CC a cardiovascular, endothelial or angiogenic disorder in a mammal, CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular CC degeneration, atherosclerosis, hypertension, arterial restenosis, CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver CC carcinoma) and wound healing. The PRO polynucleotides have applications CC in molecular biology, including use as hybridisation probes, and in CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and CC probes used in the exemplification of the present invention.

XX Sequence 128 AA;

Query Match 92.6%; Score 547; DB 23; Length 128;
 Best Local Similarity 90.0%; Pred. No. 1.7e-62;
 Matches 99; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

OY 1 HGVMKSKSKLCADECCVYTIISARAQEDYNAPDRCFFIDVKKGGQIYYYSKLVTENGA 60
 DB 19 HGIMDRILASKKLCADCCVYTIISARAQEDYNAPDRCFFIVKKGQIYYYSKLVKENG 78

OY 61 GEFNAGSVYGDHODENGVYFPPSNLYKGRVYQEAATKEPTTIDPFCE 110
 DB 79 GEFNAGSVYGDHODENGVYFPPSNLYKGRVYQEAATKEPTTIDPFCE 128

RESULT 10

AAU83627
 ID AAU83627 standard; Protein; 128 AA.

XX AAU83627;

DT 08-MAY-2002 (first entry)

DE Human PRO protein, Seq ID No 72.

XX Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
 KM breast cancer; prostate tumour; rectal tumour; liver tumour;
 KM pericyte cell proliferation; chondrocyte cell proliferation;
 KM tumour necrosis factor-alpha.

OS Homo sapiens.

PN WO200208288-A2.

PD 31-JAN-2002.

PF 29-JUN-2001; 2001MO-US21066.

XX 20-JUL-2000; 2000US-219556P.

PR 25-JUL-2000; 2000US-220585P.

PR 25-JUL-2000; 2000US-220605P.

PR 25-JUL-2000; 2000US-220607P.

PR 25-JUL-2000; 2000US-220624P.

PR 25-JUL-2000; 2000US-220638P.

PR 25-JUL-2000; 2000US-220664P.

PR 26-JUL-2000; 2000US-220893P.

PR 28-JUL-2000; 2000MO-US20710.

PR 23-AUG-2000; 2000MO-US23522.

PR 24-AUG-2000; 2000MO-US23328.

PR 15-SEP-2000; 2000US-000000P.

PR 10-NOV-2000; 2000MO-US30873.

PR 28-NOV-2000; 2000US-253646P.

PR 01-DEC-2000; 2000MO-US32678.

PR 20-DEC-2000; 2000US-0747259.

PR 20-DEC-2000; 2000MO-US34956.

PR 28-FEB-2001; 2001MO-US06520.

PR 10-MAY-2001; 2001US-0854280.

PR 25-MAY-2001; 2001MO-US17092.

PA (GETH) GENENTECH INC.

XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX WPI: 2002-172001/22.
 XX N-PSDB: ABK33571.

PT One hundred and twenty two nucleic acids encoding PRO polypeptides, PT useful for treating a PRO related disorder and for diagnosing tumours PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal PT tumour or liver tumour -

XX Claim 11; Figure 72; 359pp; English.

XX The invention relates to one hundred and twenty two nucleic acids CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides CC encode human secreted proteins. The PRO nucleic acids, polypeptides, CC agonists and antagonists are useful for treating a PRO related disorder. CC The PRO polypeptides are useful for diagnosing tumours, especially lung CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or CC liver tumour. The PRO polypeptides are useful for stimulating the CC proliferation of, or gene expression, in pericyte cells, for stimulating

CC the proliferation or differentiation of chondrocyte cells, for
 CC stimulating the release of tumour necrosis factor- α from human blood,
 CC for stimulating or inhibiting the proliferation of normal human dermal
 CC fibroblast cells. The PRO polypeptide may also be used as molecular
 CC weight markers and for tissue typing. The PRO nucleic acids have
 CC applications in molecular biology, including use as hybridisation probes,
 CC and in chromosome and gene mapping. AA083592-AA083713 represent human PRO
 CC protein sequences of the invention.

XX Sequence 128 AA;

Query Match 92.6%; Score 547; DB 23; Length 128;

Best Local Similarity 90.0%; Pred. No. 1.7e-62;

Matches 99; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 HGVFMDLSSKKLCADDECVYTISLAPQEDYNAPDCRFIDYKGGQIYVYSKLVTENGA 60
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 19 HGI FMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQIYVYSKLVKENG 78
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 61 GEFWAGSVYGDHODEMGIVGFPSNLYKEQRYVQEARKEIPTDIDFCE 110
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 79 GEFWAGSVYGDGDEMGVGVGFPRNLVKEQRYVQEARKEVPTDIDFCE 128

RESULT 11

AAU09871

ID AAU09871 standard; Protein; 128 AA.

AC AAU09871;

XX 26-FEB-2002 (first entry)

DE Novel human secreted protein #12.

XX Secreted protein; cytosolic; immunosuppressive; vulnary; vaccine;
 XX antiinflammatory; neuroprotective; nephrotoxic; cardiovascular;
 XX human; cancer; autoimmune disease; wound healing disorder; infection;
 XX haematopoietic disorder; inflammatory disorder; infertility;
 XX neurological disease; psychiatric disease; cardiovascular disease;
 XX respiratory disease; renal; gastrointestinal.

OS Homo sapiens.

PN WO200179454-A1.

XX 25-OCT-2001.

PF 11-APR-2001; 2001WO-US11797.

PR 13-APR-2000; 2000US-196603P.

PR 24-APR-2000; 2000US-199417P.

XX (SMK) SMITHKLINE BEECHAM CORP.

PA (SMK) SMITHKLINE BEECHAM PLC.

PI Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;

DR MPI: 2002-061975/08.

DR N-PSDB; AAS17583.

PT New secreted proteins or polypeptides, useful for treating e.g. cancer,
 PT autoimmune diseases, wound healing disorder, infections, haematopoietic
 PT disorders, inflammatory disorders, infertility, cancer -

XX Claim 1; Page 73-74; 92pp; English.

XX The invention relates to an isolated novel secreted polypeptide (I) and
 CC polynucleotide (II). (I) and (II) are useful for treating cancer,
 CC autoimmune diseases, wound healing disorder, infections, haematopoietic
 CC disorders, inflammatory disorders, infertility, neurological and
 CC psychiatric diseases, cardiovascular diseases, respiratory diseases,
 CC renal diseases, or gastrointestinal diseases. These may also be used to
 CC treat diseases, abnormalities and disorders caused by abnormal

CC expression, production, function and/or metabolism of the genes, as
 CC vaccines for inducing immunological response in a mammal, and in
 CC screening methods for detecting the effect of added compounds on the
 CC production of mRNA and polypeptide in cells. The polypeptides can be used
 CC as immunogens to produce antibodies immunospecific for the polypeptides,
 CC and to identify membrane-bound or soluble receptors. The polynucleotides
 CC may be used as diagnostic reagents, in chromosome localisation studies,
 CC and in tissue expression studies. The present sequence represents the
 CC amino acid sequence of novel human secreted protein #12.

XX Sequence 128 AA;

Query Match 92.6%; Score 547; DB 23; Length 128;

Best Local Similarity 90.0%; Pred. No. 1.7e-62;

Matches 99; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 HGVFMDLSSKKLCADDECVYTISLAPQEDYNAPDCRFIDYKGGQIYVYSKLVTENGA 60
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 19 HGI FMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQIYVYSKLVKENG 78
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 61 GEFWAGSVYGDHODEMGIVGFPSNLYKEQRYVQEARKEIPTDIDFCE 110
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 79 GEFWAGSVYGDGDEMGVGVGFPRNLVKEQRYVQEARKEVPTDIDFCE 128

RESULT 12

AA082672

ID AAB82672 standard; Protein; 105 AA.

AC AAB82672;

XX 02-OCT-2001 (first entry)

DE Human growth regulatory-like polypeptide (mature protein).

XX Growth regulatory-like polypeptide; human; cartilage; melanoma;
 XX neuroectodermal tumour; glioma; cancer; therapy; diagnosis.

OS Homo sapiens.

PN WO200155332-A2.

XX 02-AUG-2001.

PF 25-JAN-2001; 2001WO-US02455.

PR 25-JAN-2000; 2000US-0491404.

PR 02-MAY-2000; 2000US-0563786.

XX (HYSE-) HYSEQ INC.

PI Mize NK, Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C;

PI Drmanac RT;

DR MPI: 2001-463233/52.

DR N-PSDB; AAB26343.

PT Isolated human growth regulatory-like polypeptide useful for treating
 PT e.g. Alzheimer's disease, cancer, autoimmune disorders,
 PT hyperproliferative disorders, coagulation disorders, and nervous system
 PT disorders -

XX Claim 10; Page 117; 119pp; English.

XX The present sequence is that of a novel human growth regulatory-like
 CC polypeptide (GRP) mature protein. The sequence is predicted from
 CC a novel assembled cDNA (see AAB26343) based on Hyseq clone number
 CC 16372272. The protein has a mol.wt. of 14 kDa unglycosylated. GRP
 CC belongs to the same protein family as growth regulatory proteins,
 CC growth factors, human melanoma derived growth regulatory protein
 CC precursor (64% similarity and 45% identity over 111 amino acids)
 CC or melanoma inhibitory activity, cattle cartilage-derived
 CC retinoic acid sensitive protein (CD-RAP, 44% identity and 64%

CC similarity over 16 amino acids) and other retinoic acid-sensitive
 CC proteins. GRP polypeptides and polynucleotides of the invention
 CC can be used in the prophylaxis, treatment (including gene therapy)
 CC and diagnosis of disorders and diseases caused by, or involving,
 CC cartilage development and maintenance, inhibition of melanoma cell
 CC growth and tumours, including neuroectodermal tumours such as
 CC gliomas. The polypeptides, which include the GRP mature protein,
 CC may also have nutritional uses, cytokine and cell proliferation
 CC or differentiation activity, stem cell growth factor activity,
 CC haematopoiesis regulating activity, tissue growth activity,
 CC immunosuppressive or immunostimulant activity, activating/inhibin
 CC activity, chemotactic/chemokinetic activity, haemostatic and
 CC thrombolytic activity, use in cancer diagnosis and therapy,
 CC drug screening, receptor/ligand activity, antiinflammatory
 CC activity, and treatment of leukaemia, nervous system disorders,
 CC arthritis and inflammation.

XX
 SQ Sequence 105 AA;

Query Match 87.8%; Score 519; DB 22; Length 105;
 Best Local Similarity 90.5%; Pred. No. 5.3e-59;
 Matches 95; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 6 DKLSKKLCADCECVYITISLARAQEDYNAPDCRFIDVKKGOQIVYYSKLVTEGAGEFWA 65
 DB 1 DRLASKKLCADCECVYITISLARAQEDYNAPDCRFIDVKKGOQIVYYSKLVTEGAGEFWA 60

QY 66 GSVYGDHODEMGIVGYFPPSNLVKEQRYOATKEIPTDIDFCE 110
 DB 61 GSVYGGQDEMGVGYFPPRLVKEQRYOATKEVETTDIDFCE 105

RESULT 13
 AAB69129
 ID AAB69129 standard; Protein; 87 AA.
 XX
 AC AAB69129;
 XX
 DT 23-APR-2001 (first entry)
 XX
 DE Rat MLP protein sequence SEQ ID NO:39.
 XX
 KM MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
 KM joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
 KM cardiac; gene therapy; secretory cell function regulator; promoter;
 KM inhibitor.
 XX
 OS Rattus sp.
 XX
 PN MO200102564-A1.
 XX
 PD 11-JAN-2001.
 XX
 PF 29-JUN-2000; 2000MO-JP04278.
 XX
 PR 30-JUN-1999; 99JP-0186718.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
 PI Tanaka H;
 XX
 DR WPI; 2001-159271/16.
 XX
 PT Safe, low-toxicity secretory cell function-regulatory protein and
 PT encoded DNA, applicable as drugs, in diagnosis and development of
 PT promoters and inhibitors for preventing or treating e.g. bone and joint
 PT diseases -
 XX
 PS Example 9; Page 103; 11pp; Japanese.
 XX
 CC The present invention describes novel MLP proteins and their encoding
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiac

CC activities, and can be used in gene therapy and as secretory cell
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in
 CC the diagnosis and development of promoters and inhibitors for preventing
 CC or treating bone and joint diseases as well as pathologic angiogenesis.
 CC AAF5903 to AAF5909 and AAB6912 to AAB69132 represent sequences used
 CC in the exemplification of the present invention.

XX
 SQ Sequence 87 AA;

Query Match 76.0%; Score 449; DB 22; Length 87;
 Best Local Similarity 96.6%; Pred. No. 4.8e-50;
 Matches 84; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 DKLSKKLCADCECVYITISLARAQEDYNAPDCRFIDVKKGOQIVYYSKLVTEGAGEFWA 65
 DB 1 DKLSKKLCADCECVYITISLARAQEDYNAPDCRFIDVKKGOQIVYYSKLVTEGAGEFWA 60

QY 66 GSVYGDHODEMGIVGYFPPSNLVKEQRY 92
 DB 61 GSVYGDHODEMGIVGYFPPSNLVKEQRY 87

RESULT 14
 AAB69811
 ID AAB69811 standard; Protein; 131 AA.
 XX
 AC AAB69811;
 XX
 DT 25-MAR-2003 (updated)
 DT 26-OCT-1995 (first entry)
 XX
 DE Melanoma inhibiting protein (human).
 XX
 KM Melanoma; inhibition; cancer; melanoma; glioblastoma; neuroblastoma;
 KM small cell lung cancer; neuroectodermal tumours; immunosuppressant;
 KM phycohaemagglutinin; lymphocyte; interleukin 2; IL-2; detection;
 KM probe; fusion protein.
 XX
 OS Homo sapiens.
 XX
 PN WO9503328-A2.
 XX
 PD 02-FEB-1995.
 XX
 PF 19-JUL-1994; 94WO-EP02369.
 XX
 PR 20-JUL-1993; 93DE-4324247.
 XX
 PA (BOE) BOEHRINGER MANNHEIM GMBH.
 XX
 PI Bogdahn U, Buettner R, Kaluza B;
 XX
 DR WPI; 1995-075191/10.
 DR N-PsDB; AAQ84050; AAQ84051.
 XX
 PT New melanoma inhibiting protein and related nucleic acid -
 PT vectors, transformed cells, antibodies etc., useful for treating
 PT tumours and as immunosuppressant e.g. by gene therapy
 XX
 PS Claim 1; Page 54; 85pp; German.
 XX
 CC This protein has melanoma-inhibiting activity and can be used to
 CC treat cancer (melanoma, glioblastoma, neuroblastoma, small cell
 CC lung cancer, neuroectodermal tumours) or as an immunosuppressant
 CC (it inhibits IL-2 or phytohaemagglutinin induced proliferation of
 CC peripheral blood lymphocytes). Antibodies raised against the
 CC protein can be used to detect cell producing the protein and also
 CC for protein purification. Probes derived from DNA encoding the
 CC protein (AAQ84050, AAQ84051) can be used to detect sequences encoding
 CC the protein or related proteins. The protein may be expressed as
 CC a fusion protein (conjugated with dihydrofolate reductase (DHFR)).
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX

SQ Sequence 131 AA;

| | | | | |
|-----------------------|--------|--------------------|--------|----------------|
| Query Match | 44.2%; | Score 261.5; | DB 16; | Length 131; |
| Best Local Similarity | 45.4%; | Pred. No. 1.6e-25; | | |
| Matches | 49; | Conservative | 24; | Mismatches 30; |
| | | | | Indels 5; |
| | | | | Gaps 3; |

```

QY      2 MDLKLSSKGLCADEECVYTITSLARQGYNNAPDGRFTIDVKKKQQCIYYASKLTIVENAGGE-F-63
        :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db      27 MPTLADPKRLCADQCSHPISMAVALQYNNAPDCRFLTHRGVVYVFSTL---KGSGRLF 83
QY      64 WASSVYGDHDDQEMGI-VGSPFNLSLYNQRRYYCEATKEIPTTIDIFCEE 110
        :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db      84 WGGSVGQSDIYGDLAARGTFPPSSIVREDDQLTKRKGVDKTDKDDPFCQG 131

```

RESULT 15
AAG65614

AC AAG65614 ;

DT 07-JAN-2002 (first entry)

Human MIA protein sequence.

KM MA, melanoma inhibiting activity protein; antinflammatory; human;
KM antiarthritic; antirheumatic; antitumor; osteopathic; nephrotropic
KM immunosuppressive; ophthalmological; dermatological; antidiabetic;
KM neuroprotective; immune tolerance; T-cell tolerance.

OS Homo sapiens

PN WO200170253-A1.

PD 27-SEP-2001

PF 15-MAR-2001; 2001WO-EP02991.

PR 23-MAR-2000; 2000EP-0201063.

PA (ALKU) AKZO NOBEL NV.

PI Nelissen RLH, Verheijden GFM;

DR WPI; 2001-611446/70.

[illegible]

PT Use of melanoma inhibiting activity protein or its derivatives as
PT immune modulatory agents for the treatment of inflammatory diseases,
PT specifically rheumatoid arthritis -

PS Example 4; Page 34; 41pp; English.

The invention relates to the use of melanoma inhibiting activity (MIA) protein and/or its fragments that have anti-inflammatory effects and induce systemic immune tolerance or specific T-cell tolerance to MIA antigen, for manufacturing a preparation against inflammatory diseases and for induction of systemic immune tolerance or specific T-cell tolerance in patients suffering from or susceptible to inflammatory diseases. A fragment of MIA is useful as a therapeutic substance and is useful for manufacture of pharmaceutical preparations against inflammatory diseases such as an immune-cell mediated cartilage destruction disease, specifically rheumatoid arthritis, autoimmune diseases like Graves' disease, juvenile arthritis, primary glomerulonephritis, polyarthritis, osteoarthritis, Sjogren's syndrome, myasthenia gravis, Addison's disease, primary biliary sclerosis, uveitis, systemic lupus erythematosus, inflammatory bowel disease, multiple sclerosis or diabetes. The MIA polypeptides have specific effect on the autoreactive T-cells thus leaving the other components of the immune system intact as compared to the non-specific suppressive effect of immunosuppressive drugs. The present sequence represents a human MIA protein.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 29, 2003, 16:09:08 : Search time 15.098 Seconds
(without alignments)
1449.984 Million cell updates/sec

Title: US-10-019-455A-26
Perfect score: 591
Sequence: 1 HGVFMDLSKLCADCECV.....RVYQEAATKEIPTIDIFCE 110

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 724715 seqs, 199017464 residues

Total number of hits satisfying chosen parameters: 724715

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
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16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|------------------|-------------------|
| 1 | 547 | 92.6 | 128 | US-10-216-163-72 | Sequence 72, App1 |
| 2 | 547 | 92.6 | 128 | US-10-218-765-72 | Sequence 72, App1 |
| 3 | 547 | 92.6 | 128 | US-10-219-063-72 | Sequence 72, App1 |
| 4 | 547 | 92.6 | 128 | US-10-219-066-72 | Sequence 72, App1 |
| 5 | 547 | 92.6 | 128 | US-10-219-067-72 | Sequence 72, App1 |
| 6 | 547 | 92.6 | 128 | US-10-219-068-72 | Sequence 72, App1 |
| 7 | 547 | 92.6 | 128 | US-10-219-069-72 | Sequence 72, App1 |
| 8 | 547 | 92.6 | 128 | US-10-219-073-72 | Sequence 72, App1 |
| 9 | 547 | 92.6 | 128 | US-10-219-475-72 | Sequence 72, App1 |
| 10 | 547 | 92.6 | 128 | US-10-219-480-72 | Sequence 72, App1 |
| 11 | 547 | 92.6 | 128 | US-10-219-483-72 | Sequence 72, App1 |
| 12 | 547 | 92.6 | 128 | US-10-219-525-72 | Sequence 72, App1 |
| 13 | 547 | 92.6 | 128 | US-10-219-526-72 | Sequence 72, App1 |
| 14 | 547 | 92.6 | 128 | US-10-219-530-72 | Sequence 72, App1 |
| 15 | 547 | 92.6 | 128 | US-10-219-531-72 | Sequence 72, App1 |

ALIGNMENTS

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RESULT 1
US-10-216-163-72
Sequence 72, Application US//10216163
Publication No. US20030149239A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, V. Christopher
APPLICANT: Guiney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Matanabe, Colin L.
APPLICANT: Wood, William T.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530PIC3
CURRENT APPLICATION NUMBER: US//10/216,163
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
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PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 72
LENGTH: 128
TYPE: PRT
ORGANISM: Homo Sapien
US-10-216-163-72

Query Match 92.6%; Score 547; DB 12; Length 128;
Best Local Similarity 90.0%; Pred. No. 2,2e-59;
Matches 99; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 HGVFMDKSKKLCADEEVYITSLAPQEDYNAPDCRFIDYKGGQIYVSKLVTENGA 60
DB 19 HGIFMDRLASKKLCADEECVYITSLASQEDYNAPDCRFINVKGGQIYVSKLVKENG 78

QY 61 GEFWAGSVYGDHDEMGVIGVFPPSNLVKQRYVQATKXPIPTDIDFCE 110
DB 79 GEFWAGSVYGDHDEMGVIGVFPPSNLVKQRYVQATKXVPTDIDFCE 128

RESULT 2
US-10-218-765-72
Sequence 72, Application US/10218765
Publication No. US20030187201A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Geriltsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C19
CURRENT APPLICATION NUMBER: US/10/218,765
CURRENT FILING DATE: 2002-08-12,480
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
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PRIOR APPLICATION NUMBER: 60/063873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/081819
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PRIOR APPLICATION NUMBER: 60/081955
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PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06

PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/086392
PRIOR FILING DATE: 1998-05-22
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PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089905
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
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PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090691
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/095302
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/095318
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/095916
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/096146
PRIOR FILING DATE: 1998-08-11
PRIOR APPLICATION NUMBER: 60/096791
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 60/097986
PRIOR FILING DATE: 1998-08-26
PRIOR APPLICATION NUMBER: 60/098544
PRIOR FILING DATE: 1998-08-31
PRIOR APPLICATION NUMBER: 60/099596
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099598
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099803
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099811
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099812
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099816
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/100038
PRIOR FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: 60/100385
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100390
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100627
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100848
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/100919
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/101477
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101738
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101741
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101786
PRIOR FILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: 60/101916
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101922
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/106178

PRIOR FILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: 60/106248
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 60/106464
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 60/106905
PRIOR FILING DATE: 1998-11-03
PRIOR APPLICATION NUMBER: 60/108787
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/108801
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/108849
PRIOR FILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: 60/112422
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/113296
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/113605
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113621
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/115558
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115565
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115733
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/119549
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/123618
PRIOR FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: 60/125259
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 60/125775
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 60/126773
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: 60/127887
PRIOR FILING DATE: 1999-04-05
PRIOR APPLICATION NUMBER: 60/130232
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/131022
PRIOR FILING DATE: 1999-04-26
PRIOR APPLICATION NUMBER: 60/131270
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131291
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131445
PRIOR FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 60/134287
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/140650
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/140723
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/14037
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 60/144758
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/145698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: 60/146222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: 60/146963
PRIOR FILING DATE: 1999-08-03
PRIOR APPLICATION NUMBER: 60/149320
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/149638
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/151733
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/164418
PRIOR FILING DATE: 1999-11-09

PRIOR APPLICATION NUMBER: 60/166361
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: 60/169445
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169495
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169835

Query Match 92.6%; Score 547; DB 12; Length 128;
Best Local Similarity 90.0%; Pred. No. 2,2e-59;
Matches 99; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 1 HGVMFMDKLSKSKLCADEBCVYTISLARAQEDYNAPDCRFIDYKKGQIYYYSKLVKENG 60
Db 19 HGIFMDRLASKKLCADCECVYTISLARAQEDYNAPDCRFINVKKGQIYYYSKLVKENG 78
Qy 61 GEFWAGSVYGDHGDQEMGIVGFPSNLVKEORVYQEAETKEIPTDIDFCE 110
Db 79 GEFWAGSVYGDHGDQEMGVGIFPNLVKEORVYQEAETKEIPTDIDFCE 128

RESULT 3

US-10-219-063-72
Sequence 72, Application US/10219063
Publication No. US20030187202A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Macanabe, Colin L.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P350P1C24
CURRENT APPLICATION NUMBER: US/10/219,063
PRIOR FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 72
LENGTH: 128
TYPE: PRT
ORGANISM: Homo Sapien

US-10-219-063-72
Query Match 92.6%; Score 547; DB 12; Length 128;
Best Local Similarity 90.0%; Pred. No. 2,2e-59;
Matches 99; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 HGVFMKLSKSKLCADEECVYTTISLARAQEDYNAPDCRFIDVKKGOQIYYSKLV TENGA 60
DB 19 HGIFMDRLASKSKLCADEECVYTTISLARAQEDYNAPDCRFINVKKGQOIYYSKLV KENGA 78
QY 61 GEFWAGSVYGDGDQDEMGVGYFFPNLVKEQRYVQEAATKEIPTTIDIFFCE 110
DB 79 GEFWAGSVYGDGDQDEMGVGYFFPNLVKEQRYVQEAATKEIPTTIDIFFCE 128

RESULT 4

US-10-219-066-72
Sequence 72, Application US/10219066
Publication No. US20030187205A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530PIC27
CURRENT APPLICATION NUMBER: US/10/219,066
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079234
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 72
LENGTH: 128
TYPE: PRT
ORGANISM: Homo Sapien
US-10-219-066-72

Query Match 92.6%; Score 547; DB 12; Length 128;
Best Local Similarity 90.0%; Pred. No. 2.2e-59;
Matches 99; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 HGVFMKLSKSKLCADEECVYTTISLARAQEDYNAPDCRFIDVKKGOQIYYSKLV TENGA 60
DB 19 HGIFMDRLASKSKLCADEECVYTTISLARAQEDYNAPDCRFINVKKGQOIYYSKLV KENGA 78
QY 61 GEFWAGSVYGDGDQDEMGVGYFFPNLVKEQRYVQEAATKEIPTTIDIFFCE 110
DB 79 GEFWAGSVYGDGDQDEMGVGYFFPNLVKEQRYVQEAATKEIPTTIDIFFCE 128

RESULT 5

US-10-219-067-72

Sequence 72, Application US/10219067
Publication No. US20030187204A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530PIC51
CURRENT APPLICATION NUMBER: US/10/219,067
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 72
LENGTH: 128
TYPE: PRT
ORGANISM: Homo Sapien
US-10-219-067-72

Query Match 92.6%; Score 547; DB 12; Length 128;
Best Local Similarity 90.0%; Pred. No. 2.2e-59;
Matches 99; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 HGVFMKLSKSKLCADEECVYTTISLARAQEDYNAPDCRFIDVKKGOQIYYSKLV TENGA 60
DB 19 HGIFMDRLASKSKLCADEECVYTTISLARAQEDYNAPDCRFINVKKGQOIYYSKLV KENGA 78
QY 61 GEFWAGSVYGDGDQDEMGVGYFFPNLVKEQRYVQEAATKEIPTTIDIFFCE 110
DB 79 GEFWAGSVYGDGDQDEMGVGYFFPNLVKEQRYVQEAATKEIPTTIDIFFCE 128

RESULT 6

US-10-219-068-72
Sequence 72, Application US/10219068
Publication No. US20030187205A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.

APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C31
CURRENT APPLICATION NUMBER: US/10/219,068
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 72
LENGTH: 128
TYPE: PRT
ORGANISM: Homo Sapien
US-10-219-068-72

Query Match 92.6%; Score 547; DB 12; Length 128;
Best Local Similarity 90.0%; Pred. No. 2.2e-59;
Matches 99; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 HGFMFKLSKSKLCADEECYVITSLAQAQEDYNAPDCRFIDVKKGQIYYYSKLVENGA 60
DB 19 HGFMFKLSKSKLCADEECYVITSLAQAQEDYNAPDCRFIDVKKGQIYYYSKLVENGA 78
QY 61 GEFWAGSYGDDHODEMGIVGYPNSLVKEQRYVQATKEIPTTIDDFCE 110
DB 79 GEFWAGSYGDDHODEMGIVGYPNSLVKEQRYVQATKEIPTTIDDFCE 128

RESULT 7
US-10-219-069-72
Sequence 72, Application US/10219069
Publication No. US20030187206A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C40
CURRENT APPLICATION NUMBER: US/10/219,069
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09

PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 72
LENGTH: 128
TYPE: PRT
ORGANISM: Homo Sapien
US-10-219-069-72

Query Match 92.6%; Score 547; DB 12; Length 128;
Best Local Similarity 90.0%; Pred. No. 2.2e-59;
Matches 99; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 HGFMFKLSKSKLCADEECYVITSLAQAQEDYNAPDCRFIDVKKGQIYYYSKLVENGA 60
DB 19 HGFMFKLSKSKLCADEECYVITSLAQAQEDYNAPDCRFIDVKKGQIYYYSKLVENGA 78
QY 61 GEFWAGSYGDDHODEMGIVGYPNSLVKEQRYVQATKEIPTTIDDFCE 110
DB 79 GEFWAGSYGDDHODEMGIVGYPNSLVKEQRYVQATKEIPTTIDDFCE 128

RESULT 8
US-10-219-073-72
Sequence 72, Application US/10219073
Publication No. US20030187207A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C52
CURRENT APPLICATION NUMBER: US/10/219,073
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910

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; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-219-073-72

Query Match      92.6%; Score 547; DB 12; Length 128;
Best Local Similarity 90.0%; Pred. No. 2.2e-59;
Matches 99; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 HGFMNKLSSKKLCADEECYTTISLARQEDYNAPDCRFIDVKKGOIYYYSKLVTENGA 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 19 HGFMNRLASKKLCADDECVYTTISLASAQEDYNAPDCRFINVKKGQIYYYSKLVKNGA 78

QY 61 GEFWAGSVYGDHODEMGIVGFPSNLVKEQRYVQEATKEIPTTDIDFCE 110
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 79 GEFWAGSVYGDGDEMVGVGFPRLVKEQRYVQEATKEVPTTDIDFCE 128

RESULT 9
; Sequence 72, Application US/10219475
; Publication No. US20030187208A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C49
; CURRENT APPLICATION NUMBER: US/10/219,475
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
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; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-219-475-72

Query Match      92.6%; Score 547; DB 12; Length 128;
Best Local Similarity 90.0%; Pred. No. 2.2e-59;
Matches 99; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 HGFMNKLSSKKLCADEECYTTISLARQEDYNAPDCRFIDVKKGOIYYYSKLVTENGA 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 19 HGFMNRLASKKLCADDECVYTTISLASAQEDYNAPDCRFINVKKGQIYYYSKLVKNGA 78

QY 61 GEFWAGSVYGDHODEMGIVGFPSNLVKEQRYVQEATKEIPTTDIDFCE 110
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 79 GEFWAGSVYGDGDEMVGVGFPRLVKEQRYVQEATKEVPTTDIDFCE 128

RESULT 10
; Sequence 72, Application US/10219480
; Publication No. US20030187209A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C38
; CURRENT APPLICATION NUMBER: US/10/219,480
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-219-480-72

Query Match      92.6%; Score 547; DB 12; Length 128;
Best Local Similarity 90.0%; Pred. No. 2.2e-59;
Matches 99; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 HGFMNKLSSKKLCADEECYTTISLARQEDYNAPDCRFIDVKKGOIYYYSKLVTENGA 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 19 HGFMNRLASKKLCADDECVYTTISLASAQEDYNAPDCRFINVKKGQIYYYSKLVKNGA 78
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QY 61 GEFNAGSVYGDHODEMGIVGYFPPSNLVKQRYVOEATKEIPTDIDPFCE 110
Db 79 GEFNAGSVYGDGODEMGVGVFFPRNLVKEQRYVOEATKEVPTDIDPFCE 128

RESULT 11
US-10-219-483-72

; Sequence 72, Application US/10219483
; Publication No. US20030187210A1

GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3530P1C43

; CURRENT APPLICATION NUMBER: US/10/219,483

; PRIOR FILING DATE: 2002-08-13

; PRIOR APPLICATION NUMBER: 10/119,480

; PRIOR FILING DATE: 2002-04-09

; PRIOR APPLICATION NUMBER: 60/059113

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/062287

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/063549

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/064103

; PRIOR FILING DATE: 1997-10-31

; PRIOR APPLICATION NUMBER: 60/069873

; PRIOR FILING DATE: 1997-12-17

; PRIOR APPLICATION NUMBER: 60/078910

; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: 60/079294

; PRIOR FILING DATE: 1998-03-25

; PRIOR APPLICATION NUMBER: 60/079656

; PRIOR FILING DATE: 1998-03-26

; PRIOR APPLICATION NUMBER: 60/079728

; PRIOR FILING DATE: 1998-03-27

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 246

; SEQ ID NO 72

; LENGTH: 128

; TYPE: PRT

; ORGANISM: Homo Sapien

; US-10-219-483-72

Query Match 92.6%; Score 547; DB 12; Length 128;
Best Local Similarity 90.0%; Pred. No. 2,2e-59;
Matches 99; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 HGVFMDKLSKKLCADECEVYTTISLARAQEDYNAPDCRFIDVKKGGQIYVYSKLVTENGA 60
Db 19 HGIFMDRLASKKLCADECEVYTTISLARAQEDYNAPDCRFINVKKGQIYVYSKLVTENGA 78

QY 61 GEFNAGSVYGDHODEMGIVGYFPPSNLVKQRYVOEATKEIPTDIDPFCE 110
Db 79 GEFNAGSVYGDGODEMGVGVFFPRNLVKEQRYVOEATKEVPTDIDPFCE 128

RESULT 12

US-10-219-525-72

; Sequence 72, Application US/10219525

; Publication No. US20030187211A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C29

; CURRENT APPLICATION NUMBER: US/10/219,525

; PRIOR FILING DATE: 2002-08-13

; PRIOR APPLICATION NUMBER: 10/119,480

; PRIOR FILING DATE: 2002-04-09

; PRIOR APPLICATION NUMBER: 60/059113

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/062287

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/063549

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/064103

; PRIOR FILING DATE: 1997-10-31

; PRIOR APPLICATION NUMBER: 60/069873

; PRIOR FILING DATE: 1997-12-17

; PRIOR APPLICATION NUMBER: 60/078910

; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: 60/079294

; PRIOR FILING DATE: 1998-03-25

; PRIOR APPLICATION NUMBER: 60/079656

; PRIOR FILING DATE: 1998-03-26

; PRIOR APPLICATION NUMBER: 60/079728

; PRIOR FILING DATE: 1998-03-27

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 246

; SEQ ID NO 72

; LENGTH: 128

; TYPE: PRT

; ORGANISM: Homo Sapien

; US-10-219-525-72

Query Match 92.6%; Score 547; DB 12; Length 128;
Best Local Similarity 90.0%; Pred. No. 2,2e-59;
Matches 99; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 HGVFMDKLSKKLCADECEVYTTISLARAQEDYNAPDCRFIDVKKGGQIYVYSKLVTENGA 60
Db 19 HGIFMDRLASKKLCADECEVYTTISLARAQEDYNAPDCRFINVKKGQIYVYSKLVTENGA 78

QY 61 GEFNAGSVYGDHODEMGIVGYFPPSNLVKQRYVOEATKEIPTDIDPFCE 110
Db 79 GEFNAGSVYGDGODEMGVGVFFPRNLVKEQRYVOEATKEVPTDIDPFCE 128

RESULT 13

US-10-219-526-72

; Sequence 72, Application US/10219526

; Publication No. US20030187212A1

GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C41
CURRENT APPLICATION NUMBER: US/10/219,526
PRIOR FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 72
LENGTH: 128
TYPE: PRT
ORGANISM: Homo Sapien
US-10-219-526-72

Query Match 92.6%; Score 547; DB 12; Length 128;
Best Local Similarity 90.0%; Pred. No. 2.2e-59;
Matches 99; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 HGVMFKLSKKLCADEECYVITSLAPQEDYNAPDCRFIDVKKGGQIYYVSKLVTENGA 60
DB 19 HGIFMDRLASKKLCADDECVYITSLASQEDYNAPDCRFINVKGGQIYYVSKLVKXNGA 78

QY 61 GEFWAGSYVGDGDQDEMGVGYFPFNLVKEORVYQEAATKEIPTDIDFCE 110
DB 79 GEFWAGSYVGDGDQDEMGVGYFPFNLVKEORVYQEAATKEIPTDIDFCE 128

RESULT 14
US-10-219-530-72
Sequence 72, Application US/10219530
Publication No. US20030187213A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C54
CURRENT APPLICATION NUMBER: US/10/219,530
PRIOR FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 72
LENGTH: 128
TYPE: PRT
ORGANISM: Homo Sapien
US-10-219-530-72

Query Match 92.6%; Score 547; DB 12; Length 128;
Best Local Similarity 90.0%; Pred. No. 2.2e-59;
Matches 99; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 HGVMFKLSKKLCADEECYVITSLAPQEDYNAPDCRFIDVKKGGQIYYVSKLVTENGA 60
DB 19 HGIFMDRLASKKLCADDECVYITSLASQEDYNAPDCRFINVKGGQIYYVSKLVKXNGA 78

QY 61 GEFWAGSYVGDGDQDEMGVGYFPFNLVKEORVYQEAATKEIPTDIDFCE 110
DB 79 GEFWAGSYVGDGDQDEMGVGYFPFNLVKEORVYQEAATKEIPTDIDFCE 128

RESULT 15
US-10-219-531-72
Sequence 72, Application US/10219531
Publication No. US20030187214A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C66
CURRENT APPLICATION NUMBER: US/10/219,531
PRIOR FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656

/ PRIOR FILING DATE: 1998-03-26
/ PRIOR APPLICATION NUMBER: 60/079728
/ PRIOR FILING DATE: 1998-03-27
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 246
/ SEQ ID NO: 72
/ LENGTH: 128
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-219-531-72

Query Match 92.6%; Score 547; DB 12; Length 128;
Best Local Similarity 90.0%; Pred. No. 2.2e-59;
Matches 99; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 HGVFMDKLSSKCLCADDECVYTTISLARAQEDYNAPDCRFIDVKKGQIYYYSKLVTEGA 60
Db 19 HGIFMDRLASKKLCADDECVYTTISLARAQEDYNAPDCRFINVKKGQIYYYSKLVKENG 78
QY 61 GEFNAGSYGPDHODEMGIYGFPNSLVKEGRVYQEAATKEIPTDIDPFCE 110
Db 79 GEFNAGSYGPDHODEMGIYGFPNSLVKEGRVYQEAATKEIPTDIDPFCE 128

Search completed: December 29, 2003, 16:26:16
Job time : 16.098 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 29, 2003, 16:03:18 ; Search time 8.0112 Seconds
(without alignments)
580.961 Million cell updates/sec

Title: US-10-019-455A-26
Perfect score: 591
Sequence: 1 HGVMDLTKSKLCADECV.....RVQETATKEIPTTIDIFCE 110

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0 %
Maximum Match 100 %

Listing first 45 summaries

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32: /cgn2_6/ptodata/2/1aa/6C.COMB.pep.*
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45: /cgn2_6/ptodata/2/1aa/6P.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 261.5 | 44.2 | 131 | 1 | US-08-578-649-2 |
| 2 | 241.5 | 40.9 | 130 | 1 | US-08-578-649-5 |
| 3 | 91.5 | 15.5 | 844 | 1 | US-07-646-517B-2 |
| 4 | 82.5 | 14.0 | 54 | 3 | US-09-346-510B-21 |
| 5 | 78.5 | 13.3 | 1589 | 3 | US-09-356-952-4 |
| 6 | 77 | 13.0 | 694 | 1 | US-08-164-839-4 |
| 7 | 77 | 13.0 | 694 | 1 | US-08-164-839-4 |
| 8 | 77 | 13.0 | 695 | 1 | US-08-164-839-6 |
| 9 | 77 | 13.0 | 695 | 1 | US-08-583-799-6 |
| 10 | 73.5 | 12.4 | 48 | 3 | US-09-346-510B-24 |
| 11 | 71.5 | 12.1 | 248 | 4 | US-08-630-915A-40 |
| 12 | 71.5 | 12.1 | 509 | 4 | US-08-630-915A-194 |
| 13 | 71.5 | 12.1 | 687 | 1 | US-08-164-839-31 |
| 14 | 71.5 | 12.1 | 687 | 1 | US-08-164-839-33 |
| 15 | 71.5 | 12.1 | 687 | 1 | US-08-583-799-31 |
| 16 | 71.5 | 12.1 | 687 | 1 | US-08-583-799-33 |
| 17 | 71.5 | 12.1 | 688 | 1 | US-08-164-839-70 |
| 18 | 71.5 | 12.1 | 688 | 1 | US-08-164-839-72 |
| 19 | 71.5 | 12.1 | 688 | 1 | US-08-583-799-70 |
| 20 | 71.5 | 12.1 | 688 | 1 | US-08-583-799-72 |
| 21 | 71.5 | 12.1 | 688 | 1 | US-08-630-915A-38 |
| 22 | 69 | 11.7 | 57 | 4 | US-08-630-915A-136 |
| 23 | 68.5 | 11.6 | 58 | 4 | US-08-630-915A-210 |
| 24 | 67.5 | 11.4 | 333 | 4 | US-09-562-737-6 |
| 25 | 67 | 11.3 | 57 | 4 | US-08-630-915A-125 |
| 26 | 67 | 11.3 | 57 | 4 | US-08-630-915A-219 |
| 27 | 67 | 11.3 | 788 | 4 | US-08-630-915A-30 |

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|----|------|------|-----|---|----------------------|-------------------|
| 28 | 66.5 | 11.3 | 56 | 4 | US-08-630-915A-137 | Sequence 137, App |
| 29 | 66.5 | 11.3 | 56 | 4 | US-08-630-915A-217 | Sequence 217, App |
| 30 | 66 | 11.2 | 322 | 4 | US-08-630-915A-198 | Sequence 198, App |
| 31 | 66 | 11.2 | 389 | 4 | US-09-252-991A-18644 | Sequence 18644, A |
| 32 | 65.5 | 11.1 | 469 | 4 | US-09-252-991A-30596 | Sequence 30596, A |
| 33 | 65 | 11.0 | 57 | 4 | US-08-630-915A-139 | Sequence 139, App |
| 34 | 65 | 11.0 | 244 | 4 | US-09-198-452A-457 | Sequence 457, App |
| 35 | 65 | 11.0 | 280 | 1 | US-08-434-255-8 | Sequence 8, Appli |
| 36 | 65 | 11.0 | 280 | 1 | US-08-459-967-8 | Sequence 8, Appli |
| 37 | 65 | 11.0 | 280 | 1 | US-08-460-327-8 | Sequence 8, Appli |
| 38 | 65 | 11.0 | 280 | 1 | US-08-459-871-8 | Sequence 8, Appli |
| 39 | 65 | 11.0 | 280 | 3 | US-09-024-532-2 | Sequence 2, Appli |
| 40 | 65 | 11.0 | 280 | 4 | US-09-104-623A-2 | Sequence 2, Appli |
| 41 | 65 | 11.0 | 280 | 4 | US-09-019-532-2 | Sequence 2, Appli |
| 42 | 65 | 11.0 | 280 | 4 | US-09-417-359A-2 | Sequence 2, Appli |
| 43 | 65 | 11.0 | 370 | 1 | US-08-434-255-6 | Sequence 6, Appli |
| 44 | 65 | 11.0 | 370 | 1 | US-08-459-967-6 | Sequence 6, Appli |
| 45 | 65 | 11.0 | 370 | 1 | US-08-460-327-6 | Sequence 6, Appli |

ALIGNMENTS

RESULT 1
US-08-578-649-2
; Sequence 2, Application US/08578649
; Patent No. 570366

GENERAL INFORMATION:
APPLICANT: Ulrich Bogdan

APPLICANT: Reinhard Butner

APPLICANT: Brigitte Kaluza

TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:
ADDRESS: Felle & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 MB storage diskette

COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-July-1993

ATTORNEY/AGENT INFORMATION:
NAME: Andrew L. Tiajoleff
REGISTRATION NUMBER: 31,575

REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-578-649-2

Query Match 44.2%; Score 261.5; DB 1; Length 131;
Best local similarity 45.4%; Pred. No. 2,4e-26;
Matches 49; Conservative 24; Mismatches 30; Indels 5; Gaps 3;

5 MDLSSKSLCADECVTTISLARQEDYNAPCRFDIVKKGQIYYYSKVTENGAGE-P 63

Db 27 MPKLDRLKCADQECQHPISMAVALQDTWAPDCRFLTHRGQVYVFSKL---KGRGLF 83

QY 64 WAGSVYGDHODEMGI-VGYFSPNLVKEORVQOATKEIPTDIDFCE 110
Db 84 WGSVQGDYVGDPLARLIGYFSPSIVREDQTLKPKGVADVTDKWDYQ 131

RESULT 2

US-08-578-649-5
Sequence 5, Application US/08578649

Patent No. 5770366

GENERAL INFORMATION:

APPLICANT: Ulrich Bogdan

APPLICANT: Reinhard Butner

APPLICANT: Brigitte Kaluza

TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felle & Lynch

STREET: 805 Third Avenue

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch 1.44 MB storage diskette

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/578,649

FILING DATE: 29-July-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 43 24 247.2

FILING DATE: 20-July-1993

ATTORNEY/AGENT INFORMATION:

NAME: Andrew L. Tiajoleff

REGISTRATION NUMBER: 31,575

REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 130 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-578-649-5

Query Match 40.9%; Score 241.5; DB 1; Length 130;
Best Local Similarity 45.4%; Pred. No. 9.6e-24;
Matches 49; Conservative 21; Mismatches 33; Indels 5; Gaps 3;

QY 5 MDKSSKRLADCECVYTISLARAQEDYNAPDCRFIDVKKGOQIYVSKLVTEENGAGE-F 63
Db 26 MPKLDRLKCADQECQHPISMAVALQDTWAPDCRFLTHRGQVYVFSKL---KGRGLF 82

QY 64 WAGSVYGDHODEMGI-VGYFSPNLVKEORVQOATKEIPTDIDFCE 110
Db 84 WGSVQGDYVGDPLARLIGYFSPSIVREDQTLKPKGVADVTDKWDYQ 130

RESULT 3
US-07-646-537B-2
Sequence 2, Application US/07646537B

Patent No. 5348864

GENERAL INFORMATION:

APPLICANT: Bardacid, Mariano

TITLE OF INVENTION: Yav Proto-Oncogene Protein

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Bristol-Myers Squibb Company
STREET: P.O. Box 4000

CITY: Princeton

STATE: New Jersey

COUNTRY: U.S.A.

ZIP: 08543-4000

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/646,537B

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Gaul, Timothy J.

REGISTRATION NUMBER: 33,111

REFERENCE/DOCKET NUMBER: DC10

TELECOMMUNICATION INFORMATION:

TELEPHONE: (609) 921-4526

TELEFAX: (609) 921-5901

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 844 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-646-537B-2

Query Match 15.5%; Score 91.5; DB 1; Length 844;
Best Local Similarity 32.9%; Pred. No. 0.0053;
Matches 23; Conservative 14; Mismatches 20; Indels 13; Gaps 3;

QY 26 ARAQEDYNAPDCRFIDVKKGOQIYVSKLVTEENGAGEFFMAGSVYGDHODEMGIYGFPSN 85
Db 786 AKARDPFCARDRSELSTLKEDII---KIUNKGQGGQWRRGEIYGR-----IGWFPN 834

QY 86 LYKEQRYOE 95
Db 835 YVEED-YSE 842

RESULT 4
US-09-346-510B-21
Sequence 21, Application US/09346510B

Patent No. 6281014

GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

APPLICANT: Wang, Yinxian

TITLE OF INVENTION: SH3-Containing Protein, DNA and Uses Thereof

FILE REFERENCE: D6221CIP

CURRENT APPLICATION NUMBER: US/09/346,510B

PRIOR FILING DATE: 1999-07-01

PRIOR APPLICATION NUMBER: 08/871,732

NUMBER OF SEQ ID NOS: 32

SEQ ID NO 21

LENGTH: 54

TYPE: PRT

ORGANISM: unknown

FEATURE:

NAME/KEY: Domain

OTHER INFORMATION: amino acid sequence of Yav SH3 domain

US-09-346-510B-21

Query Match 14.0%; Score 82.5; DB 3; Length 54;
Best Local Similarity 32.3%; Pred. No. 0.0016;
Matches 20; Conservative 13; Mismatches 18; Indels 11; Gaps 2;

QY 28 AOEYNAPDCRFIDVKKGOQIYVSKLVTEENGAGEFFMAGSVYGDHODEMGIYGFPSN 87
Db 1 AYDFCARDRSELSTLKEDII---KIUNKGQGGQWRRGEIYGR-----VGWPNYV 49

QY 88 KE 89
DB 50 EE 51

RESULT 5
US-09-356-952-4

Sequence 4, Application US/09356952
Patent No. 6117663
GENERAL INFORMATION:
APPLICANT: Borjick-Sjodin, Ann
APPLICANT: Margalit, S. M.
APPLICANT: Bor-Sogai, Dafna
APPLICANT: Cole, Philip
APPLICANT: Kuriyan, John
TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE
TITLE OF INVENTION: THERMOF
FILE REFERENCE: 600-1-228N
CURRENT APPLICATION NUMBER: US/09/356,952
CURRENT FILING DATE: 1999-07-19
EARLIER APPLICATION NUMBER: 60/093,631
EARLIER FILING DATE: 1998-07-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO: 4
LENGTH: 1589
TYPE: PRP
ORGANISM: Saccharomyces cerevisiae
US-09-356-952-4

Query Match 13.3%; Score 79.5; DB 3; Length 1589;
Best Local Similarity 27.0%; Pred. No. 0.64;
Matches 24; Conservative 18; Mismatches 36; Indels 11; Gaps 4;

QY 8 LSSKLCADCECVYITSLRAQEDVAP-----DCRFIDVKGQGIYYSKLVENGAGE 62
DB 45 LSSPSTSELTIRPIGIVAAVDENVYPIKXSSQLSSVQGGETIYLNK-----NSSG- 99
QY 63 FVAGSYGHDHDEMGVGVFNSLVKXQR 91
DB 100 WMDGLVIDDSNGKVN-RGMFPQNGRPLR 127

RESULT 6
US-08-164-839-4

Sequence 4, Application US/08164839
Patent No. 5514573
GENERAL INFORMATION:
APPLICANT: YASUEDA, HISASHI
APPLICANT: NAKANISHI, KAZUO
APPLICANT: MOTOKI, MASAO
APPLICANT: NAGASE, KAZUO
APPLICANT: MATSUI, HIROSHI
TITLE OF INVENTION: GENE ENCODING TRANSGLUTAMINASE DERIVED
TITLE OF INVENTION: FROM FISH
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/164,839
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/004,729
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5514573man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-599-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)412-3000
TELEFAX: (703)413-2220

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 694 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-164-839-4

Query Match 13.0%; Score 77; DB 1; Length 694;
Best Local Similarity 27.5%; Pred. No. 0.31;
Matches 22; Conservative 20; Mismatches 28; Indels 10; Gaps 3;

QY 31 DYNAPDCRFIDVKGQGIYYSKLVENGAG---EFVAGSYGHDHDEMGVGVFNSLV 87
DB 392 EVNADTIYWIYQDQGR-----RKITEDHASVGNKISTKSVYGNHEDVTLHYKFBGSG 446
QY 88 KEGRVQATKEI--PTTDI 105
DB 447 KEREVYKAGRRVTPSPNEI 466

RESULT 7
US-08-583-799-4

Sequence 4, Application US/08583799
Patent No. 5607849
GENERAL INFORMATION:
APPLICANT: YASUEDA, HISASHI
APPLICANT: NAKANISHI, KAZUO
APPLICANT: MOTOKI, MASAO
APPLICANT: NAGASE, KAZUO
APPLICANT: MATSUI, HIROSHI
TITLE OF INVENTION: GENE ENCODING TRANSGLUTAMINASE DERIVED
TITLE OF INVENTION: FROM FISH
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,799
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/004,729
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5607849man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-599-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)412-3000
TELEFAX: (703)413-2220

TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 694 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-583-799-4

Query Match 13.0%; Score 77; DB 1; Length 694;
Best Local Similarity 27.5%; Pred. No. 0.31;
Matches 22; Conservative 20; Mismatches 28; Indels 10; Gaps 3;

QY 31 DYNAPDCRFIDVKKGOIIVYSKLTENGAG---EFWAGSVYGDHODENGIVGFPNSLV 87
DB 392 EVNADTIYWIIVQKQGR-----RKITEDHASVGKNISTKSYGNHREDVTLHKYIPESGQ 446
QY 88 KEQRVYQATKEI--PTTDI 105
DB 447 KEREVYKKAGRRVTEPSNEI 466

RESULT 8

US-08-164-839-6
Sequence 6, Application US/08164839

PATENT No. 5514573
GENERAL INFORMATION:
APPLICANT: YASUEDA, HISASHI
APPLICANT: NAKANISHI, KAZUO
APPLICANT: MOTOKI, MASAO
APPLICANT: NAGASE, KAZUO
APPLICANT: MATSUI, HIROSHI
TITLE OF INVENTION: GENE ENCODING TRANSGLUTAMINASE DERIVED
TITLE OF INVENTION: FROM FISH
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/164,839
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/004,729
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5514573man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-599-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)412-3000
TELEFAX: (703)413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 695 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-164-839-6

Query Match 13.0%; Score 77; DB 1; Length 695;
Best Local Similarity 27.5%; Pred. No. 0.31;

Matches 22; Conservative 20; Mismatches 28; Indels 10; Gaps 3;

QY 31 DYNAPDCRFIDVKKGOIIVYSKLTENGAG---EFWAGSVYGDHODENGIVGFPNSLV 87
DB 393 EVNADTIYWIIVQKQGR-----RKITEDHASVGKNISTKSYGNHREDVTLHKYIPESGQ 447
QY 88 KEQRVYQATKEI--PTTDI 105
DB 448 KEREVYKKAGRRVTEPSNEI 467

RESULT 9
US-08-583-799-6
Sequence 6, Application US/08583799

PATENT No. 5607849
GENERAL INFORMATION:
APPLICANT: YASUEDA, HISASHI
APPLICANT: NAKANISHI, KAZUO
APPLICANT: MOTOKI, MASAO
APPLICANT: NAGASE, KAZUO
APPLICANT: MATSUI, HIROSHI
TITLE OF INVENTION: GENE ENCODING TRANSGLUTAMINASE DERIVED
TITLE OF INVENTION: FROM FISH
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,799
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/004,729
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5607849man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-599-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)412-3000
TELEFAX: (703)413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 695 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-583-799-6

Query Match 13.0%; Score 77; DB 1; Length 695;
Best Local Similarity 27.5%; Pred. No. 0.31;
Matches 22; Conservative 20; Mismatches 28; Indels 10; Gaps 3;

QY 31 DYNAPDCRFIDVKKGOIIVYSKLTENGAG---EFWAGSVYGDHODENGIVGFPNSLV 87
DB 393 EVNADTIYWIIVQKQGR-----RKITEDHASVGKNISTKSYGNHREDVTLHKYIPESGQ 447
QY 88 KEQRVYQATKEI--PTTDI 105
DB 448 KEREVYKKAGRRVTEPSNEI 467

RESULT 10
US-09-346-5108-24
; Sequence 24 Application US/093465108
; Patent No. 6281014
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Wang, Yinxian
; TITLE OF INVENTION: SH3-Containing Protein, DNA and Uses Thereof
; FILE REFERENCE: D6221CJP
; CURRENT APPLICATION NUMBER: US/09/346,5108
; CURRENT FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: 08/871,732
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 24
; LENGTH: 48
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 2...49
; OTHER INFORMATION: amino acid sequence of Vav SH3 domain at position 2
; OTHER INFORMATION: through position 49 of SEQ ID No. 6281014 21
US-09-346-5108-24

Query Match 12.4%; Score 73.5; DB 3; Length 48;
Best Local Similarity 31.6%; Pred. No. 0.021;
Matches 18; Conservative 11; Mismatches 17; Indels 11; Gaps 2;

31 DYNAPDCFFIDVKKQCOIYVSKLTENGAGEFMAAGSYGDDHGMGIVGFPNSLV 87
Db 3 DFCARDSELSLKEDIT---KIINKGQGGWNRGEIYGR-----VGMFPANYV 48

RESULT 11
US-08-630-915A-40
; Sequence 40 Application US/08630915A
; Patent No. 6309820
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: HOFFMAN, No. 6309820h
; APPLICANT: KAY, Brian K.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; TITLE OF INVENTION: USING SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,915A
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; INFORMATION FOR SEQ ID NO: 40:

SEQUENCE CHARACTERISTICS:
; LENGTH: 248 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-630-915A-40

Query Match 12.1%; Score 71.5; DB 4; Length 248;
Best Local Similarity 36.8%; Pred. No. 0.38;
Matches 21; Conservative 8; Mismatches 13; Indels 15; Gaps 4;

44 KGOIYVSKLTENGAGEFMAAGSYGDDHGMGIVGFPNSLV--KEQRYQEAATK 98
Db 60 EGSEILVTK-----DGEWMTGSI-GDSS-----GIFPSNYVVKRQDESFSGASK 103

RESULT 12
US-08-630-915A-194
; Sequence 194 Application US/08630915A
; Patent No. 6309820
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: HOFFMAN, No. 6309820h
; APPLICANT: KAY, Brian K.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; TITLE OF INVENTION: USING SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,915A
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELE: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 194:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-630-915A-194

Query Match 12.1%; Score 71.5; DB 4; Length 509;
Best Local Similarity 36.8%; Pred. No. 1.1;
Matches 21; Conservative 8; Mismatches 13; Indels 15; Gaps 4;

44 KGOIYVSKLTENGAGEFMAAGSYGDDHGMGIVGFPNSLV--KEQRYQEAATK 98
Db 321 EGSEILVTK-----DGEWMTGSI-GDSS-----GIFPSNYVVKRQDESFSGASK 364

RESULT 13
US-08-164-839-31
Sequence 31, Application US/08164839
Patent No. 5514573
GENERAL INFORMATION:
APPLICANT: YASUEDA, HISASHI
APPLICANT: NAKANISHI, KAZUO
APPLICANT: MOTOKI, MASAO
APPLICANT: NAGASE, KAZUO
APPLICANT: MATSUI, HIROSHI
TITLE OF INVENTION: GENE ENCODING TRANSGLUTAMINASE DERIVED
FROM FISH
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/164,839
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/004,729
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5514573man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-599-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)412-3000
TELEFAX: (703)413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 687 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-164-839-31

Query Match 12.1%; Score 71.5; DB 1; Length 687;
Best Local Similarity 26.0%; Pred. No. 1.6; Indels 13; Gaps 4;
Matches 27; Conservative 19; Mismatches 45

QY 7 KLSKKLCADEECVYTISLAPAGEVYAPDCRFIDVKKGGQIYV-----SKL-VTE 57
DB 356 ELSDGEVCCPCPYTAIKEGNLSVKYDAP---FIFAEVNADIIYMWAGGGERKKIDVDQ 412

QY 58 NGAGE-FWAGSVYGDHODEMGIYGFPSNLVKEGRVYQEAATKEI 100
DB 413 SGVGNISTKSLYGDYREDVTLHYKYPEGSKEREYVQKAGHRI 456

RESULT 14
US-08-164-839-33
Sequence 33, Application US/08164839
Patent No. 5514573
GENERAL INFORMATION:
APPLICANT: YASUEDA, HISASHI
APPLICANT: NAKANISHI, KAZUO
APPLICANT: MOTOKI, MASAO
APPLICANT: NAGASE, KAZUO
APPLICANT: MATSUI, HIROSHI
TITLE OF INVENTION: GENE ENCODING TRANSGLUTAMINASE DERIVED

TITLE OF INVENTION: FROM FISH
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/164,839
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/004,729
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5514573man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-599-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)412-3000
TELEFAX: (703)413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 687 amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-164-839-33

Query Match 12.1%; Score 71.5; DB 1; Length 687;
Best Local Similarity 26.0%; Pred. No. 1.6;
Matches 27; Conservative 19; Mismatches 45; Indels 13; Gaps 4;

QY 7 KLSKKLCADEECVYTISLAPAGEVYAPDCRFIDVKKGGQIYV-----SKL-VTE 57
DB 356 ELSDGEVCCPCPYTAIKEGNLSVKYDAP---FIFAEVNADIIYMWAGGGERKKIDVDQ 412

QY 58 NGAGE-FWAGSVYGDHODEMGIYGFPSNLVKEGRVYQEAATKEI 100
DB 413 SGVGNISTKSLYGDYREDVTLHYKYPEGSKEREYVQKAGHRI 456

RESULT 15
US-08-583-799-31
Sequence 31, Application US/08583799
Patent No. 5607849
GENERAL INFORMATION:
APPLICANT: YASUEDA, HISASHI
APPLICANT: NAKANISHI, KAZUO
APPLICANT: MOTOKI, MASAO
APPLICANT: NAGASE, KAZUO
APPLICANT: MATSUI, HIROSHI
TITLE OF INVENTION: GENE ENCODING TRANSGLUTAMINASE DERIVED
FROM FISH
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,799
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/004,729
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: O'Brien, No. 5607849man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-599-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)412-3000
TELEFAX: (703)413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 687 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-583-799-31

Query Match 12.1%; Score 71.5; DB 1; Length 687;
Best Local Similarity 26.0%; Pred. No. 1.6; Indels 13; Gaps 4;
Matches 27; Conservative 19; Mismatches 45

QY 7 KLSKSLCADDECVYITSLAEOEDYNAPDCRFIDVKGQIYVY-----SKL-VTE 57
Db 356 ELSDGEYCCGCPCTVTAIKGNLSVKYDAP---FIFAEVNADILTYMAGGGERKKIDVDQ 412

QY 58 NGAGE-FMAGSYVDHODEMGIYGFPSNLVKEORVYGEATKEI 100
Db 413 SGVGNISTKSLYGDYREDVTLHYKYPEGSKKERREYVCKAGHRI 456

Search completed: December 29, 2003, 16:11:51
Job time: 9.0112 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 29, 2003, 16:11:59 ; Search time 1810.69 Seconds

(without alignments)
2485.278 Million cell updates/sec

Title: US-10-019-455a-26

Perfect score: 591
Sequence: 1 HGVMDLSSKULCADEECV.....RVQEAATKEIPTDIPFCE 110

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
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-DB=GenEmbl -GMMT=fastap -SUFFIX=ise -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdt -LIST=45
-DOCALLIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=45 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
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-NO MMAP -LARGEOQUERY -NEG.SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -Ygapop=10 -Ygapext=0.5 -Delop=6 -Delext=7

Database :

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20: em_om: *
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30: em_hgt_hum: *
31: em_hgt_inv: *
32: em_hgt_other: *
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34: em_hgt_pin: *
35: em_hgt_rtd: *
36: em_hgt_mam: *
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40: em_hgt_mus: *
41: em_hgt_other: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 591 | 100.0 | 330 | 6 | BD010817 Novel pol |
| 2 | 591 | 100.0 | 330 | 6 | BD093118 Novel pol |
| 3 | 591 | 100.0 | 384 | 6 | BD010805 Novel pol |
| 4 | 591 | 100.0 | 384 | 6 | BD093106 Novel pol |
| 5 | 591 | 100.0 | 929 | 10 | AF243504 Mus muscu |
| 6 | 591 | 100.0 | 947 | 6 | BD010821 Novel pol |
| 7 | 591 | 100.0 | 947 | 6 | BD093122 Novel pol |
| 8 | 591 | 100.0 | 958 | 10 | MMU243939 Mus muscu |
| 9 | 591 | 100.0 | 1054 | 10 | AF233333 Mus muscu |
| 10 | 574 | 97.1 | 330 | 6 | BD010836 Novel pol |
| 11 | 574 | 97.1 | 330 | 6 | BD093137 Novel pol |
| 12 | 574 | 97.1 | 384 | 6 | BD010835 Novel pol |
| 13 | 574 | 97.1 | 384 | 6 | BD093136 Novel pol |
| 14 | 547 | 92.6 | 330 | 6 | BD010816 Novel pol |
| 15 | 547 | 92.6 | 330 | 6 | BD093117 Novel pol |
| 16 | 547 | 92.6 | 384 | 6 | BD010802 Novel pol |
| 17 | 547 | 92.6 | 384 | 6 | BD093103 Novel pol |
| 18 | 547 | 92.6 | 521 | 6 | AX358818 Sequence |
| 19 | 547 | 92.6 | 521 | 6 | AX362311 Sequence |
| 20 | 547 | 92.6 | 521 | 6 | AX454774 Sequence |
| 21 | 547 | 92.6 | 521 | 6 | AX491252 Sequence |
| 22 | 547 | 92.6 | 846 | 9 | AF233261 Homo sapi |
| 23 | 547 | 92.6 | 865 | 9 | AF243505 Homo sapi |
| 24 | 547 | 92.6 | 923 | 6 | BD010820 Novel pol |
| 25 | 547 | 92.6 | 923 | 6 | BD093121 Novel pol |
| 26 | 547 | 92.6 | 1422 | 9 | HSR42552 Homo sapi |
| 27 | 505 | 85.4 | 307 | 6 | BD010830 Novel pol |
| 28 | 505 | 85.4 | 307 | 6 | BD093131 Novel pol |
| 29 | 465.5 | 78.8 | 484 | 5 | AF233518 Gallus ga |
| 30 | 445 | 75.3 | 261 | 6 | BD010829 Novel pol |
| 31 | 445 | 75.3 | 261 | 5 | BD093130 Novel pol |
| 32 | 399 | 67.5 | 466 | 5 | AF233519 Rana cace |
| 33 | 298.5 | 50.5 | 21581 | 2 | AC106161 Rattus no |
| 34 | 293.5 | 44.4 | 442 | 6 | AX331430 Mus muscu |
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| 36 | 262.5 | 44.4 | 442 | 6 | AX331430 Sequence |
| 37 | 261.5 | 44.2 | 330 | 6 | AX42859 Sequence 18 |
| 38 | 261.5 | 44.2 | 330 | 6 | AX016802 Sequence |
| 39 | 261.5 | 44.2 | 336 | 12 | BT007074 Homo sapi |
| 40 | 261.5 | 44.2 | 336 | 12 | BT007075 Synthetic |
| 41 | 261.5 | 44.2 | 459 | 6 | A42942 Sequence 1 |
| 42 | 261.5 | 44.2 | 459 | 6 | AX016785 Sequence |
| 43 | 261.5 | 44.2 | 459 | 6 | AX252508 Sequence |
| 44 | 261.5 | 44.2 | 459 | 6 | AX287209 Sequence |
| 45 | 261.5 | 44.2 | 459 | 9 | HSWGRPWA X75450 H. sapiens m |

ALIGNMENTS

RESULT 1

BD010817 330 bp DNA linear PAT 31-JAN-2002

LOCUS BD010817 Novel polypeptide and DNA thereof.

DEFINITION BD010817.1 GI:18639190

ACCESSION BD010817.1

VERSION JP 200106994-A/18.

KEYWORDS Mus sp.

SOURCE Mus sp.

ORGANISM Mus sp.

REFERENCE 1 (bases 1 to 330)

AUTHORS Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y., Yoshimura, K. and Tanaka, H.

TITLE Novel polypeptide and DNA thereof

JOURNAL Patent: JP 200106994-A 18 21-MAR-2001;

COMMENT TAKEDA CHEMICAL INDUSTRIES LTD

OS Mus sp. (mouse)

PN JP 200106994-A/18

PD 21-MAR-2001

PF 29-JUN-2000 JP 2000195911

PR

PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI SHINICHI MOGI.

PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA

PC C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P9/00,A61P19/02, PC A61P19/08, PC C07K14/47,C07K16/18,C12N1/21,C12N5/10,G01N33/15,G01N33/50, PC G01N33/53//

PC C12P21/08,C12N15/00,A61K37/02,C12N5/00

CC

FH Key Location/Qualifiers

FT source 1..330

FT /organism="Mus sp. (mouse)"

FEATURES

source 1..330

/organism="Mus sp."

/mol_type="genomic DNA"

/db_xref="taxon:10095"

BASE COUNT 91 a 60 c 92 g 87 t

ORIGIN

Alignment Scores:

Pred. No.: 5,4e-62 Length: 330

Score: 591.00 Matches: 110

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: Gaps: 0

US-10-019-455a-26 (1-110) x BD010817 (1-330)

QY 1 HisGlyValPheMetAspLysLeuSerLysLysLeuCysAlaAspGluGluCysVal 20

DB 1 CATGGTATTATGATTAACCTTCTCTTAAGAGGTGTGGCGATGAGAGAGTGTTC 60

QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40

DB 61 TTTACTATTCTCTGGCAAGACACAGAAAGTTCAATGCCCGCATGTATGCTTCTTC 120

QY 41 AspValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60

DB 121 GATGTCAAGAAAGGCGACAGATCTATGTTTACTCCAAAGCTGTAAACGAAACGAGACT 180

QY 61 GlyGluPheThrPalaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80

DB 181 GGAGAGTTTGGGCTGGCGAGTGTATGATGACCCAGGATGAGATGGGAATTGTAGCT 240

QY 81 TyrPheProSerAsnLeuValLysGlnGlnArgValTyrGlnGluAlaThrLysGluIle 100

DB 241 TATTTCCCGCAACTTGTGTGAAGAGCAGCGCTGTATACAGAGAGCCACCAAGAGATC 300

QY 101 ProThrThrAspIleAspPheCysGlu 110

DB 301 CCAACCAAGGATATGACTTCTCTGTGAA 330

RESULT 2

LOCUS BD093118 330 bp DNA linear PAT 27-AUG-2002

DEFINITION BD093118 Novel polypeptide and its DNA.

ACCESSION BD093118

VERSION BD093118.1 GI:22638706

KEYWORDS WO 0102564-A/18.

SOURCE Mus sp.

ORGANISM Mus sp.

REFERENCE 1 (bases 1 to 330)

AUTHORS Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y., Yoshimura, K. and Tanaka, H.

TITLE Novel polypeptide and its DNA

JOURNAL Patent: WO 0102564-A 18 11-JAN-2001;

COMMENT TAKEDA CHEMICAL INDUSTRIES LTD YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA

OS Mus sp. (mouse)

PN WO 0102564-A/18

PD 11-JAN-2001

PF 29-JUN-2000 WO 20001P004278

PR 30-JUN-1999 JP 99P 186718

PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA

PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA

PC C12N15/12,C12N5/10,C12P21/02,C07K14/47,C07K16/18,A61K45/00, PC A61K38/17, PC A61K39/395,A61K49/16,A61P19/02,A61P19/08,A61K31/7088// (C12P21/02,C12R1:19)

CC

FH Key Location/Qualifiers

FT source 1..330

FT /organism="Mus sp."

FT /mol_type="genomic DNA"

FT /db_xref="taxon:10095"

BASE COUNT 91 a 60 c 92 g 87 t

ORIGIN

Alignment Scores:

Pred. No.: 5,4e-62 Length: 330

Score: 591.00 Matches: 110

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: Gaps: 0

US-10-019-455a-26 (1-110) x BD093118 (1-330)

QY 1 HisGlyValPheMetAspLysLeuSerLysLysLeuCysAlaAspGluGluCysVal 20

DB 1 CATGGTATTATGATTAACCTTCTCTTAAGAGGTGTGGCGATGAGAGAGTGTTC 60

QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40

DB 61 TTTACTATTCTCTGGCAAGACACAGAAAGTTCAATGCCCGCATGTATGCTTCTTC 120

QY 41 AspValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60

DB 121 GATGTCAAGAAAGGCGACAGATCTATGTTTACTCCAAAGCTGTAAACGAAACGAGACT 180

QY 61 GlyGluPheThrPalaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80

DB 181 GGAGAGTTTGGGCTGGCGAGTGTATGATGACCCAGGATGAGATGGGAATTGTAGCT 240

QY 81 TyrPheProSerAsnLeuValLysGlnGlnArgValTyrGlnGluAlaThrLysGluIle 100

DB 241 TATTTCCCGCAACTTGTGTGAAGAGCAGCGCTGTATACAGAGAGCCACCAAGAGATC 300

| | | | |
|--|---|--|-----------------|
| Oy | 101 | ProthirtaspisileasppheCys6lu | 110 |
| Db | 301 | CCAAACGAGATTTGACTTCTTGTA | 330 |
| RESULT 3 | | | |
| LOCUS | BD010805 | 384 bp | DNA |
| DEFINITION | Novel polypeptide and DNA thereof. | | linear |
| VERSION | BD010805 | | PAT 31-JAN-2002 |
| KEYWORDS | JP 2001069994-A/6. | | |
| SOURCE | Mus sp. | | |
| ORGANISM | Mus sp. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Ito,Y., Nishi,K., Ogi,X., Okubo,S., Mogi,S., Noguchi,Y., Yoshimura,K. and Tanaka,H. Novel polypeptide and DNA thereof Patent: JP 2001069994-A 6 21-MAR-2001; | | |
| TITLE | JOURNAL | | |
| COMMENT | OS Mus sp. (mouse) PN JP 2001069994-A/6 PD 21-MAR-2001 PF 29-JUN-2000 JP 2000195911 PR YASUAKI ITO,KAZUNORI NISHI,KAZUHIRO OGI,SHOICHI OKUBO, PI PI SHINICHI MOGI, PI YUKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA PC C12N5/09,A61K38/00,A61K45/00,A61K48/00,A61P9/00,A61P19/02, PC A61P19/08, PC C07K14/47,C07K16/18,C12N1/21,C12N5/10,G01N33/15,G01N33/50, PC G01N33/53// PC C12P21/08,C12N15/00,A61K37/02,C12N5/00 CC FH key Location/Qualifiers FT source 1..384 FT /organism='Mus sp.' Location/Qualifiers 1..384 /mol_type='genomic DNA' /db_xref='taxon:10095' | | |
| BASE COUNT | 98 a | 68 c | 111 g 107 t |
| ORIGIN | | | |
| Alignment Scores: | | | |
| Pred. No.: | 6.35e-62 | Length: | 384 |
| Score: | 591.00 | Matches: | 110 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 6 | Gaps: | 0 |
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| Oy | 1 | HiscglValPhemcAspLysLeuSerSerLysLysLeuCysAlaAspGlugLcysVal | 20 |
| Db | 55 | CATGGTAGATTTAAGCATTAACCTTCCTCTTAAGAGATTGTGTGGGATGAAGAAGTGTGC | 114 |
| Oy | 21 | TyrThrIseIseIeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle | 40 |
| Db | 115 | TATACTATTCTCTGGCAAGACACAGGAAGATTACAATGCCCCAGACTGAGTTATC | 174 |
| Oy | 41 | AspValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValTrnGluAsrGlyAla | 60 |
| Db | 175 | GATGTCAAGAAAGGCGACAGCATCTATGTTCACCAAGCTGCTAACAGAAACGGAGCT | 234 |
| Oy | 61 | GlyGluPheTrpAlaGlySerValTyrGlyAspHisglnAspGluMetGlyIleValGly | 80 |
| Db | 235 | GGAAGATTITGGCTGGCAGAGTTTATTAGTGTAACCAACGAGATGAGATGGGAATTGTAGCT | 294 |

| | | | | | |
|--|-----|---|-----|--------|-----------------|
| Qy | 8 | TyrpHeptoseSerLeuValIlysgluGlnArgValTyrGlnGluAlaTrrIlysgluIle | 100 | | |
| Db | 295 | TATTTCCCGACGACTTGTGTGAAGACACCGGTGTATCCAGAGGCCACCAAGAGATC | 354 | | |
| Qy | 101 | ProThrThraSpIleaePhephecYseglu | 110 | | |
| Db | 355 | CCAACCAAGGATATGACTTCTCTGTGAA | 384 | | |
| RESULT 4 | | | | | |
| BD093106 | | 384 bp | DNA | linear | PAT 27-AUG-2002 |
| LOCUS | | | | | |
| DEFINITION | | | | | |
| ACCESSION | | | | | |
| VERSION | | | | | |
| KEYWORDS | | | | | |
| SOURCE | | | | | |
| ORGANISM | | | | | |
| REFERENCE | | | | | |
| AUTHORS | | | | | |
| TITLE | | | | | |
| JOURNAL | | | | | |
| COMMENT | | | | | |
| FEATURES | | | | | |
| source | | | | | |
| BASE COUNT | | | | | |
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| Score: | | | | | |
| Percent Similarity: | | | | | |
| Best Local Similarity: | | | | | |
| Query Match: | | | | | |
| DB: | | | | | |
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| Qy | 1 | HieGlyValPheMetAapLysLeuSerSerLysIlyseuGysAlaaspGluGluCysVal | 20 | | |
| Db | 55 | CATGGTATTTTATTTATGATTAACCTTTCTTCAAGAGTTGTGTCGGATGAGGAGTGTCTC | 114 | | |
| Qy | 21 | TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle | 40 | | |
| Db | 115 | TATACATATTTCTCTGGCAGAGCAACGAGAAAGATTACATGCCCAAGCTGTAGGTTTCATC | 174 | | |
| Qy | 41 | AspValIlysgIyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla | 60 | | |
| Db | 175 | GATGTCAAGAAAGGACGACGATCTATGTTTACTTCCAGCTGGTTACAGAAAGCGAGCT | 234 | | |
| Qy | 61 | GlyGluPheThrAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly | 80 | | |

Db 235 GGAGAGTTTGGCTGCGCTGTTTATGTTGACCAACGATGAGATGGGAATTGAGCT 294

Qy 81 TYPHROSERANLEUVALYSGIUNARVALTYRGINGUALATHRLYSGIULLE 100

Db 295 TATTTCCCGACCACTTGGAAGAGACGCGTGTATACAGAGAGCCACCAAGAGATC 354

Qy 101 ProthThraspPhepPhepCysGlu 110

Db 355 CCAACACGAGATATGACTTCTGTGTGAA 384

RESULT 5

AF243504 929 bp mRNA linear ROD 26-DEC-2000

LOCUS AF243504 Mus musculus fibrocyte-derived protein (Fdp) mRNA, complete cds.

DEFINITION AF243504.1 GI:11991841

ACCESSION AF243504.1 GI:11991841

VERSION

KEYWORDS

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE Cohen-Salmon, M., Frenz, D., Liu, W., Verpy, E., Voegelting, S. and Petit, C. Fdp, a new fibrocyte-derived protein related to MIA/CD-RAP, has an in vitro effect on the early differentiation of the inner ear mesenchyme

JOURNAL J. Biol. Chem. 275 (51), 40036-40041 (2000)

MEDLINE 20568254

PUBMED 10998416

REFERENCE 2 (bases 1 to 929)

AUTHORS Cohen-Salmon, M., Frenz, D., Verpy, E., Voegelting, S. and Petit, C.

TITLE Direct Submission

JOURNAL Submitted (09-MAR-2000) Biotechnologies, Institut Pasteur, 25 rue du Dr. Roux, Paris 75015, France

FEATURES

source

1..929

/organism="Mus musculus"

/mol_type="mRNA"

/strain="BALB/c"

/db_xref="taxon:10090"

/chromosome="2"

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/gene="Fdp"

9..395

/gene="Fdp"

/codon_start=1

/product="fibrocyte-derived protein"

/protein_id="AAG2355.1"

/db_xref="GI:11991842"

/translation="MARILLILGGLVVLCAGHGVPMDKLSKKLCADEECVYTSLA RAOEDVAPPCRFIDVKKGOIIVYKSLVLENAGRMWASVYGDHDEMGITGYPS NLVKEGVYQEARKEIPTTIDPFCE"

BASE COUNT 260 a 156 c 220 g 293 t

ORIGIN

Alignment Scores:

Pred. No.: 1.64e-61 Length: 929

Score: 591.00 Matches: 110

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 10 Gaps: 0

US-10-019-455A-26 (1-110) x AF243504 (1-929)

Qy 1 HisGlyValPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysVal 20

Db 63 CATGGTGAATTATGGAATAAAGCTTCTCTAAGAAAGTTGTGTGGAGATGAGAGTGTGTC 122

Qy 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspLysArgAlaProAspCysArgPheIle 40

Db 123 TATACTATTCTCTGGCAGAGACAGAGAAATTACAATGCCCGACTGAGTTCATC 182

Qy 41 AspVallyslslysglgnlnlleTyrValTyrSerLysLeuValTTrGluAsnGlyAla 60

Db 183 GATGTCAGAAAGGCGCGACATATCTTACTCCAAAGCTGTGTAACAGAAACGAGCT 242

Qy 61 GlyGluPheTTPAlaGlySerValTYRGlyAspHisGlnAspGluMetGlyIleValGly 80

Db 243 GGAGAGTTTGGCTGCGAGTGTATGTTGACCAACGATGAGATGGGAATTGAGT 302

Qy 81 TYPHROSERANLEUVALYSGIUNARVALTYRGINGUALATHRLYSGIULLE 100

Db 303 TATTTCCCGACCACTTGGAAGAGACGCGTGTATACAGAGAGCCACCAAGAGATC 362

Qy 101 ProthThraspPhepPhepCysGlu 110

Db 363 CCAACACGAGATATGACTTCTGTGTGAA 392

RESULT 6

BD010821 947 bp DNA linear PAT 31-JAN-2002

LOCUS BD010821 Novel polypeptide and DNA thereof.

DEFINITION BD010821

ACCESSION BD010821.1 GI:18639194

VERSION JP 2001069994-A/22.

KEYWORDS

SOURCE Mus sp.

ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 947)

AUTHORS Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y., Yoshimura, K. and Tanaka, H.

TITLE Novel polypeptide and DNA thereof

JOURNAL Patent: JP 2001069994-A 22 21-MAR-2001; TAKEDA CHEMICAL INDUSTRIES LTD

COMMENT

OS Mus sp. (mouse)

PN JP 2001069994-A/22

PD 21-MAR-2001

PF 29-JUN-2000 JP 2000195911

PR

PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI SHINICHI MOGI,

PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA

PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC A61P19/08, PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC G01N33/53//

PC C12P21/08, C12N15/00, A61K37/02, C12N5/00

CC

FF Key

FT source

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location/Qualifiers

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BASE COUNT 279 a 158 c 221 g 289 t

ORIGIN

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Score: 591.00 Matches: 110

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-10-019-455A-26 (1-110) x BD010821 (1-947)

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QY 21 TTTThlleserleuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
 DB 125 TTTACTATTTCCTCTGCAAGAGACAGAGAAATTAACATGCCCAAGACTGTGATC 184
 QY 41 AspVallylsylGlyGlnGlnIleTyrValTyrSerlyLeuValThrGluAsnGlyAla 60
 DB 185 GATGTCAAGAAAGGACAGACATCTATGTTTACTCCAAAGCTGGTACAGAAAACGAGCT 244
 QY 61 GlyGluPheTyrPalaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
 DB 245 GAGAGATTTTGGGCTGGCAGTGTATTGTGACCAACAGATGAGATGGGAATTGTAGCT 304
 QY 81 TyrPheProSerAsnLeuVallylsylGlnArgValTyrGlnGluAlaThrlysgluile 100
 DB 305 TATTTCCCAAGCAACTGTGTGAAGGACAGCGGTGTATACAGAGAGCCCAAGAGATC 364
 QY 101 ProThrThrAspIleAspPheCysGlu 110
 DB 365 CCAACCAAGATATTGACTTCTGTGTGA 394

RESULT 7
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 LOCUS Novel polypeptide and its DNA.
 DEFINITION BD093122
 ACCESSION BD093122.1 GI:22638710
 VERSION WO 0102564-A/22.
 KEYWORDS Mus sp.
 SOURCE Mus sp.
 ORGANISM Mus sp.

REFERENCE
 AUTHORS Eukariota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 947)
 Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y., Yoshimura, K. and Tanaka, H.
 Novel polypeptide and its DNA
 Patent: WO 0102564-A 22 11-JAN-2001;
 TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
 COMMENT OS Mus sp. (mouse)
 PN WO 0102564-A/22
 PD 11-JAN-2001
 PF 29-JUN-2000 WO 2000JP004278
 PR 30-JUN-1999 JP 99P 186718
 PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI MOGI,

PI MOGI,
 PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
 PC C12N15/12, C12N5/10, C12P21/02, C07K14/47, C07K16/18, A61K45/00, PC A61K38/11,
 PC A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/7086//C12P21/PC 02, C12R1.19)
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BASE COUNT 279 a 158 c 221 g 289 t
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 Best Local Similarity: 100.00% Mismatches: 0
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 DB: 6 Gaps: 0

US-10-019-455a-26 (1-110) x BD093122 (1-947)

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 QY 21 TTTThrlleserleuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
 DB 125 TTTACTATTTCCTCTGCAAGAGACAGAGAAATTAACATGCCCAAGACTGTGATC 184
 QY 41 AspVallylsylGlyGlnGlnIleTyrValTyrSerlyLeuValThrGluAsnGlyAla 60
 DB 185 GATGTCAAGAAAGGACAGACATCTATGTTTACTCCAAAGCTGGTACAGAAAACGAGCT 244
 QY 61 GlyGluPheTyrPalaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
 DB 245 GAGAGATTTTGGGCTGGCAGTGTATTGTGACCAACAGATGAGATGGGAATTGTAGCT 304
 QY 81 TyrPheProSerAsnLeuVallylsylGlnArgValTyrGlnGluAlaThrlysgluile 100
 DB 305 TATTTCCCAAGCAACTGTGTGAAGGACAGCGGTGTATACAGAGAGCCCAAGAGATC 364
 QY 101 ProThrThrAspIleAspPheCysGlu 110
 DB 365 CCAACCAAGATATTGACTTCTGTGTGA 394

RESULT 8
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 LOCUS Mus musculus mRNA for melanoma inhibitory activity-like protein
 DEFINITION (Mial gene).
 ACCESSION AJ243939
 VERSION AJ243939.1 GI:12619174
 KEYWORDS melanoma inhibitory activity-like protein; Mial gene.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukariota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1
 Rendtorff, N.D., Frodin, M., Attie-Bltach, T., Vekmans, M. and Tommerup, N.
 Identification and characterization of an inner ear-expressed human melanoma inhibitory activity (MIA)-like gene (MIAL) with a frequent polymorphism that abolishes translation
 Genomics 71 (1), 40-52 (2001)
 MEDLINE 21100875
 PUBMED 1161796
 REFERENCE 2 (bases 1 to 958)
 AUTHORS Rendtorff, N.D.
 TITLE Direct Submission
 JOURNAL Submitted (20-JUL-1999) Rendtorff N.D., Department of Medical Genetics, Institute of Medical Biochemistry and Genetics, Blegdamsvej 3, 2200 Copenhagen N, DENMARK
 COMMENT Related sequence: AJ242552.
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 CDS

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US-10-019-455A-26 (1-110) X MMJ243939 (1-958)

[illegible]

| RESULT 9 | AF233333 | LOCUS | AF233333 | 1054 bp | linear | ROD 06-JUL-2000 |
|------------|----------------------------|-------------------------------|----------|---------|--------|-----------------|
| DEFINITION | Mus musculus | otoraplin mRNA, complete cds. | | | | |
| ACCESSION | AF233333 | | | | | |
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| SOURCE | Mus musculus (house mouse) | | | | | |

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US-10-019-455A-26 (1-110) X AF233333 (1-1054)

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| Db | 72 | CATGGTGAATTAAAGGATAAACTTTCTTAAAGAAGTTGTGGCGAAGAGAGTGTC | 131 |
| Qy | 21 | TyrThrIleSerIeuaIaargAlaGlnGluaspIYrAenAlaProaspCyArPheIle | 40 |
| Db | 132 | TATCTATTCTTCTGGCAAGAGCGCAGAGAGATTACAAATGCCCAAGACTGTAGGTTCACT | 191 |
| Qy | 41 | AspValIySlySgIyGlnGlnIleTYrValTYrSerIySeuValIthrGluasnGlyVaIa | 60 |
| Db | 192 | GATGTCAAGAAAGGCGACAGATCTAATGTTACTCCAAAGCTGTATACAGAAAACGAGACT | 251 |
| Qy | 61 | GlyGluPheTrpAlaGlySerValTYrGlyAspHisGlnaspGluMeGlyIleValGly | 80 |
| Db | 252 | GGAGAAGTTTGGCTGGCAGTGTATTATGTGACCACCGATGAGATGGCAATTGTAGCT | 311 |
| Qy | 81 | TyrTherProSerAenLeuValIySgIuGlnArgValTYrGlnGluAlaIthrIySgIuIle | 100 |
| Db | 312 | TATTTCCCAACAATTGGTGAAGAGAGCGGTATACCAAGAGGCCACCAAGAGATC | 371 |
| Qy | 101 | ProThrIAspIleaspPhePheCySgIu | 110 |
| Db | 372 | CCAACCACGAGATTGACTTCTTCGTGA | 401 |

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| LOCUS | Novel polypeptide and DNA thereof. | | | | |
| DEFINITION | BD010836 | | | | |
| ACCESSION | BD010836 | | | | |
| VERSION | BD010836.1 GI:18639209 | | | | |
| KEYWORDS | UP 2001065994-A/37. | | | | |
| SOURCE | Rattus sp. | | | | |
| ORGANISM | Rattus sp. | | | | |

| REFERENCE | AUTHORS | TITLE | JOURNAL | COMMENT |
|--------------------|---|-----------------------------------|---|---------|
| 1 (bases 1 to 330) | Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y., Yoshimura, K. and Tanaka, H. | Novel polypeptide and DNA thereof | Parent: JP 2001069994-A 37 21-MAR-2001; | |
| | | | TAKEDA CHEMICAL INDUSTRIES LTD | |
| | | OS Rattus sp. (rat) | | |
| | | PN JP 2001069994-A/37 | | |
| | | PD 21-MAR-2001 | | |
| | | PF 29-JUN-2000 JP 2000195911 | | |
| | | PR | | |
| | PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI SHINICHI MOGI, | | | |
| | PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA | | | |
| | PC C12A15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, A61P19/08, | | | |

PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC
G01N33/53//
PC C12P21/08, C12N15/00, A61K37/02, C12N5/00
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DB 61 TATACCATTTCTCTGCGAAGACACAGCAAGACTCAATCAAGCCCGAGCTGTGATTCATC 120
QY 41 AspValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
DB 121 AATGTCAGAGAAAGGCGACAGATCTATGTTTATTCAGAGCTGTAAACAGAAATGAGACT 180
QY 61 GlyGluPheThrAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
DB 181 GGGGCAATTCGGCTGGCAGTGTTAAGTGACCAACAGATGAGATGGGAATTTGGGT 240
QY 81 TyrPheProSerAsnLeuValLysGluGlnArgValTyrGlnAlaAlaThrLysGluIle 100
DB 241 TATTTCCCAAGCACTGTTTGAAGACCAAGAGTGTACCAAGGCCCAAGAGATT 300
QY 101 ProThrThrAspIleAspPhePheCysGlu 110
DB 301 CCAACCAAGATATTGACTTCTCTGTGAA 330
RESULT 11
BD093137 330 bp DNA linear PAT 27-AUG-2002
LOCUS Novel polypeptide and its DNA.
DEFINITION BD093137
ACCESSION BD093137.1 GI:22638725
VERSION WO 0102564-A/37.
KEYWORDS Rattus sp.
SOURCE Rattus sp.
ORGANISM Rattus sp.
REFERENCE 1 (bases 1 to 330)
AUTHORS Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
Yoshimura, K. and Tanaka, H.
TITLE Novel polypeptide and its DNA
JOURNAL Patent: WO 0102564-A 37 11-JAN-2001;
TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO
OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,
HIDEYUKI TANAKA
OS Rattus sp. (rat)
PN WO 0102564-A/37
PD 11-JAN-2001
PF 29-JUN-2000 WO 2000JP004278

PR 30-JUN-1999 JP 99P 186718
PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI
MOGI,
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/12, C12N5/10, C12P21/02, C07K14/47, C07K16/18, A61K45/00, PC
A61K38/17
PC A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/7088// (C12P21/
02, C12R1:19)
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FH Key Location/Qualifiers
source 1..330
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/mol_type="genomic DNA"
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BASE COUNT 91 a 62 c 91 g 86 t
ORIGIN
Alignment Scores:
Pred. No.: 5,91e-60 Length: 330
Score: 574.00 Matches: 106
Percent Similarity: 99.09% Conservative: 3
Best Local Similarity: 96.36% Mismatches: 1
Query Match: 97.12% Indels: 0
Gaps: 0
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QY 21 TyrThrIleSerLeuAlaArgAlaGlnGlnAspTyrAsnAlaProAspCysArgPheIle 40
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QY 41 AspValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
DB 121 AATGTCAGAGAAAGGCGACAGATCTATGTTTATTCAGAGCTGTAAACAGAAATGAGACT 180
QY 61 GlyGluPheThrAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
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QY 81 TyrPheProSerAsnLeuValLysGluGlnArgValTyrGlnAlaAlaThrLysGluIle 100
DB 241 TATTTCCCAAGCACTGTTTGAAGACCAAGAGTGTACCAAGGCCCAAGAGATT 300
QY 101 ProThrThrAspIleAspPhePheCysGlu 110
DB 301 CCAACCAAGATATTGACTTCTCTGTGAA 330
RESULT 12
BD010835 384 bp DNA linear PAT 31-JAN-2002
LOCUS Novel polypeptide and DNA thereof.
DEFINITION BD010835
ACCESSION BD010835.1 GI:18639208
VERSION JP 2001069994-A/36.
KEYWORDS Rattus sp.
SOURCE Rattus sp.
ORGANISM Rattus sp.
REFERENCE 1 (bases 1 to 384)
AUTHORS Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
Yoshimura, K. and Tanaka, H.
TITLE Novel polypeptide and DNA thereof
JOURNAL Patent: JP 2001069994-A 36 21-MAR-2001;
TAKEDA CHEMICAL INDUSTRIES LTD
OS Rattus sp. (rat)
PN JP 2001069994-A/36

PD 21-MAR-2001
PE 29-JUN-2000 JP 2000195911
PR
PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI
SHINICHI MOGI,
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC
A61P19/08,
PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC
G01N33/53//
PC C12P21/08, C12N15/00, A61K37/02, C12N5/00
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FH Key Location/Qualifiers
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FT /organism="Rattus sp. (rat)"
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BASE COUNT 98 a 72 c 109 g 105 t
ORIGIN

Alignment Scores:
Pred. No.: 6,96e-60 Length: 384
Score: 574.00 Matches: 106
Percent Similarity: 99.09% Conservative: 3
Best Local Similarity: 96.36% Mismatches: 1
Query Match: 97.12% Indels: 0
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Db 115 TATACCATTTCTCTGGCAAGAGCAGACAGACTTAACATGCCCGGACGTGTGATC 174

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Db 175 AATGTCAGAAAGGAGCAGATCTATGTTATTCACAGCTGTACAGAAATGAGCT 234

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Db 235 GGGGCATTTCTGGCTGTGAGTGTATGTTATGACACACAGATGAGATGGGATTGTGGGT 294

QY 81 TyrPheProSerAsnLeuValLysGlnGlnArgValTyrGlnGluAlaThrLysGluIle 100
Db 295 TATTTCCCGACGACCTGTGTAGAGCAACAGATGTACAGAGGCCACCAAGAGATT 354

QY 101 ProThrThrAspIleAspPhePheCysGlu 110
Db 355 CCACACCGAGATTTGACTTCTTCTGTGA 384

RESULT 13
BD093136 384 bp DNA linear PAT 27-AUG-2002
LOCUS Novel polypeptide and its DNA.
DEFINITION
ACCESSION BD093136
VERSION BD093136.1 GI:22638724
KEYWORDS WO 0102564-A/36.
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 384)
Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
Yoshimura, K. and Tanaka, H.
Novel polypeptide and its DNA

JOURNAL
Patent: WO 0102564-A 36 11-JAN-2001;
TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO
OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,
HIDEYUKI TANAKA
OS Rattus sp. (rat)
PN WO 0102564-A/36
PD 11-JAN-2001
PE 29-JUN-2000 WO 2000JP004278
PR 30-JUN-1999 JP 99P 186718
PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI
MOGI,
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/12, C12N5/10, C07K14/47, C07K16/18, A61K45/00, PC
A61K38/17,
PC A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/7088// (C12P21/
02, C12R1:19)
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Best Local Similarity: 96.36% Mismatches: 1
Query Match: 97.12% Indels: 0
DB: Gaps: 0

US-10-019-455a-26 (1-110) x BD093136 (1-384)

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LOCUS Novel polypeptide and DNA thereof.
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ACCESSION BD010816
VERSION BD010816.1 GI:18639189
KEYWORDS JP 2001069994-A/17.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 330)

AUTHORS Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y., Yoshimura, K. and Tanaka, H.
 TITLE Novel polypeptide and DNA thereof
 JOURNAL Patent: JP 2001069994-A 17 21-MAR-2001;
 COMMENT TAKEDA CHEMICAL INDUSTRIES LTD
 OS Homo sapiens (human)
 PN JP 2001069994-A/17
 PD 21-MAR-2001
 PR 29-JUN-2000 JP 2000195911
 PI YASUOKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI MOGI,
 YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
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 ACCESSION BD093117
 VERSION BD093117.1 GI:22638705
 KEYWORDS WO 0102564-A/17.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 330)
 AUTHORS Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y., Yoshimura, K. and Tanaka, H.
 TITLE Novel polypeptide and its DNA
 JOURNAL Patent: WO 0102564-A 17 11-JAN-2001;
 COMMENT TAKEDA CHEMICAL INDUSTRIES LTD, YASUOKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
 OS Homo sapiens (human)
 PN WO 0102564-A/17
 PD 11-JAN-2001
 PR 29-JUN-2000 WO 2000JP004278
 PR 30-JUN-1999 JP 99P 186718
 PI YASUOKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI MOGI,
 YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
 PC C12N15/12, C12N5/10, C12P21/02, C07K14/47, C07K16/18, A61K45/00, PC
 A61K38/17,
 PC A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/7088//C12P21/
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 Pred. No.: 1,03e-56 Length: 330
 Score: 547.00 Matches: 99
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 Best Local Similarity: 90.00% Mismatches: 4
 Query Match: 92.55% Indels: 0
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 Db 301 CCCACACGAGATTTGACTTCTTCTGCGAG 330
 Search completed: December 29, 2003, 19:57:20
 Job time: 1812.69 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 29, 2003, 16:23:14 : Search time 1138.05 Seconds
(without alignments)
2349.180 Million cell updates/sec

Title: US-10-019-455a-26
Perfect score: 591
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0 %
Maximum Match 100 %

Listing first 45 summaries

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-DOCLIGN=200 -THR.SCOR=5-pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
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12: gb_est3:*
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28: gb_gss1:*

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29: gb_gss2:.*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 7 | 591 | 100.0 | 630 | 13 | BQ568471 |
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| 13 | 539 | 91.2 | 604 | 13 | BQ567343 |
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| 19 | 362 | 61.3 | 280 | 13 | BQ568785 |
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| 21 | 309.5 | 52.4 | 3240 | 11 | AK047965 |
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| 23 | 274.5 | 46.4 | 678 | 10 | BB647928 |
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ALIGNMENTS

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DEFINITION clone gila3b10 5', mRNA sequence.
ACCESSION BQ570035
VERSION BQ570035.1 GI:21473352
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 398)

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|---------|---|
| AUTHORS | Kachar, B. |
| TITLE | EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing |
| JOURNAL | Unpublished |
| COMMENT | Contact: Kachar, B. e-mail: bka@u.washington.edu |

| FEATURES | Location/Qualifiers |
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city, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy, 14.3% 2, 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in Genbank and have known function; 23% have hits in Genbank, but do not have known function; 12% are uncharacterized ESTs and 20% are unidentified."

| | | | | |
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US-10-019-455A-26 (1-110) x BQ570035 (1-398,

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RESULT 2

BQ564607

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| LOCUS | BQ564607 | 488 bp | mRNA | linear | EST 19-JUN-200 |
| DEFINITION | g119h02.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA | | | | |

ACCESSIO

VERSION

KEYWORDS

SOURCE

ORGAN I

REFERENCE

KEEPER
ATTENTION

AUTHOR
TITLE

1111

ТОПНА

COMMENT

CONTENTS

FEATURES

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 /note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR GigaPack III Gold Cloning Kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with GigaPack III Gold and, upon titration on XL1 Blue MR⁺ cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's Exsist interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAAACAGTATGAC) and 25⁺ strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 143 a 83 c 135 g 127 t

ORIGIN

Alignment Scores:

Pred. No.: 4.38e-73 Length: 488

Score: 591.00 Matches: 110

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 13 Gaps: 0

US-10-019-455a-26 (1-110) x B0564607 (1-488)

QY 1 HisGlyValPheMetAspIysLeuSerLysLysLeuCyAlAspGluCysVal 20

DB 61 CATGGTATTTATGATATACTTCTTTAAGAGTTGTGGCATAGAGTGTGC 120

QY 21 TyrThrIleSerIleuAlaArgAlaGluGluAspTyrAsnAlaProAspCysArgPheIle 40

DB 121 TATACATATTTCTTGGCAGACAGACAGAAATTCAATGCCCACTGTGTTTCATC 180

QY 41 AspValIleLysGluGlnGlnIleTyrValIYrSerLysLeuValThrcGluGngValA 60

DB 181 GAGTCAAGAAAGGAGGAGGAGATCTATGTTACTCCAGCTGTAAACAGAAAGAGCT 240

QY 61 GtGluPheThrAlaGlySerValTyrGtYAspHisGluAspGluMecGlyIleValGly 80

DB 241 GGAGAGTTTGGGCTGGCGTGTTTTGTGACCCAGAGATGAGTGGAAATTGAGGT 300

QY 81 TyrPheProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIle 100

DB 301 TATTTCCAGCAACTTGTGAAAGGAGCGGTATACAGAGGCCCAAGAGATC 360

QY 101 ProThrThrAspIleAspPheCysGlu 110

DB 361 CCAACCAGGATATGACTTCTCTGTGAA 390

RESULT 3

B056498 514 bp mRNA linear EST 19-JUN-2002

LOCUS B056498

DEFINITION Gl109c02.y1 Mouse Organ of Corti cDNA pluescript Mus musculus cDNA

ACCESSION B056498

VERSION B056498.1 GI:21471815

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 514)

AUTHORS Kachar, B.

TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing

JOURNAL Unpublished

COMMENT Contact: Kachar, B.

Structural Cell Biology

National Institute of Deafness and other Communication Disorders

50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA

Tel: 301-402-1599

Fax: 301-402-1765

Email: kachar@nidcd.nih.gov

Plate: 109 row: c column: 02

Seq primer: M13Rpl reverse primer (ABI)

location/Qualifiers

1..514

/organism="Mus musculus"

/mol_type="mRNA"

/strain="BALB/c"

/db_xref="taxon:10090"

/clone="g119h02"

/sex="male and female"

/dev_stage="Post natal day 5 to 13"

/clone_lib="Mouse Organ of Corti cDNA pluescript"

/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit

(catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning Kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase H. Phase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XL1 Blue MRF⁺ cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's Exsist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96 (TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAAACAGCTATAC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 13% are uncharacterized ESTs and 20% are unidentified.

BASE COUNT 147 a 85 c 143 g 139 t
ORIGIN

Alignment Scores:

Prod. No.: 4,71e-73 Length: 514
Score: 591.00 Matches: 110
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-019-455a-26 (1-110) x B0566498 (1-514)

QY 1 HISGLVVAIPHEWETASPLYSLEUSESESLVLSLEUCYALAAPOGLUGLUYSVAL 20
DB 59 CATGGTCTATTATGATTAACCTTTCTTAAAGATTGTGCGGATGAGAGGTGTG 118
QY 21 TTTTThTt 40
DB 119 TATACATTCTTCGCAAGAGACAGAGATTACATGCCAGACTGTAGTTTATC 178
QY 41 ASPVALLVSLGLYGLINGINILLETYVALTYRSELYLEUVALTHRCGLUASNLVALA 60
DB 179 GATGTAAAGAAAGGAGAGATCTATGTTTACTCCAACTGTATAAGAAAAAGGACT 238
QY 61 GLYGLUPHETRALAGYSEVALTYRGLYASPHISGLIASPGLMEGLYILEVALGLY 80
DB 239 GGAAGATTGGGCTGGCACTGTTTATGTTGACCCAGATGAGATGAGGAAATTGAGCT 298

QY 81 TyRheProSeRasAnLeuValTyGluGlnAryValTyGlnGluAaThryGluIle 100
DB 299 TATTTCGCCAGCAACTTGGTGAAGAGACGCGTATACAGAGGCGACCAAGAGATC 358
QY 101 ProThrThraPpIleAaPhePheCyGlu 110
DB 359 CCAACCAAGATATGACTTCTCTGTGAA 368

RESULT 4

B0564134

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1..534
/organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
/db_xref="taxon:10090"
/clone="g11d01"
/sex="male and female"
/dev_stage="post natal day 5 to 13"
/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning Kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase H. Phase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden)

534 bp mRNA linear EST 19-JUN-2002
g11d01.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA
clone g11d01 5', mRNA sequence.
B0564134
B0564134.1 GI:21467451
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 534)
EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
Unpublished
Contact: Kachar, B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: kachar@nidcd.nih.gov
Plate: 11 row: d column: 01
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers

and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XL1 Blue MRF⁺ cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 µl of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAAACAGCTATGACC) and 25x strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA) and analyzed on 3700 automated capillary sequencers using POPS polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 155 a 87 c 148 g 144 t

ORIGIN

Alignment Scores:

Pred. No.: 4.97e-73 Length: 534
Score: 591.00 Matches: 110
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-10-019-455a-26 (1-110) x B0564134 (1-534)

QY 1 HisGlyValPheMetAspLysLeuSerLysLeuGlyCysAlaAspGluGluCysVal 20
DB 57 CATGCTGATTATTAGATTAACCTTCTTCAAGAGTTGTGTGGCATGAGAGTGTCTC 116
QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
DB 117 TATACATTTCTCTGGCAGAGCACAGAGAGATTACATGCCCCAGACTGTAGTTCATC 176
QY 41 AspValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
DB 177 GATGTCAAGAAAGGGCAGCAGATGATTATCTCCAGCTGGTAACAGAAACGGAGCT 216
QY 61 GLyGluPheTpaIaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
DB 237 GGAAGATTTTGGGTGGCAGCTGTTATGTCGACCAACAGATGAGTGGAAATTTGAGGT 296
QY 81 TyrPheProSerAsnLeuValLysGluGlnArgValTyrGlnGlnIleAlaThrLysGluIle 100
DB 297 TATTTCCCAAGCAACTGGTGAAGAGACAGCGTATATACAGAGGACCAACAGAGATC 356
QY 101 ProThrThrAspIleAspPhePheCysGlu 110
DB 357 CCAACCAAGATATGACTTCTCTGTGAA 386

RESULT 5

LOCUS B0569741

DEFINITION g1135f01.y1 Mouse Organ of Corti cDNA pb1uescript Mus musculus cDNA

ACCESSION B0569741

VERSION B0569741.1

KEYWORDS EST.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.
AUTHORS 1 (bases 1 to 560)
TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
JOURNAL Unpublished
COMMENT Contact: Kachar, B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: kachar@nidcd.nih.gov
Plate: 135 row: f column: 01
Seq primer: M13Rpl reverse primer (ABI).
Location/Qualifiers
1..560
/organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
/db_xref="taxon:10090"
/clone="g1135f01"
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/clone_lib="Mouse Organ of Corti cDNA pb1uescript"
/note="Organ: Organ of Corti; Vector: pb1uescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 µg mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with Xho I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XL1 Blue MRF⁺ cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 µl of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAAACAGCTATGACC) and 25x

Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 DB: 13
 Gaps: 0

US-10-019-455a-26 (1-110) x BQ568471 (1-608)

QY 1 HisGlyValI PheMetAspIysLeuSerIysIysLeuCysAlaAspGluGluCysVal 20
 Db 67 CATGCTGATTTATGATTAACCTTCTCTTAAGAGTTGTGGCGATGAGAGGTGTC 126
 QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
 Db 127 TATACATTTCTCTGCGAAGACACAGAGATTCATGCCCCAGACTGTAGGTTCATC 186
 QY 41 AspValIysGlyGlnGlnIleTyrValTyrSerIysLeuValThrGluAsnGlyAla 60
 Db 187 GATGTCAGAAAGGCGACAGATCTATGTTTCTCAAGCTGTGACAGAAACGAGACT 246
 QY 61 GlyGluPheTyrPalaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
 Db 247 CGAGAGTTTGGCGCTGGCAGTGTATATGTCACACAGATGAGATGGAATTTGAGT 306
 QY 81 TyrPheProSerAsnLeuValIysGluGluArgValTyrGlnGluAlaThrLysGluIle 100
 Db 307 TATTCCCGCAGCACTGTGTGAGAGCAGCGTGTATACAGAGAGCCACCAAGAGATC 366
 QY 101 ProThrAspIleAspPheGlyGlu 110
 Db 367 CCACCGAGGATTTGACTTCTCTGTGA 396

RESULT 7

LOCUS BQ568471 630 bp mRNA linear EST 19-JUN-2002
 DEFINITION g1108904.Y1 Mouse Organ of Corti cDNA pluscscript Mus musculus CDNA
 clone g1108904 5', mRNA sequence.
 ACCESSION BQ568471
 VERSION BQ568471.1 GI:21471788
 KEYWORDS EST
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
 1 (bases 1 to 630)
 Kachar, B.
 EST analysis of gene expression in the mouse Organ of Corti at the
 onset of hearing
 Unpublished
 Contact: Kachar, B.
 Structural Cell Biology
 National Institute of Deafness and other Communication Disorders
 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
 Tel: 301-402-1599
 Fax: 301-402-1765
 Email: kacharb@nidcd.nih.gov
 Plate: 108 row: 9 column: 04
 Seq primer: M13RP1 reverse primer (ABI).
 Location/Qualifiers
 1..630
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="BALB/c"
 /db_xref="taxon:10090"
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 /dev_stage="Post natal day 5 to 13"
 /clone_lib="Mouse Organ of Corti cDNA pluscscript"
 /note="Organ: Organ of Corti; Vector: pluscscript; The
 organ of Corti (OC) was fine dissected from a total of 386
 OC as follows: 102 samples from post-natal (P) day 5; 72
 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
 14 from P12 and 24 from P13. After killing animals by
 cervical dislocation followed by decapitation, the bulla

JOURNAL COMMENT
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 FEATURES
 source

US-10-019-455a-26 (1-110) x BQ568471 (1-630)
 QY 1 HisGlyValI PheMetAspIysLeuSerIysIysLeuCysAlaAspGluGluCysVal 20
 Db 67 CATGCTGATTTATGATTAACCTTCTCTTAAGAGTTGTGGCGATGAGAGGTGTC 126
 QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
 Db 127 TATACATTTCTCTGCGAAGACACAGAGATTCATGCCCCAGACTGTAGGTTCATC 186
 QY 41 AspValIysGlyGlnGlnIleTyrValTyrSerIysLeuValThrGluAsnGlyAla 60

BASE COUNT

178 a 111 c 167 g 174 t

Alignment Scores:

Pred. No.: 6,29e-73 Length: 630
 Score: 591.00 Matches: 110
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 13 Gaps: 0

US-10-019-455a-26 (1-110) x BQ568471 (1-630)

QY 1 HisGlyValI PheMetAspIysLeuSerIysIysLeuCysAlaAspGluGluCysVal 20
 Db 67 CATGCTGATTTATGATTAACCTTCTCTTAAGAGTTGTGGCGATGAGAGGTGTC 126
 QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
 Db 127 TATACATTTCTCTGCGAAGACACAGAGATTCATGCCCCAGACTGTAGGTTCATC 186
 QY 41 AspValIysGlyGlnGlnIleTyrValTyrSerIysLeuValThrGluAsnGlyAla 60

was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR GigaPack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug RNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMuLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with GigaPack III Gold and, upon titration on XL1 Blue MRF⁺ cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's EXSist interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concerto96 (TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGGAACGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

/strain="BALB/c"
 /db xref="taxon:10090"
 /clone="g142903"
 /sex="male and female"
 /dev_stage="post natal day 5 to 13"
 /clone_lib="Mouse Organ of Corti cDNA plibuescript"
 /note="Organ: Organ of Corti; Vector: plibuescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack Kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR GigaPack III Gold Cloning Kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (IMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with GigaPack III Gold and, upon titration on XL1 Blue MRF cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's Exsist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the grown in 96-well, 2 ml growth plate, plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAAACAGCTGTAAC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 2% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT
 ORIGIN

145 a 78 c 131 g 120 t

Alignment Scores:

Pred. No.: 2,14e-72 Length: 474
 Score: 586.00 Matches: 109
 Percent Similarity: 99.09% Conservative: 0
 Best Local Similarity: 99.09% Mismatches: 1
 Query Match: 99.15% Indels: 0
 DB: 13 Gaps: 0

US-10-019-455a-26 (1-110) x B0565637 (1-474)

QY 1 HisGlyValPheMetAspLeuSerSerIysIleLeuCysAlaAspGluGlyVal 20
 Db 68 CAGCGGTATTATGATAAAGCTTCTTAATGTTGGCGGATGAGAGTGTGTC 127

QY 21 TyrThrIleSerLeuAlaArgAlaGluIleAspTyrAsnAlaProAspCysArgPheIle 40
 Db 128 TATCTATTATTTCTGCGAAGACAGACAGAAATTACAAGCCCGACGTTGTTTCATC 187

QY 41 AspValIleSerGluGluGlnIleTyrValTyrSerIleLeuValThrGluGlnGlyAla 60
 Db 188 GAGGTCAAGAAAGGAGGAGCATCTATGTTACTCCAACTGGTAAACAGAAACGAGCT 247

QY 61 G1G1PheThrPalaGlySerValTyrGlyAspHisG1AspG1umetG1yleValG1y 80
 Db 248 GGAAGATTTTGGCTGGCTGCACTGTTTGTGTACCCACAGATGAGTGGAAATTGAGCT 307

QY 81 TyrPheProSerAsnLeuValIysGluGlnArgValTyrGlnGluAlaThrIysGluIle 100
 Db 308 TATTTCCCGACCAACTTGTGGAAGAGACGCGTATACAGAGGCGCAAGAGATC 367

QY 101 ProThrThrAspIleAspPhePheCysGlu 110
 Db 368 CCAACCGAGATATGACTTCTTGTGAA 397

RESULT 11
 B0566932
 LOCUS B0566932 409 bp mRNA linear EST 19-JUN-2002
 DEFINITION g173g09.y1 Mouse Organ of Corti cDNA plibuescript Mus musculus cDNA
 clone g173g09 5', mRNA sequence.
 ACCESSION B0566932
 VERSION B0566932.1 GI:21470249
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 409)
 REFERENCE Kachar,B.
 TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
 JOURNAL Unpublished
 COMMENT Contact: Kachar,B.
 Structural Cell Biology
 National Institute of Deafness and other Communication Disorders
 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
 Tel: 301-402-1599
 Fax: 301-402-1765
 Email: kachar@nidcd.nih.gov
 Plate: 73 row: g column: 09
 Seq primer: M13RPI reverse primer (ABI).
 Location/Qualifiers
 1. 409
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="BALB/c"
 /db xref="taxon:10090"
 /clone="g173g09"
 /sex="male and female"
 /dev_stage="post natal day 5 to 13"
 /clone_lib="Mouse Organ of Corti cDNA plibuescript"
 /note="Organ: Organ of Corti; Vector: plibuescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack Kit

(catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and the Uni-Zap XR GigaPack III Gold Cloning Kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly, 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep600 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1,000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phasmid was packaged with GigaPack III Gold and, upon titration on XL1 Blue MRP cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExSist1 Intelectance resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well 2 ml growth plate. Plasmid DNA was purified from 200 μ l of saturated culture with the Concert 96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CACGAACGCTATACC) and 25' strand specific BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

| | | | | |
|------------|-------|------|-------|-------|
| BASE COUNT | 102 a | 75 c | 121 g | 111 f |
| ORIGIN | | | | |

Alignment Scores:

| | | | |
|------------------------|----------|---------------|-----|
| Pred. No.: | 1.61e-69 | Length: | 409 |
| Score: | 565.00 | Matches: | 108 |
| Percent Similarity: | 98.18% | Conservative: | 0 |
| Best Local Similarity: | 98.18% | Mismatches: | 1 |
| Query Match: | 95.60% | Indels: | 1 |
| DB: | 13 | Gaps: | 0 |

US-10-019-455A-26 (1-110) X BQ566932 (1-409)

| | | |
|----|--|-----|
| QY | HiGIYVaLpHeMcAsPlySLeUsSeRrLySLvSLeCYaI1-AsgGIuGLCYvA | 20 |
| Db | 81 CAtGGGTAtTTTATGcATNAACCTTTCTTAAAGMAcCTTGtGCTTGATAGcAGAtGGT | 146 |
| QY | 20 IYrThrILeSerLeuAlaRgSLaGInGLuSPYrAsnAlAProSPCYaRgPheI1 | 40 |
| Db | 141 CTNACATATTCTCGGCAAGACCAcGGAAGTTTCAATGCCCGCAcGTAGTTCAT | 200 |
| QY | 40 eAspValLySLvSGLyGInGLInLeYrYValIYrSeRySLvSLValThrgIuAsnGLYAl | 60 |
| Db | 201 CGATGCTCAcAAAGGGcAGcAGATCTATCTTATCTCCAAcGTGGTAAcGAAGAAcGGAGC | 260 |
| QY | 60 aGlyuPHeTrpAlaGLySerValTYrGLyAspHISGLuAspGluMetGLYIleValGL | 80 |
| Db | 261 TGAGAGcTTTGGcGTGGcAGcAGTGTATTATGATACCAcCAcGAGTGTGAATGGcAATTTGAGG | 320 |

| Qy | Db |
|---|--|
| 80 YTYRPEPQSSRSASLSEVALLVYGLNGLSARVATLTCINGLNLATHRYLVSGLVIL | 321 TATATTTCCCCACGCACTGGTGTAAAGACACACGGTATACCAAGSAGCCCAAGAGGAT |
| 100 ePpRThTThaapIleasPpnaephCys 109 | |
| 381 CCCAACCAACGCGCATTTGACTTCTTCTGT 408 | |

| | |
|------------|--|
| RESULT | 12 |
| LOCUS | B0565411 |
| DEFINITION | B0565411 490 bp mRNA linear EST 19-JUN-2007 g137b2.1 Mouse Organ of Corti cDNA plus transcript Mus musculus CDNA clone g137b2.5, mRNA sequence. |
| ACCESSION | B0565411 |
| VERSION | B0565411.1 GI:21468728 |
| KEYWORDS | EST. |
| SOURCE | Mus musculus (house mouse) |
| ORGANISM | Mus musculus |

| | |
|-----------|---|
| REFERENCE | 1 (bases 1 to 490) |
| AUTHORS | Kachar,B. |
| TITLE | EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing |
| JOURNAL | Unpublished |
| COMMENT | Contact: Kachar,B. |

| FEATURES | Location/Qualifiers |
|----------|---------------------|
| source | 1. .490 |

and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XL1 Blue MR⁺ cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in Genbank and have known function; 23% have hits in Genbank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 191 a 77 c 109 g 112 t
ORIGIN
Alignment Scores:
Pred. No.: 5,4e-68 Length: 490
Score: 555.00 Matches: 103
Percent Similarity: 99.09% Conservative: 6
Best Local Similarity: 93.64% Mismatches: 1
Query Match: 93.91% Indels: 0
DB: 13 Gaps: 0
US-10-019-455A-26 (1-110) X BQ565411 (1-490)
QY 1 HisG1ValPheMetAspLysLeuSerLysLysLeuCysAlaAspGluGluCysVal 20
Db 141 CAGGGGATTTATGGAATTAATCTTTTAAATAATTTGTGCGGATTAAGAGTGTTC 200
QY 21 TTTTTh1SerLeuAlaArgAlaGluAspTyrAsnAlaProAspCysArgPhe1le 40
Db 201 TATACTATTCTCTGSCAAGACAGCAAGAAATTTCAATGCCCAACTGATGCTTATTC 260
QY 41 AspValLysGluGluGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
Db 261 GATGTCAAAAAGGCGAGCAAAATCTATGTTTCTCCAACTGGTAAACAAAACGAGACT 320
QY 61 GlyGluPheThrAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
Db 321 GGAATATTTTGGCTGTGAGTGTTTATGGGACCCACGAGATGAATGGGAATTTAGGT 380
QY 81 TTTPhPheSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIle 100
Db 381 TATTTTCCCAACCACTGTTGTAAGAGGAGCGGTGATATCCAGAGGCCCAAGAGAGATC 440
QY 101 ProThrThrAsp1LeaSpPheCysGlu 110
Db 441 CCACACCGAGATTTGACTTCTTGGGAA 470
RESULT 13
BQ567343 604 bp mRNA linear EST 19-JUN-2002
LOCUS BQ567343
DEFINITION g186d08.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA
ACCESSION BQ567343
VERSION BQ567343.1 GI:21470660
KEYWORDS EST.

SOURCE
ORGANISM Mus musculus (house mouse)
MUS musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 604)
REFERENCE
AUTHORS Kachar, B.
TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
JOURNAL
COMMENT Unpublished
Contact: Kachar, B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: kachar@nidcd.nih.gov
Plate: 88 row: d column: 08
Seq primer: M13RPI reverse primer (ABI).
FEATURES
source
location/Qualifiers
1..604
/organism="Mus musculus"
/mol_type="RNA"
/strain="BALB/c"
/db_xref="taxon:10090"
/clone="g186d08"
/sex="male and female"
/dev_stage="post natal day 5 to 13"
/clone_lib="Mouse Organ of Corti cDNA pBluescript"
/note="Organ: Mouse Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning Kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dt) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMuLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Palo Alto, CA) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XL1 Blue MR⁺ cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCTATGACC) and 25%

strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in Genbank and have known function; 23% have hits in Genbank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 178 a 108 c 152 g 166 t

ALIGNMENT SCORES:

Pred. No.: 1,336-65 Length: 604
Score: 539.00 Matches: 100
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 91.20% Indels: 0
DB: 13 Gaps: 0

US-10-019-455A-26 (1-110) x BQ567343 (1-604)

QY 11 LysLysLeuCyAlaAspGluGluCysValTyrThrIleSerLeuAlaArgIleGluGlu 30
DB 1 MAGAGCTGTGTGGGATGAGAGTGTGTCTATCTTCTGCGAAGACACAGAA 60
QY 31 ASPYAspAlaProAspCysArgPheIleAspValLysGlyGlnGlnIleTyrVal 50
DB 61 GATTACATGCGCCAGACTGTAGTTCATCGATGTCAGAAAGGCGAGATCATGTT 120
QY 51 TTTSerLysLeuValThrGlnGlnGlyAlaGlyGluPheTyrAlaGlySerValTyrGly 70
DB 121 TACTCCAGACTGTATACAGAAACGAGCTGAGAGTTTGGCGCGAGATGTTATTATG 180
QY 71 ASPHISGlnAspGluMetGlyIleValGlyTyrPheProSerAsnLeuValLysGlnGln 90
DB 181 GACCCACAGAGTGTAGTGGAAATGTAGTATTTCCCGACACTTGTGTGAAGAGAG 240
QY 91 AGValTyrGlnGlnAlaThrLysGlnIlePheProThrAspIleAspPhePheCysGlu 110
DB 241 CGTGTATACAGAGGCCACCAAGAGAGATCCACACGAGATATGATCTTCTGTGAA 300

RESULT 14 BY232622 365 bp mRNA linear EST 10-DEC-2002
LOCUS BY232622 RIKEN full-length enriched, adult inner ear Mus musculus
DEFINITION CDNA clone F930026J20 5', mRNA sequence.
ACCESSION BY232622
VERSION BY232622.1 GI:26413732
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 365)
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Otsu, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojbori, T., Baldarelli, R., Hill, D.P., Bulic, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, D.A., Brad, D., Brusa, V., Chochia, C., Corbani, L.E., Cousins, S., Dalia, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimond, S., Gustlich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Keizler, R.W., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pereira, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramchandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, G., Ring, B.Z., Ringwald, M., Sander, A., Schneider, C., Sempere, C.A., Seton

TITLE

JOURNAL MEDLINE
PUBMED
22354683

COMMENT

M., Shinada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verrado, R., Wagner, L., Mahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilm, L.G., Wynshaw-Boris, A., Yangisawa, M., Yang, I., Yang, L., Yuan, Z., Zou, L., Zhu, Y., Zimmer, A., Cammici, P., Hayatsu, N., Hirozane-Kishikawa, T., Komori, H., Nakamura, M., Sakazume, N., Sato, K., Shitaki, T., Waki, K., Kawai, T., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterson, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

12466851
Contact: Yoshinide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-resgsc.riken.go.jp/
URL: http://genome.gsc.riken.go.jp/
Aizawa, K., Akimura, T., Arakawa, T., Cammici, P., Fukuda, S., Hirozane, T., Imocani, K., Ishii, Y., Itoh, M., Kawai, J., Komori, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numata, K., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shitaki, T., Tagami, M., Waki, K., Watanishi, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Kirk W. Beisel (Boys Town National Research Hospital 555 North 30th Street Omaha, NE 68131 USA) whose assistance we gratefully acknowledge. Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.
Location/Qualifiers

FEATURES

source

1. 365
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="F930026J20"
/tissue_type="inner ear"
/dev_stage="adult"
/clone_lib="RIKEN full-length enriched, adult inner ear"
BASE COUNT 97 a 60 c 110 g 98 t

ORIGIN

ALIGNMENT SCORES:

Pred. No.: 2,126-60 Length: 365
Score: 500.00 Matches: 95
Percent Similarity: 98.96% Conservative: 0
Best Local Similarity: 98.96% Mismatches: 1
Query Match: 84.60% Indels: 0
DB: 13 Gaps: 0

US-10-019-455A-26 (1-110) x BY232622 (1-365)

QY 1 HisGlyValPheMetAspLysLeuSerSerLysLysLeuCyAlaAspGluGluCysVal 20
 Db 78 CAGGCTATTATTGATTAAGTCTTCTTAAGAGTGTGTGGATGAGAGTGTGTC 137
 QY 21 TyThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
 Db 138 TATACCTATTCTCTGGCAGAGACACAGAAAGATTACATCCCACTGTAGTTCATC 197
 QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGluAla 60
 Db 198 GATGTCAAGAAAGGCGCAGATCTATGTTTACTCCAGCTGTGTAAACAGAAACGAGCT 257
 QY 61 G1GluPheTyrPalajSerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
 Db 258 CGAGAGTTGGGCGTGGCAGTGTATTAGTGACACACAGATGATGATGGGAATTGAGGT 317
 QY 81 TyPheProSerAsnLeuValLysGluGlnArgValTyrGlnGluAla 96
 Db 318 TATTCCCAAGCAACTGTGTGAAGACACAGCTGTATACAGAGAGGCC 365
 RESULT 15 485 bp mRNA linear EST 19-JUN-2002
 BQ565179 485 bp mRNA linear EST 19-JUN-2002
 LOCUS g132a07.y1 Mouse Organ of Corti cDNA Bluescript Mus musculus cDNA
 DEFINITION clone g132a07 5', mRNA sequence.
 ACCESSION BQ565179
 VERSION BQ565179
 KEYWORDS BQ565179.1 GI:21468496
 SOURCE EST.
 ORGANISM Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 485)
 Kachar, B.
 EST analysis of gene expression in the mouse Organ of Corti at the
 onset of hearing
 Unpublished
 JOURNAL Contact: Kachar, B.
 Structural Cell Biology
 National Institute of Deafness and other Communication Disorders
 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
 Tel: 301-402-1599
 Fax: 301-402-1765
 Email: kacharbeniddc.nih.gov
 Plate: 32 row: a column: 07
 Seq primer: M13RPI reverse primer (ABI).
 Location/Qualifiers
 1..485
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="BALB/c"
 /db_xref="taxon:10090"
 /clone="g132a07"
 /sex="male and female"
 /dev_stage="Post natal day 5 to 13"
 /note="Organ: Organ of Corti; Vector: pBluescript; The
 organ of Corti (OC) was fine dissected from a total of 386
 OC as follows: 102 samples from post-natal (p) day 5; 72
 from p6; 60 from p7; 46 from p8; 18 from p9; 20 from p10;
 14 from p12 and 24 from p13. After killing animals by
 cervical dislocation followed by decapitation, the bulla
 was removed and opened in Leibowitz medium. The bony
 capsule of the cochlea was clipped away, stria vascularis
 and spiral ligament were removed and the sensory
 epithelium was carefully dissected out of the modiolus.
 Total RNA was extracted using the micro Fasttrack kit
 (catalog # K1593-02; Invitrogen, Carlsbad, CA), according
 to manufacturer's instructions. Reverse transcription and
 library construction were carried out with the Uni-Zap XR
 vector kit (catalog # 237211, Stratagene) and Uni-Zap XR
 Gigapack III Gold Cloning kit (catalog # 237612), both
 from Stratagene (La Jolla, CA, USA), according to

manufacturer's instructions. Briefly: 1.5 ug mRNA was
 reverse transcribed using a hybrid oligo(dT) linker-primer
 that contains an Xho I site. First strand synthesis was
 primed with the linker-primer and transcribed using
 Moloney murine leukemia virus reverse transcriptase
 (MMLV-RT) and 5-methyl dCTP. The second strand was
 synthesized with DNA polymerase and RNase H. Complementary
 DNA was blunt ended with Pfu DNA polymerase, ligated with
 EcoR I adapters in the presence of ligase and digested
 with Xho I. The cDNA was sequentially size fractionated
 over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden)
 and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA)
 columns to enrich for cDNAs greater than 400bp and 1000 bp
 , respectively. The cDNA was then directionally ligated to
 the Uni-Zap XR vector, which had been predigested with
 EcoR I and Xho I. The phagemid was packaged with Gigapack
 III Gold and, upon titration on X11 Blue MRF⁺ cells, the
 yield of the phage library was estimated to be 11,100,000
 recombinants. Stratagene's Exsist⁺ interference
 resistance helper phage (catalogue # 211203) was adopted
 to rescue plasmid DNA from the phages. Upon plating of the
 rescued library, individual cDNA clones were selected and
 grown in 96-well, 2 ml growth plate. Plasmid DNA was
 purified from 200 ul of saturated culture with the
 Concert96(TM) plasmid purification kit (Invitrogen,
 Carlsbad, CA) as instructed by the manufacturer. ESTs from
 the 5' end of the cDNA clones were generated with the
 universal M13 reverse primer (CAGGAACAGCTATGACC) and 253
 strength BigDye terminator sequencing chemistry (Applied
 Biosystems, Foster City, CA). Sequencing reactions were
 performed on MJ Tetrad thermal cyclers (MJ Research,
 Waltham, MA), and analyzed on 3700 automated capillary
 sequencers using POPs polymer (Applied Biosystems, Foster
 City, CA). The frequency distribution of the library is
 as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10;
 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of
 genes are present in GenBank and have known function; 23%
 have hits in GenBank, but do not have assigned function;
 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 146 a 92 c 122 g 125 t
 ORIGIN

Alignment Scores:

Pred. No.: 6,92e-52 Length: 485
 Score: 441.00 Matches: 81
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 74.62% Indels: 0
 DB: 13 Gaps: 0

US-10-019-455A-26 (1-110) x BQ565179 (1-485)

QY 30 GUAAPTYrAsnAlaProAspCysArgPheIleAspValLysGlyGlnGlnIleTyr 49
 Db 2 CAAAGTTTCATGCCCCCAGACTGTAGTTCATCATGTCAAGAAAGCGCACATCTAT 61
 QY 50 ValTyrSerLysLeuValThrGluAsnGlyAlaGlyGluPheTyrPalajSerValTyr 69
 Db 62 GTTACTCCAAAGCTGTACAGAAACGACGCTGAGAGTTTGGGCTGCAGAGTTTAT 121
 QY 70 G1AspHisGlnAspGluMetGlyIleValGlyTyrPheProSerAsnLeuValLysGlu 89
 Db 122 GGTGACCCACAGAGATGAGATGGGAATTGTAGTTATTTCCCACTGTGTAGAGAG 181
 QY 90 G1AspValTyrGlnGlnAlaThrLysGlnIleProThrTyrAspIleAspPheCys 109
 Db 182 CAGCTGTATTCACAGAGGCCACCAAGAGATCCCAACACGAGATTTGACTTCTGT 241
 QY 110 G1u 110
 Db 242 GAA 244

Tue Dec 30 10:20:45 2003

us-10-019-455a-26.rpt

Page 15

Search completed: December 29, 2003, 22:00:50
Job time : 1140.05 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 29, 2003, 16:10:49 ; Search time 132.647 Seconds
(without alignments)
2238.558 Million cell updates/sec

Title: US-10-019-455a-26

Sequence: 1 HGVFMDKSKKLCADDECV.....RYGEATKEPTTIDIFPCE 110

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2552756 segs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:
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-Q=/cgn2.1/USPTO.spool/US10019455/runat.29122003.160347.230/app.query.fasta_1.1770
-DB=N Geneseg 19Jun03 -QFMT=fasta+ -SUFFIX=ring -MINMATCH=0.1 -LOOPEXT=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=bloms62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCNU -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10019455.@CGN1.1.0 @runat.29122003.160347.230 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WATP -DSPLOCK=100 -LONGLOC
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -XGAPOP=10 -XGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N_Geneseg_19Jun03:*
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2: /SIDSI/gcgdata/geneseg/geneseg-n-emb1/NA1981.DAT:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.

and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-----------|--------------------|
| 1 | 591 | 100.0 | 330 | AAFS9080 | Mouse MLP nucleot |
| 2 | 591 | 100.0 | 384 | AAFS9080 | Mouse MLP nucleot |
| 3 | 591 | 100.0 | 947 | AAFS9084 | Mouse MLP nucleot |
| 4 | 574 | 97.1 | 330 | AAFS9089 | Rat MLP nucleotide |
| 5 | 574 | 97.1 | 384 | AAFS9098 | Rat MLP nucleotide |
| 6 | 547 | 92.6 | 330 | AAFS9075 | Human MLP nucleot |
| 7 | 547 | 92.6 | 384 | AAFS9065 | Human MLP nucleot |
| 8 | 547 | 92.6 | 387 | AA517583 | DNA encoding novel |
| 9 | 547 | 92.6 | 426 | AAH26341 | Human growth regul |
| 10 | 547 | 92.6 | 521 | ABU95740 | Human angiogenesis |
| 11 | 547 | 92.6 | 521 | ABU88251 | Human PRO9873 CDNA |
| 12 | 547 | 92.6 | 521 | ABK33571 | CDNA encoding huma |
| 13 | 547 | 92.6 | 891 | AAH98228 | Human EST-derived |
| 14 | 547 | 92.6 | 891 | AAH26342 | Human growth regul |
| 15 | 547 | 92.6 | 923 | AAFS9083 | Human MLP nucleot |
| 16 | 547 | 92.6 | 1201 | AAH26343 | Human growth regul |
| 17 | 505 | 85.4 | 307 | AAFS9093 | Rat MLP nucleotide |
| 18 | 445 | 75.3 | 261 | AAFS9092 | Rat MLP nucleotide |
| 19 | 262.5 | 44.4 | 442 | ABU63502 | Breast cancer rela |
| 20 | 262.5 | 44.4 | 442 | ABU64012 | Breast cancer rela |
| 21 | 261.5 | 44.2 | 330 | AAQ84061 | Sequence encoding |
| 22 | 261.5 | 44.2 | 459 | AAQ84050 | Sequence encoding |
| 23 | 261.5 | 44.2 | 459 | AAI70083 | Melanoma inhibitor |
| 24 | 261.5 | 44.2 | 459 | AAI8732 | Human antisense ol |
| 25 | 261.5 | 44.2 | 555 | ABV59223 | Human prostate exp |
| 26 | 259.5 | 43.9 | 433 | AAH47783 | Recombinant human |
| 27 | 241.5 | 40.9 | 581 | AAQ84052 | Sequence encoding |
| 28 | 219.5 | 37.1 | 305 | AAQ84055 | Amplified fragment |
| 29 | 218 | 36.9 | 1060 | AAFS92140 | Human PRO19670 CDN |
| 30 | 218 | 36.9 | 1060 | ABU74460 | Human CDNA encodin |
| 31 | 218 | 36.9 | 1060 | ABU95738 | Human angiogenesis |
| 32 | 218 | 36.9 | 1060 | ABU88249 | Human PRO19670 CDN |
| 33 | 218 | 36.9 | 1060 | ACA57963 | Human PRO19670 CDN |
| 34 | 218 | 36.9 | 1060 | ACA58892 | CDNA encoding huma |
| 35 | 218 | 36.9 | 1060 | ACA60445 | Novel human secret |
| 36 | 218 | 36.9 | 1060 | ACA63455 | CDNA encoding huma |
| 37 | 218 | 36.9 | 1060 | ABX98433 | Human CDNA encodin |
| 38 | 218 | 36.9 | 1060 | ABX98935 | Novel human secret |
| 39 | 218 | 36.9 | 1060 | ACA05980 | Human secreted/tri |
| 40 | 218 | 36.9 | 1060 | ABX98024 | Human PRO polynuci |
| 41 | 218 | 36.9 | 1060 | ABX78808 | Human PRO polynuci |
| 42 | 218 | 36.9 | 1060 | ABX75821 | Human CDNA encodin |
| 43 | 218 | 36.9 | 1060 | ABX77026 | Human PRO polynuci |
| 44 | 218 | 36.9 | 1060 | ABX16866 | Human CDNA encodin |
| 45 | 218 | 36.9 | 1061 | AA546205 | Human DNA encoding |

ALIGNMENTS

RESULT 1
AAFS9080
AAFS9080 standard; DNA, 330 BP.
23-APR-2001 (first entry)

Mouse MLP nucleotide sequence SEQ ID NO:25.

MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
cardiac; gene therapy; secretory cell function regulator; promoter;
inhibitor; ds.

XX Mus musculus.
XX OS
XX

PN MO200102564-A1.
 XX
 PD 11-JAN-2001.
 XX
 PF 29-JUN-2000; 2000MO-JP04278.
 XX
 PR 30-JUN-1999; 99JP-0186718.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K,
 PI Tanaka H;
 XX
 DR WPI; 2001-159271/16.
 DR P-PSDB; AAB69127.
 XX
 PT Safe, low-toxicity secretory cell function-regulatory protein and
 PT encoded DNA, applicable as drugs, in diagnosis and development of
 PT promoters and inhibitors for preventing or treating e.g. bone and joint
 PT diseases -
 XX
 PS Claim 10; Page 98; 11pp; Japanese.
 XX
 CC The present invention describes novel MLP proteins and their encoding
 CC DNAs. The MLP proteins and DNAs have anti-inflammatory and cardiac
 CC activities, and can be used in gene therapy and as secretory cell
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in
 CC the diagnosis and development of promoters and inhibitors for preventing
 CC or treating bone and joint diseases as well as pathologic angiogenesis.
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
 CC in the exemplification of the present invention.
 XX
 SQ Sequence 330 BP; 91 A; 60 C; 92 G; 87 T; 0 other;
 SQ
 Alignment Scores:
 Pred. No.: 4 28e-75 Length: 330
 Score: 591.00 Matches: 110
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 0
 US-10-019-455A-26 (1-110) x AAF59080 (1-330)
 QY 1 HisGlyValPheMetAspLysLeuSerLysLysLeuCysAlaAspGluGluCysVal 20
 DB 1 CATGGTGTATTATGATTAACCTTCTCTTAAGAAAGTTGTGGGATGAGAGTGTGTC 60
 QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
 DB 61 TATACATAATTTCTCTGGCAAGACGACGAGAAATTAACGCCCACTGTGGTTCATC 120
 QY 41 AspValLysLysGlnGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
 DB 121 GATGTCAAGAAAGGACGACGATCTATGTTTACTCCAACTGTAAACAAAAACGAGCT 180
 QY 61 GlyGluPheTyrAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
 DB 181 GGAAGAGTTTGGGCTGGCAGTGTATTATGGTGACCAACGAGATGATGGAAATTGTAAGT 240
 QY 81 TyrPheProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIle 100
 DB 241 TATTTCCCGCAGCACTGTGGTGAAGGAGCGCGTGTATACAGAGGCCACCAAGGAGATC 300
 QY 101 ProThrThraspLysaspPhePheCysGlu 110
 DB 301 CCAACCAAGGATTTGACTTCTTCTGTGA 330
 RESULT 2
 AAF59068
 ID AAF59068 standard; DNA; 384 BP.
 XX
 AC AAF59068;

XX
 DT 23-APR-2001 (first entry)
 XX
 DE Mouse MLP nucleotide sequence SEQ ID NO:10.
 XX
 KW MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
 KW joint disease; pathologic angiogenesis; diagnosis; anti-inflammatory;
 KW cardiac; gene therapy; secretory cell function regulator; promoter;
 KW inhibitor; ds.
 XX
 OS Mus musculus.
 XX
 PN MO200102564-A1.
 XX
 PD 11-JAN-2001.
 XX
 PF 29-JUN-2000; 2000MO-JP04278.
 XX
 PR 30-JUN-1999; 99JP-0186718.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K,
 PI Tanaka H;
 XX
 DR WPI; 2001-159271/16.
 DR P-PSDB; AAB69125.
 XX
 PT Safe, low-toxicity secretory cell function-regulatory protein and
 PT encoded DNA, applicable as drugs, in diagnosis and development of
 PT promoters and inhibitors for preventing or treating e.g. bone and joint
 PT diseases -
 XX
 PS Claim 11; Page 93; 11pp; Japanese.
 XX
 CC The present invention describes novel MLP proteins and their encoding
 CC DNAs. The MLP proteins and DNAs have anti-inflammatory and cardiac
 CC activities, and can be used in gene therapy and as secretory cell
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in
 CC the diagnosis and development of promoters and inhibitors for preventing
 CC or treating bone and joint diseases as well as pathologic angiogenesis.
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
 CC in the exemplification of the present invention.
 XX
 SQ Sequence 384 BP; 98 A; 68 C; 111 G; 107 T; 0 other;
 SQ
 Alignment Scores:
 Pred. No.: 5 28e-75 Length: 384
 Score: 591.00 Matches: 110
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 0
 US-10-019-455A-26 (1-110) x AAF59068 (1-384)
 QY 1 HisGlyValPheMetAspLysLeuSerLysLysLeuCysAlaAspGluGluCysVal 20
 DB 55 CATGGTGTATTATGATTAACCTTCTCTTAAGAAAGTTGTGGGATGAGAGTGTGTC 114
 QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
 DB 115 TATACATAATTTCTCTGGCAAGACGACGAGAAATTAACGCCCACTGTGGTTCATC 174
 QY 41 AspValLysLysGlnGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
 DB 175 GATGTCAAGAAAGGACGACGATCTATGTTTACTCCAACTGTAAACAAAAACGAGCT 234
 QY 61 GlyGluPheTyrAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
 DB 235 GGAAGAGTTTGGGCTGGCAGTGTATTATGGTGACCAACGAGATGATGGAAATTGTAAGT 294
 QY 81 TyrPheProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIle 100

```

DB 295 TATTCCCGACGACTGTGTGAGGAGCGGTGTATACGAGGAGCCACCAAGAGATC 354
QY 101 ProThrThrAspIleAspPhePheCysGlu 110
DB 355 CCAACCGAGATATTGACTTCTTGTGAA 384

RESULT 3
AAFS9084
ID AAF59084 standard: DNA, 947 BP.
XX
AC AAF59084;
XX
DT 23-APR-2001 (first entry)
XX
DE Mouse MLP nucleotide sequence SEQ ID NO:30.
XX
KM MLP, MIA; melanoma inhibitory activity; cancer; bone disease;
KM joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
KM cardiant; gene therapy; secretory cell function regulator; promoter;
KM inhibitor; ds.
XX
OS Mus musculus.
XX
PN W0200102564-A1.
XX
PD 11-JAN-2001.
XX
PF 29-JUN-2000; 2000WO-JP04278.
XX
PR 30-JUN-1999; 99JP-0186718.
XX
PA (TAKE ) TAKEDA CHEM IND LTD.
XX
PI Itch Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
PI Tanaka H;
XX
DR WPI; 2001-159271/16.
XX
PT Safe, low-toxicity secretory cell function-regulatory protein and
PT encoded DNA, applicable as drugs, in diagnosis and development of
PT promoters and inhibitors for preventing or treating e.g. bone and joint
PT diseases -
XX
PS Example 2; Page 100-101, 111pp; Japanese.
XX
CC The present invention describes novel MLP proteins and their encoding
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
CC activities, and can be used in gene therapy and as secretory cell
CC function regulators. The MLP proteins and DNAs can be used in drugs, in
CC the diagnosis and development of promoters and inhibitors for preventing
CC or treating bone and joint diseases as well as pathologic angiogenesis.
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
CC in the exemplification of the present invention.
XX
SQ Sequence 947 BP; 279 A; 158 C; 221 G; 289 T; 0 other;

Alignment Scores:
Pred. No.: 1,836-74 Length: 947
Score: 591.00 Matches: 110
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-10-019-455a-26 (1-110) x AAF59084 (1-947)

QY 1 HisGlyValIlePheMetAspLysLeuSerIleLysLeuValAspGluCysVal 20
DB 65 CATGGTGTATTATGATTAACCTTCTCTAAGAGTGTGTGCGAGTGAAGAGTGTGTC 124
QY 21 TyrThrIleSerIleuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40

```

```

DB 125 TATACTATTCTCTGCGAAGACAGCAAGATTACATGCCCCAGACTGTACGTTTCATC 184
QY 41 AspValIleLysGlyGlnGlnIleIleTyrValIleTyrSerLysLeuValThrGluSerGlyAla 60
DB 185 GATGTCAGAAAGGAGGACGACGATCTATGTTTACTCCAGCTGTATACAGAAACGAGACT 244
QY 61 GlyIlePheThrPalaGlySerValIleTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
DB 245 GGAGAGTTTGGCTGCGACGTGTTTATGGTGACCAACGATGAGATGGGAATTGTAGGT 304
QY 81 TyrPheProSerAsnLeuValIleGlyGlnGlnArgValIleTyrGlnGluAlaThrLysGluIle 100
DB 305 TATTCCCGACGACTGTGTGAGGAGCGGTGTATACGAGGAGCCACCAAGAGATC 364
QY 101 ProThrThrAspIleAspPhePheCysGlu 110
DB 365 CCAACCGAGATATTGACTTCTTGTGAA 394

RESULT 4
AAFS9099
ID AAF59099 standard: DNA, 330 BP.
XX
AC AAF59099;
XX
DT 23-APR-2001 (first entry)
XX
DE Rat MLP nucleotide sequence SEQ ID NO:48.
XX
KM MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
KM joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
KM cardiant; gene therapy; secretory cell function regulator; promoter;
KM inhibitor; ds.
XX
OS Rattus sp.
XX
PN W0200102564-A1.
XX
PD 11-JAN-2001.
XX
PF 29-JUN-2000; 2000WO-JP04278.
XX
PR 30-JUN-1999; 99JP-0186718.
XX
PA (TAKE ) TAKEDA CHEM IND LTD.
XX
PI Itch Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
PI Tanaka H;
XX
DR WPI; 2001-159271/16.
DR P-PSDB; AAB69131.
XX
PT Safe, low-toxicity secretory cell function-regulatory protein and
PT encoded DNA, applicable as drugs, in diagnosis and development of
PT promoters and inhibitors for preventing or treating e.g. bone and joint
PT diseases -
XX
PS Claim 12; Page 107; 111pp; Japanese.
XX
CC The present invention describes novel MLP proteins and their encoding
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
CC activities, and can be used in gene therapy and as secretory cell
CC function regulators. The MLP proteins and DNAs can be used in drugs, in
CC the diagnosis and development of promoters and inhibitors for preventing
CC or treating bone and joint diseases as well as pathologic angiogenesis.
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
CC in the exemplification of the present invention.
XX
SQ Sequence 330 BP; 91 A; 62 C; 91 G; 86 T; 0 other;

Alignment Scores:
Pred. No.: 1,156-72 Length: 330
Score: 574.00 Matches: 106
Percent Similarity: 99.09% Conservative: 3

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```

XX DE DNA encoding novel secreted protein #12.
XX
XX Secreted protein; cytostatic; immunosuppressive; vulnereary; vaccine;
XX antiinflammatory; neuroprotective; nephrotoxic; cardiovascular;
XX human; cancer; autoimmune disease; wound healing disorder; infection;
XX haematopoietic disorder; inflammatory disorder; infertility;
XX neurological disease; psychiatric disease; cardiovascular disease;
XX respiratory disease; renal; gastrointestinal; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..387
XX FT /*tag= a
XX FT /product= "Human secreted protein"
XX
XX MO200179454-A1.
XX
XX 25-OCT-2001.
XX
XX 11-APR-2001; 2001WO-US11797.
XX
XX 13-APR-2000; 2000US-196603P.
XX 24-APR-2000; 2000US-199417P.
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;
XX
XX WPI; 2002-061975/08.
XX P-PSDB; AAU09871.
XX
XX New secreted proteins or polypeptides, useful for treating e.g. cancer,
XX autoimmune diseases, wound healing disorder, infections, haematopoietic
XX disorders, inflammatory disorders, infertility, cancer
XX
XX Claim 2; Page 44; 92pp; English.
XX
XX The invention relates to an isolated novel secreted polypeptide (I) and
XX polynucleotide (II). (I) and (II) are useful for treating cancer,
XX autoimmune diseases, wound healing disorder, infections, haematopoietic
XX disorders, inflammatory disorders, infertility, neurological and
XX psychiatric diseases, cardiovascular diseases, respiratory diseases,
XX renal diseases, or gastrointestinal diseases. These may also be used to
XX treat diseases, abnormalities and disorders caused by abnormal
XX expression, production, function and/or metabolism of the genes, as
XX vaccines for inducing immunological response in a mammal, and in
XX screening methods for detecting the effect of added compounds on the
XX production of mRNA and polypeptide in cells. The polypeptides can be used
XX as immunogens to produce antibodies immunospecific for the polypeptides,
XX and to identify membrane-bound or soluble receptors. The polynucleotides
XX may be used as diagnostic reagents, in chromosome localisation studies,
XX and in tissue expression studies. The present sequence represents the
XX coding sequence of novel human secreted protein #12.
XX
XX Sequence 387 BP; 101 A; 70 C; 106 G; 110 T; 0 other;
XX
XX Alignment Scores:
XX Pred. No.: 1.04e-68 Length: 387
XX Score: 547.00 Matches: 99
XX Percent Similarity: 96.36% Conservative: 7
XX Best Local Similarity: 90.00% Mismatches: 4
XX Query Match: 92.55% Indels: 0
XX DB: 24 Gaps: 0
XX
XX US-10-019-455a-26 (1-110) x AAS17583 (1-387)
XX
XX QY 1 H18G1VVA1PhemecetaplylsleuSerLysLysLeuCyala1aapGluGluCysVal 20
XX DB 55 CATGGAATATTTATGACCGCTGAGCTTCCAGAGAGCTCTGTCAGATGATGATGTC 114

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QY 21 TYRThrIleSerLeuAlaArgAlaGlnGluAspTYRAsnAlaProAspCysArgPheIle 40
DB 115 TATACTATTTCCTGGCTAGTCTCAAGAAAGTTTAAATGCCCGGACTGTGATTCATT 174
QY 41 AspValIleValGlyGlnGlnIleTYRValTYRserLysLeuValThrGluAsnGlyAla 60
DB 175 AACGTTAAAAAGGAGAGATCTATGTGATCTCAAGCTGGTAAAGAAATGAGACT 234
QY 61 GlyGluPheThrAlaGlySerValTYRgluAspHisGlnAspGluMetGlyIleValGly 80
DB 235 GGAGAAATTTGGCTGGCAGTGTATGATGATGCGCAGACAGATGGAGTCTGCGGT 294
QY 81 TYRPhenProSerAsnLeuValIleGlnGlnArgValTYRglnGluAlaThrLysGluIle 100
DB 295 TATTTCCCGCAGAACCTGTCTCAAGGAACGCGTGTGTACAGAAAGCTTACCAAGGAAGT 354
QY 101 ProThrThrAspIleAspPhePheCysGlu 110
DB 355 CCCACACGAGATATTGACTTCTTCTGCGAG 384
XX
XX RESULT 9
XX AAH26341
XX ID AAH26341 standard; cDNA; 426 BP.
XX
XX AC AAH26341;
XX
XX DT 02-OCT-2001 (first entry)
XX
XX DE Human growth regulatory-like polypeptide clone 16372272.
XX
XX KW Growth regulatory-like polypeptide; human; cartilage; melanoma;
XX neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;
XX ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200155332-A2.
XX
XX PD 02-AUG-2001.
XX
XX PF 25-JAN-2001; 2001WO-US02455.
XX
XX PR 25-JAN-2000; 2000US-0491404.
XX 02-MAY-2000; 2000US-0563786.
XX
XX PA (HYSE-) HYSEQ INC.
XX
XX PI Mize NK, Boyle BJ, Ford JE, Artetburn WC, Tang YT, Liu C;
XX Drmanac RT;
XX
XX WPI; 2001-483233/52.
XX
XX Isolated human growth regulatory-like polypeptide useful for treating
XX e.g. Alzheimer's disease, cancer, autoimmune disorders,
XX hyperproliferative disorders, coagulation disorders, and nervous system
XX disorders -
XX
XX Example 1; Page 114; 119pp; English.
XX
XX The present sequence is that of Hyseq clone identification number
XX 16372272, which was obtained from a human thymus cDNA library
XX using standard PCR with primers specific for vector sequences
XX flanking the inserts, sequencing by hybridisation sequence
XX signature analysis, and Sanger sequencing techniques. This
XX expressed sequence tag was used in the assembly of a full-length
XX cDNA sequence (see AAH26343) encoding a novel human growth
XX regulatory-like polypeptide (GRP, see AAB82671). The GRP
XX belongs to the same protein family as growth regulatory proteins,
XX growth factors, human melanoma derived growth regulatory protein
XX precursor (64% similarity and 45% identity over 111 amino acids)
XX or melanoma inhibitory activity, cattle cartilage-derived
XX retinoic acid sensitive protein (CD-RAP, 44% identity and 64%
XX similarity over 126 amino acids) and other retinoic acid-sensitive

```

CC proteins. GRP polypeptides and polynucleotides of the invention
 CC can be used in the prophylaxis, treatment (including gene therapy)
 CC and diagnosis of disorders and diseases caused by, or involving,
 CC cartilage development and maintenance, inhibition of melanoma cell
 CC growth and tumors, including neuroendocrine tumors such as
 CC gliomas. The polynucleotides can also be used to design probes
 CC and primers, for chromosome and gene mapping, in the recombinant
 CC production of protein, in the generation of antisense, ribozyme and
 CC peptide-nucleic acid molecules, and to produce transgenic animals.
 XX
 SQ Sequence 426 BP; 119 A; 73 C; 113 G; 120 T; 1 other;
 Alignment Scores:
 Pred. No.: 1,19e-68 Length: 426
 Score: 547.00 Matches: 99
 Percent Similarity: 96.36% Conservative: 7
 Best Local Similarity: 90.00% Mismatches: 4
 Query Match: 92.55% Indels: 0
 DB: 22 Gaps: 0
 US-10-019-455a-26 (1-110) x AAH26341 (1-426)
 QY 1 HHSGLVAlPhMeAspLysLeuSerLysLysLeuCyAlaAspGluCysVal 20
 DB 73 CATGGAATATTATATGACCGCTACCTCCAGAAAGCTCTGTGAGATGATGATGTC 132
 QY 21 TTTTTLleSerLeuAlaArSAlaGlnGluAspLysAsnAlaProAspCysArgPheIle 40
 DB 133 TATACTATTCTCTGCTGCTAGTCTCAAGAAAGTTATATGCCCGAGATGATGATCTT 192
 QY 41 AspValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
 DB 193 AACGTTAAAAAGCGCAGACGATCTATGTGTAACAAAGCTGTAAAGAAATGCACT 252
 QY 61 GlyGluPheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
 DB 253 GGAGAAATTTGGGCTGGCAGTGTATATGATGCGCCAGACGAGATGGAGTGTGGCT 312
 QY 81 TTTTPhProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIle 100
 DB 313 TATTTCCCGCAGAACTTGTCTCAGAAACAGCTGTGTCTCCAGAAAGCTTCAAGAGATT 372
 QY 101 ProThrTrpAspLysAspPhePheCysGlu 110
 DB 373 CCCACACGAGATATTGACTTCTTCTGCGAG 402
 RESULT 10
 ABL95740
 ID ABL95740 standard; cDNA; 521 BP.
 XX
 AC ABL95740;
 XX
 DT 19-JUL-2002 (first entry)
 DE Human angiogenesis related cDNA PRO9873 SEQ ID NO: 359.
 XX
 KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
 KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
 KW cardiac; cytoskeletal; antiangiogenic; hypotensive; vulnerary;
 KW antiarteriosclerotic; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200208284-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 09-JUL-2001; 2001WO-US21735.
 XX
 PR 20-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 25-JUL-2000; 2000US-220664P.
 PR 28-JUL-2000; 2000WO-US20710.

PR 02-AUG-2000; 2000US-222695P.
 PR 17-AUG-2000; 2000US-0643657.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23338.
 PR 07-SEP-2000; 2000US-230978P.
 PR 15-SEP-2000; 2000US-000000P.
 PR 18-SEP-2000; 2000US-0664610.
 PR 18-SEP-2000; 2000US-0665350.
 PR 24-OCT-2000; 2000US-242922P.
 PR 08-NOV-2000; 2000US-0709238.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000US-0747259.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 22-JAN-2001; 2001US-0767609.
 PR 28-FEB-2001; 2001US-0766498.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0808689.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 30-MAY-2001; 2001WO-US17092.
 PR 30-MAY-2001; 2001US-0870574.
 PR 30-MAY-2001; 2001WO-US17443.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 28-JUN-2001; 2001WO-US00000.
 XX
 PA (GETH) GENENTECH INC.
 PA (BAKE) BAKER K P.
 PA (FERR) FERRARA N.
 PA (GERB) GERBER H.
 PA (GERR) GERRITSEN M E.
 PA (GODD) GODDARD A.
 PA (GODO) GODOWSKI P J.
 PA (GURN) GURNEY A L.
 PA (HILL) HILLAN K J.
 PA (MARS) MARSTERS S A.
 PA (PANT) PAN J.
 PA (PAON) PAONI N F.
 PA (STEP) STEPHAN J F.
 PA (WATA) WATANABE C K.
 PA (WILL) WILLIAMS P M.
 PA (WOOD) WOOD W I.
 XX
 PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W,
 XX
 DR WPI: 2002-171999/22.
 DR P-PSDB; ABB95602.
 XX
 PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal -
 XX
 PS Claim 1, Fig 359; 567pp; English.
 XX
 CC The present invention provides the protein and coding sequences of human
 CC PRO proteins. These are useful for treating or diagnosing a
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac
 CC hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumor
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The present sequence is a coding sequence of the invention.


```

DB 152 TATACATATTCTCTGGCTAGTGTCTCAGAGATTAATAGCCCCGAGCTAGATTCATT 211
QY 41 ASPVALVSLVSGLYGLINGLNLLETyrValTYrSerLYsLeuValThrGLuAspGLYAla 60
DB 212 AACGTTAAAAAGGCGAGCATGTATGTACTAAAGCTGTGTAAGAAAAATGGAGCT 271
QY 61 GLYGLUPHETPAlAGLYSERVALTYrGLYAspPHISGInAspGLuMetGLY11LeuAlGLY 80
DB 272 GGAGAAATTTGGGCTGCGAGTCTTTATGCTATGCGCCAGAGAGATGGAGTCTGGCT 331
QY 81 TYrPheProSerAsnLeuValLYSGluGlnArgValTYrGLuGlnAlaThrLYSGluLe 100
DB 332 TATTTCCCGAGAACTGGTCAAGGAACGCGTGTGTACAGGAAGTACCAAGGAAGTT 391
QY 101 ProThrThrAspPLeaSphephecYsGLu 110
DB 392 CCCACCAAGATATTGACTTCTTCTGCGAG 421

RESULT 12
ABK33571
ID ABK33571 standard; cDNA, 521 BP.
XX ABK33571;
XX
XX 08-MAY-2002 (first entry)
XX
XX cDNA encoding human PRO protein, Seq ID No 71.
XX
XX Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
XX breast cancer; prostate tumour; rectal tumour; liver tumour;
XX pericyte cell proliferation; chondrocyte cell proliferation;
XX tumour necrosis factor-alpha; gene; ss.
XX
XX Homo sapiens.
XX
XX WO200208288-A2.
XX
XX 31-JAN-2002.
XX
XX 29-JUN-2001; 2001WO-US21066.
XX
XX 20-JUL-2000; 2000US-219556P.
XX 25-JUL-2000; 2000US-220885P.
XX 25-JUL-2000; 2000US-220605P.
XX 25-JUL-2000; 2000US-220607P.
XX 25-JUL-2000; 2000US-220624P.
XX 25-JUL-2000; 2000US-220638P.
XX 25-JUL-2000; 2000US-220664P.
XX 25-JUL-2000; 2000US-220686P.
XX 26-JUL-2000; 2000US-220893P.
XX 28-JUL-2000; 2000WO-US20710.
XX 23-AUG-2000; 2000WO-US23522.
XX 24-AUG-2000; 2000WO-US23328.
XX 15-SEP-2000; 2000US-000000P.
XX 10-NOV-2000; 2000WO-US30873.
XX 28-NOV-2000; 2000US-253646P.
XX 01-DEC-2000; 2000WO-US32678.
XX 20-DEC-2000; 2000US-0747259.
XX 20-DEC-2000; 2000WO-US34956.
XX 28-FEB-2001; 2001WO-US06520.
XX 10-MAY-2001; 2001US-0854280.
XX 25-MAY-2001; 2001WO-US17092.
XX
XX (GENTECH) GENENTECH INC.
XX
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
XX PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WT;
XX DR MPI; 2002-172001/22.
XX P-PSDB; AAU83627.
XX
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
XX

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PT useful for treating a PRO related disorder and for diagnosing tumours
PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
PT tumour or liver tumour.
XX
XX Claim 2; Figure 71; 359pp; English.
XX
XX The invention relates to one hundred and twenty two nucleic acids
XX encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
XX encode human secreted proteins. The PRO nucleic acids, polypeptides,
XX agonists and antagonists are useful for treating a PRO related disorder.
XX The PRO polypeptides are useful for diagnosing tumours, especially lung
XX cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
XX liver tumour. The PRO polypeptides are useful for stimulating the
XX proliferation of, or gene expression, in pericyte cells, for stimulating
XX the proliferation or differentiation of chondrocyte cells, for
XX stimulating the release of tumour necrosis factor-alpha from human blood,
XX for stimulating or inhibiting the proliferation of normal human dermal
XX fibroblast cells. The PRO polypeptide may also be used as molecular
XX weight markers and for tissue typing. The PRO nucleic acids have
XX applications in molecular biology, including use as hybridisation probes,
XX and in chromosome and gene mapping. ABK33536-ABK33657 represent human
XX PRO protein coding sequences of the invention.
XX
XX Sequence 521 BP; 167 A; 86 C; 131 G; 137 T; 0 other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 1,57e-68 Length: 521
XX Score: 547.00 Matches: 99
XX Percent Similarity: 96.36% Conservative: 7
XX Best Local Similarity: 90.00% Mismatches: 4
XX Query Match: 92.55% Indels: 0
XX DB: 24 Gaps: 0
XX
XX US-10-019-455A-26 (1-110) x ABK33571 (1-521)
XX
XX QY 1 HisGLYValPheMetAspLYsLeuSerSerLYsLeuCYsAlaAspGLuGLYVal 20
XX 92 CATGGAATATTATGACCGCTTAGCTTCCAGAAAGCTCTGTGCAGATATGATGCTGTC 151
DB 152 TATACATATTCTCTGGCTAGTGTCTCAGAGATTAATAGCCCCGAGCTAGATTCATT 211
QY 21 TYrThrILESerLeuAlaArgAlaGLuAspTYrAsnAlaProAspCYsArgPheILE 40
DB 152 TATACATATTCTCTGGCTAGTGTCTCAGAGATTAATAGCCCCGAGCTAGATTCATT 211
QY 41 ASPVALVSLVSGLYGLINGLNLLETyrValTYrSerLYsLeuValThrGLuAsnGLYAla 60
DB 212 AACGTTAAAAAGGCGAGCATGTATGTACTCAAAAGCTGTGTAAGAAAAATGGAGCT 271
QY 61 GLYGLUPHETPAlAGLYSERVALTYrGLYAspPHISGInAspGLuMetGLY11LeuAlGLY 80
DB 272 GGAGAAATTTGGGCTGCGAGTCTTTATGCTATGCGCCAGAGAGATGGAGTCTGGCT 331
QY 81 TYrPheProSerAsnLeuValLYSGluGlnArgValTYrGLuGlnAlaThrLYSGluLe 100
DB 332 TATTTCCCGAGAACTGGTCAAGGAACGCGTGTGTACAGGAAGTACCAAGGAAGTT 391
QY 101 ProThrThrAspPLeaSphephecYsGLu 110
DB 392 CCCACCAAGATATTGACTTCTTCTGCGAG 421

RESULT 13
AAH98228
ID AAH98228 standard; cDNA; 891 BP.
XX AAH98228;
XX
XX 12-OCT-2001 (first entry)
XX
XX Human EST-derived coding sequence SEQ ID NO: 85.
XX
XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
XX tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
XX diagnostics; forensic test; gene mapping; genetic disorder;
XX biodiversity; gene therapy; nutrition; ss.
XX

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XX OS Homo sapiens.
XX PN WO200154477-A2.
XX PD 02-AUG-2001.
XX PF 25-JAN-2001; 2001WO-US02687.
XX PR 25-JAN-2000; 2000US-0491404.
XX PR 17-JUL-2000; 2000US-0617746.
XX PR 03-AUG-2000; 2000US-0631451.
XX PR 15-SEP-2000; 2000US-0663870.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V,
XX PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX DR WPI; 2001-476164/51.
XX DR P-PSDB; AAM23569.
XX PT Isolated polypeptide for treatment of diseases, diagnostics, raising
XX PT antibodies and research use.
XX PS Claim 1; Page 236; 1275pp; English.
XX CC The present invention provides the protein and coding sequences of novel
XX CC proteins from a variety of organisms, including human, dog, cat, horse,
XX CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
XX CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
XX CC from the organism of interest. They can be used in diagnostics,
XX CC forensics, gene mapping, identification of mutations, to assess
XX CC biodiversity and for nutritional purposes. The present sequence is a cDNA
XX CC of the invention.
XX SQ Sequence 891 BP; 272 A; 146 C; 214 G; 259 T; 0 other;

Alignment Scores:
Score: 3.28e-68 Length: 891
Percent Similarity: 547.00 Matches: 99
Best Local Similarity: 96.36% Conservative: 7
Query Match: 92.55% Mismatches: 4
DB: 22 Indels: 0 Gaps: 0

US-10-019-455A-26 (1-110) x AAH98228 (1-891)
QY 1 HisGlyValPheMetAspLysLeuSerLysLysLysCysAlaAspGluGluCysVal 20
DB 73 CATGAAATATTATGACCGCTAGCTTCCAAAGAGCTGTGTCAGATGATGAGTGTTC 132
QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysAspPheIle 40
DB 133 TATACATTTCTCTCGGCTAGCGCCCAAGAGATTATATCCCGGAGCTGATTCATT 192
QY 41 AspValLysIysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
DB 193 AACCTTAAAAAGGCGACAGATCTATGTACTCAAAAGCTGTAAAGAAATGAGAGCT 252
QY 61 G1yGluIleThrPalaGlySerValTyrGluAspHisGlnAspGluMetGlyIleValGly 80
DB 253 GAGAGAAATTTGGGCTGGCAGTGTATTATGATGGCCAGACGAGATGGAGTCTGGGT 312
QY 81 TyrPheProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIle 100
DB 313 TATTTCCCGCAGAACTTGCTCAAGAGACCGCTGTACCAAGAACTTACCAAGAGATT 372
QY 101 ProThrThrAspIleAspPhePheCysGlu 110
DB 373 CCCACACGAGATATGACTTCTTCGAG 402
RESULT 14

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AAH26342
ID AAH26342 standard; cDNA; 891 BP.
XX AC AAH26342;
XX DT 02-OCT-2001 (first entry)
XX DE Human growth regulatory-like polypeptide partial cDNA clone.
XX KW Growth regulatory-like polypeptide; human; cartilage; melanoma;
XX KW neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;
XX KW se.
XX OS Homo sapiens.
XX PN WO200155332-A2.
XX PD 02-AUG-2001.
XX PF 25-JAN-2001; 2001WO-US02455.
XX PR 25-JAN-2000; 2000US-0491404.
XX PR 02-MAY-2000; 2000US-0563786.
XX PA (HYSE-) HYSEQ INC.
XX PI Mize NK, Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C,
XX PI Drmanac RT;
XX DR WPI; 2001-48323/52.
XX CC Isolated human growth regulatory-like polypeptide useful for treating
XX CC e.g. Alzheimer's disease, cancer, autoimmune disorders,
XX CC hyperproliferative disorders, coagulation disorders, and nervous system
XX CC disorders.
XX PS Claim 1; Page 115; 119pp; English.
XX CC The present sequence is that of a novel nucleic acid that was
XX CC assembled from human thymus cDNA library-derived Hyseq clone
XX CC identification number 16372272 (see AAH26341). A recursive
XX CC algorithm was used to extend the clone by pulling additional
XX CC sequences from different databases. A full-length sequence (see
XX CC AAH26343) encoding novel human growth regulatory-like polypeptide
XX CC (GRLP, see AAH82671) was subsequently obtained. Human GRLP
XX CC belongs to the same protein family as growth regulatory proteins,
XX CC growth factors, human melanoma derived growth regulatory protein,
XX CC precursor (64% similarity and 45% identity over 111 amino acids)
XX CC or melanoma inhibitory activity, cattle cartilage-derived
XX CC retinoic acid sensitive protein (CD-RAP, 44% identity and 64%
XX CC similarity over 126 amino acids) and other retinoic acid-sensitive
XX CC proteins. GRLP polypeptides and polynucleotides of the invention
XX CC can be used in the prophylaxis, treatment (including gene therapy)
XX CC and diagnosis of disorders and diseases caused by, or involving,
XX CC cartilage development and maintenance, inhibition of melanoma cell
XX CC growth and tumours, including neuroectodermal tumours such as
XX CC gliomas. The polynucleotides can also be used to design probes
XX CC and primers, for chromosome and gene mapping, in the recombinant
XX CC production of protein, in the generation of antisense, ribozyme and
XX CC peptide-nucleic acid molecules, and to produce transgenic animals.
XX SQ Sequence 891 BP; 272 A; 146 C; 214 G; 259 T; 0 other;

Alignment Scores:
Score: 3.28e-68 Length: 891
Percent Similarity: 547.00 Matches: 99
Best Local Similarity: 96.36% Conservative: 7
Query Match: 92.55% Mismatches: 4
DB: 22 Indels: 0 Gaps: 0

US-10-019-455A-26 (1-110) x AAH26342 (1-891)

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```

QY      1 HisGlyValPheMetAspLysLeuSerLysLysLeuCysAlaAspGluCysVal 20
DB      73 CATGAAATATTATGACCGCTTACGCTTCCAGAAAGCTTGTGAGATGATGATGTC 132
QY      21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
DB      133 TATACATATTTCTTGGCTAGTCTCCAAAGATATATATGCCCCGAGCTGAGATTCAAT 192
QY      41 AspValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
DB      193 AACGTTAAAAAGGCGACGACGATCTATGCTCAAGCTGTAAAGAAATGAGAGCT 252
QY      61 GlyGluPheTpaIaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
DB      253 CGAGAAATTTGGCGTGGCAGTGTATTATGTTATGTCGCGCAGAGAGTGGAGTGGGT 312
QY      81 TyrPheProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIle 100
DB      313 TATTTCCCGACGAACTTGTGTCAGAGACACGCTGTCTACAGAAAGCTACCAAGAAAGTT 372
QY      101 ProThrThrAspIleAspPhePheCysGlu 110
DB      373 CCCACACGAGATATGACTTCTTCTGCGAG 402

RESULT 15
AAF59083
ID      AAF59083 standard; DNA; 923 BP.
AC      AAF59083;
XX
XX      23-APR-2001 (first entry)
XX
XX      Human MLP nucleotide sequence SEQ ID NO:29.
XX
XX      MLP; MTA; melanoma inhibitory activity; cancer; bone disease;
XX      joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
XX      cardiant; gene therapy; secretory cell function regulator; promoter;
XX      inhibitor; ds.
XX
XX      Homo sapiens.
XX
XX      WO200102564-A1.
XX
XX      11-JAN-2001.
XX
XX      29-JUN-2000; 200QWO-JP04278.
XX
XX      30-JUN-1999; 99JP-0186718.
XX
XX      (TAKE ) TAKEDA CHEM IND LTD.
XX
XX      Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
XX      Tanaka H;
XX
XX      WPI; 2001-159271/16.
XX
XX      Safe, low-toxicity secretory cell function-regulatory protein and
XX      encoded DNA, applicable as drugs, in diagnosis and development of
XX      promoters and inhibitors for preventing or treating e.g. bone and joint
XX      diseases -
XX
XX      Example 1; Page 99-100; 11pp; Japanese.
XX
XX      The present invention describes novel MLP proteins and their encoding
XX      DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
XX      activities, and can be used in gene therapy and as secretory cell
XX      function regulators. The MLP proteins and DNAs can be used in drugs, in
XX      the diagnosis and development of promoters and inhibitors for preventing
XX      or treating bone and joint diseases as well as pathologic angiogenesis.
XX      AAF59063 to AAF59089 and AAF59122 to AAF59132 represent sequences used
XX      in the exemplification of the present invention.
XX
XX      Sequence 923 BP; 303 A; 147 C; 213 G; 260 T; 0 other;

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Alignment Scores:
Pred. No.: 3,45e-68
Score: 547.00
Percent Similarity: 96.36%
Best Local Similarity: 90.00%
Query Match: 92.55%
DB: 22
Gaps: 0

US-10-019-455a-26 (1-110) x AAF59083 (1-923)
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DB      88 CATGAAATATTATGACCGCTTACGCTTCCAGAAAGCTTGTGAGATGATGATGTC 147
QY      21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
DB      148 TATACATATTTCTTGGCTAGTCTCCAAAGATATATATGCCCCGAGCTGAGATTCAAT 207
QY      41 AspValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
DB      208 AACGTTAAAAAGGCGACGACGATCTATGCTCAAGCTGTAAAGAAATGAGAGCT 267
QY      61 GlyGluPheTpaIaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
DB      268 CGAGAAATTTGGCGTGGCAGTGTATTATGTTATGTCGCGCAGAGAGTGGAGTGGGT 327
QY      81 TyrPheProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIle 100
DB      328 TATTTCCCGACGAACTTGTGTCAGAGACACGCTGTCTACAGAAAGCTACCAAGAAAGTT 387
QY      101 ProThrThrAspIleAspPhePheCysGlu 110
DB      388 CCCACACGAGATATGACTTCTTCTGCGAG 417

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Search completed: December 29, 2003, 16:41:11
 Job time : 133.647 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 29, 2003, 19:57:30 ; Search time 246.807 Seconds
(without alignments)
1527.048 Million cell updates/sec

Title: US-10-019-455a-26
Perfect score: 591
Sequence: 1 HGVEMDKUSKKLCADECEV.....RYGEATKEIPTTDIDFCE 110

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2244575 seqs, 1713117285 residues
Total number of hits satisfying chosen parameters: 4489150

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_6/USPTO.spool/US10019455/runat.29122003.160349.366/app.query.fasta.1.1770
-DB=Published Applications NA -QMT=fastcap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=bl0sum62
-TRANS=human0.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR M=N=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0
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-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Published Applications NA.*
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12: /cgn2_6/ptodata/2/pubpna/US09E_PUBCOMB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US09F_PUBCOMB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
17: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
18: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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|------------|-------|-------------|--------|-------|-------------|

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| 2 | 547 | 92.6 | 521 | 13 | US-10-216-163-71 |
| 3 | 547 | 92.6 | 521 | 13 | US-10-218-765-71 |
| 4 | 547 | 92.6 | 521 | 13 | US-10-219-063-71 |
| 5 | 547 | 92.6 | 521 | 13 | US-10-219-066-71 |
| 6 | 547 | 92.6 | 521 | 13 | US-10-219-067-71 |
| 7 | 547 | 92.6 | 521 | 13 | US-10-219-068-71 |
| 8 | 547 | 92.6 | 521 | 13 | US-10-219-069-71 |
| 9 | 547 | 92.6 | 521 | 13 | US-10-219-073-71 |
| 10 | 547 | 92.6 | 521 | 13 | US-10-219-475-71 |
| 11 | 547 | 92.6 | 521 | 13 | US-10-219-480-71 |
| 12 | 547 | 92.6 | 521 | 13 | US-10-219-483-71 |
| 13 | 547 | 92.6 | 521 | 13 | US-10-219-525-71 |
| 14 | 547 | 92.6 | 521 | 13 | US-10-219-526-71 |
| 15 | 547 | 92.6 | 521 | 13 | US-10-219-530-71 |
| 16 | 547 | 92.6 | 521 | 13 | US-10-219-531-71 |
| 17 | 547 | 92.6 | 521 | 13 | US-10-219-532-71 |
| 18 | 547 | 92.6 | 521 | 13 | US-10-219-533-71 |
| 19 | 547 | 92.6 | 521 | 13 | US-10-223-081-359 |
| 20 | 547 | 92.6 | 521 | 13 | US-10-230-437-71 |
| 21 | 547 | 92.6 | 521 | 13 | US-10-232-228-71 |
| 22 | 547 | 92.6 | 521 | 13 | US-10-223-082-359 |
| 23 | 547 | 92.6 | 521 | 15 | US-10-227-084-71 |
| 24 | 547 | 92.6 | 521 | 15 | US-10-230-163-71 |
| 25 | 547 | 92.6 | 521 | 15 | US-10-230-338-71 |
| 26 | 547 | 92.6 | 521 | 15 | US-10-218-631-71 |
| 27 | 547 | 92.6 | 521 | 15 | US-10-227-873-71 |
| 28 | 547 | 92.6 | 521 | 15 | US-10-219-076-71 |
| 29 | 547 | 92.6 | 521 | 15 | US-10-216-159A-71 |
| 30 | 547 | 92.6 | 521 | 15 | US-10-218-849-71 |
| 31 | 547 | 92.6 | 521 | 15 | US-10-227-873-71 |
| 32 | 547 | 92.6 | 521 | 15 | US-10-227-883-71 |
| 33 | 547 | 92.6 | 521 | 15 | US-10-219-076-71 |
| 34 | 547 | 92.6 | 521 | 15 | US-10-230-434-71 |
| 35 | 547 | 92.6 | 521 | 15 | US-10-219-003-71 |
| 36 | 547 | 92.6 | 521 | 15 | US-10-219-075-71 |
| 37 | 547 | 92.6 | 521 | 15 | US-10-219-464-71 |
| 38 | 547 | 92.6 | 521 | 15 | US-10-219-466-71 |
| 39 | 547 | 92.6 | 521 | 15 | US-10-219-467-71 |
| 40 | 547 | 92.6 | 521 | 15 | US-10-219-481-71 |
| 41 | 547 | 92.6 | 521 | 15 | US-10-230-260-71 |
| 42 | 547 | 92.6 | 521 | 15 | US-10-232-231-71 |
| 43 | 547 | 92.6 | 521 | 15 | US-10-232-233-71 |
| 44 | 547 | 92.6 | 521 | 15 | US-10-216-165-71 |
| 45 | 547 | 92.6 | 521 | 15 | US-10-218-956-71 |

ALIGNMENTS

RESULT 1
US-10-216-038-1
Sequence 1, Application US/10216038
Publication No. US20030124573A1
GENERAL INFORMATION:
APPLICANT: Mize, Nancy K
APPLICANT: Boyle, Bryan J
APPLICANT: Ford, John E
APPLICANT: Arterburn, Matthew C
APPLICANT: Tang, Y Tom
APPLICANT: Liu, Chenghua
APPLICANT: Dmanac, Radje T
APPLICANT: Sjaastad, Michael
TITLE OF INVENTION: Methods and Materials Relating to No. US20030124573A1 Growth F
FILE REFERENCE: HVS-7CIP
CURRENT APPLICATION NUMBER: US/10/216,038
PRIOR FILING DATE: 2002-08-08
PRIOR APPLICATION NUMBER: US 09/563,786
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR FILING DATE: 2000-01-25
NUMBER OF SEQ ID NOS: 8

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; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 426
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (426)..(426)
; OTHER INFORMATION: n = A, T, G, or C
US-10-216-038-1

Alignment Scores:
Pred. No.: 1,11e-76 Length: 426
Score: 547.00 Matches: 99
Percent Similarity: 96.36% Conservative: 7
Best Local Similarity: 90.00% Mismatches: 4
Query Match: 92.55% Indels: 0
DB: Gaps: 0

US-10-019-455a-26 (1-110) x US-10-216-038-1 (1-426)

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QY 21 TyrThrIleSerLeuAlaArgAlaGluAspTyrAsnAlaProAspCysArgPheIle 40
Db 133 TATACATTTCTCTGCTAGCTGCTCAGAGATTATTAAGCCCGAGATGATTCATT 192
QY 41 AspValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
Db 193 AACGTTAAATAAGGCGACGATCTATGCTACTCAAGCTGTATAAGATAATGAGCT 252
QY 61 GlyGluPheTyrPalaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
Db 253 GGAGAAATTTGGCTGGCTGCTGTTTATGCTGATGCGACGAGAGATGGAGATCGTGGCT 312
QY 81 TyrPheProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIle 100
Db 313 TATTTCCCGAGAACTGTGTCAAGAACAGCTGTGTACAGAGAGATCAAGAGAGATT 372
QY 101 ProThrThrAspIleAspPhePheCysGlu 110
Db 373 CCCACACGAGATTTGACTTCTTCTGCGAG 402

RESULT 2
US-10-216-163-71
; Sequence 71, Application US/10216163
; Publication No. US20030149239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P13
; CURRENT APPLICATION NUMBER: US/10/216,163
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
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; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-216-163-71

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Pred. No.: 1,48e-76 Length: 521
Score: 547.00 Matches: 99
Percent Similarity: 96.36% Conservative: 7
Best Local Similarity: 90.00% Mismatches: 4
Query Match: 92.55% Indels: 0
DB: Gaps: 0

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QY 101 ProThrThrAspIleAspPhePheCysGlu 110
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RESULT 3
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; Sequence 71, Application US/10218765
; Publication No. US20030187201A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P13
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FILE REFERENCE: P3530P1C19
CURRENT APPLICATION NUMBER: US/10/218,765
CURRENT FILING DATE: 2002-08-12
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PRIOR FILING DATE: 2002-04-09
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PRIOR APPLICATION NUMBER: 60/111270
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PRIOR APPLICATION NUMBER: 60/111291
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PRIOR APPLICATION NUMBER: 60/111445
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PRIOR APPLICATION NUMBER: 60/169445
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169495
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169835

Alignment Scores:

Pred. No.: 1,48e-76 Length: 521
Score: 547.00 Matches: 99
Percent Similarity: 96.36% Conservative: 7
Best Local Similarity: 90.00% Mismatches: 4
Query Match: 92.55% Indels: 0
DB: 13 Gaps: 0

US-10-019-455a-26 (1-110) x US-10-219-063-71 (1-521)

1 HisGlyValPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysVal 20
92 CATGAAATATTATTTGACCGCTCTAGCTTCCAGAAAGCTCTGTGCAAGATATGATGCTGTC 151
21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
152 TATACTATTCTCTGCTAGTGTCTCAAGAAAGATTATAAGCCCGGACCTGATTCATT 211
41 AspValLysLysGlnGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
212 AAGCTTAAAAAGGCGAGAGATCTATGTGTACTCAAAAGCTGTAAAGAAAAATGGAGCT 271
61 GAGGAAATTTGGAGCTGAGAGCTTTTGTGATGGCCAGAGAGAGATGGAGCTCGTGGT 331
272 GAGGAAATTTGGAGCTGAGAGCTTTTGTGATGGCCAGAGAGAGATGGAGCTCGTGGT 331
81 TyrPheProSerAsnLeuValLysGlnGlnArgValTyrGlnGluAlaThrLysGluIle 100
332 TATTTCCCAAGAACTTGTCAAGGAAAGCGCTGTGTACCAAGAAAGCTACCAAGAAAGT 391
101 ProThrThrAspIleAspPheCysGlu 110
392 CCCACCAAGATATGACTTCTTCTGCGAG 421

RESULT 4
US-10-219-063-71
Sequence 71, Application US/10219063
Publication No. US20030187202A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530P1C24

CURRENT APPLICATION NUMBER: US/10/219,063

CURRENT FILING DATE: 2002-08-13

PRIOR APPLICATION NUMBER: 10/119,480

PRIOR FILING DATE: 2002-04-09

PRIOR APPLICATION NUMBER: 60/059113

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/062287

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/063549

PRIOR FILING DATE: 1997-10-28

PRIOR APPLICATION NUMBER: 60/064103

PRIOR FILING DATE: 1997-10-31

PRIOR APPLICATION NUMBER: 60/069873

PRIOR FILING DATE: 1997-12-17

PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/079294

PRIOR FILING DATE: 1998-03-25

PRIOR APPLICATION NUMBER: 60/079656

PRIOR FILING DATE: 1998-03-26

PRIOR APPLICATION NUMBER: 60/079728

PRIOR FILING DATE: 1998-03-27

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 246

SEQ ID NO 71

LENGTH: 521

TYPE: DNA

ORGANISM: Homo Sapien

US-10-219-063-71

US-10-019-455a-26 (1-110) x US-10-219-063-71 (1-521)

Alignment Scores:

Pred. No.: 1,48e-76 Length: 521
Score: 547.00 Matches: 99
Percent Similarity: 96.36% Conservative: 7
Best Local Similarity: 90.00% Mismatches: 4
Query Match: 92.55% Indels: 0
DB: 13 Gaps: 0

1 HisGlyValPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysVal 20
92 CATGAAATATTATTTGACCGCTCTAGCTTCCAGAAAGCTCTGTGCAAGATATGATGCTGTC 151
21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
152 TATACTATTCTCTGCTAGTGTCTCAAGAAAGATTATAAGCCCGGACCTGATTCATT 211
41 AspValLysLysGlnGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
212 AAGCTTAAAAAGGCGAGAGATCTATGTGTACTCAAAAGCTGTAAAGAAAAATGGAGCT 271
61 GAGGAAATTTGGAGCTGAGAGCTTTTGTGATGGCCAGAGAGAGATGGAGCTCGTGGT 331


```
Db 272 GGAGATTGGCTGGCAGTGTATGATGGCCAGACGAGATGGAGTGGGT 331
Qy 81 TyrPheProSerAsnLeuValIysGluGlnArgValIYrGlnGluAlaThrIysGluIle 100
Db 332 TATTCCCGAGCACTGTGTCAAGAACGCGTGTGTACCAAGAGTACCAAGAGAGT 391
Qy 101 ProThrThrAspIleAspPhePheCysGlu 110
Db 392 CCCACCACGAGATATTGACTTCTTCTGGAG 421

RESULT 5
US-10-219-066-71
; Sequence 71, Application US/10219066
; Publication No. US20030187203A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerltsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gueney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC27
; CURRENT APPLICATION NUMBER: US/10/219,066
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-066-71

Alignment Scores:
Pred. No.: 1,48e-76 Length: 521
Score: 547.00 Matches: 99
Percent Similarity: 96.36% Conservative: 7
Best Local Similarity: 92.00% Mismatches: 4
Query Match: 92.55% Indels: 0
DB: 13 Gaps: 0

US-10-019-455a-26 (1-110) x US-10-219-066-71 (1-521)

Qy 1 HisGlyValAlaPheMetAspIysLeuSerIysIysLeuCysAlaAspGluGluCysVal 20
Db 92 CATGGAATATTATGACCGCTGTAGCTTCCAAAGAGCTGTGTGAGATGATGATGTGTGTC 151
```

```
Qy 21 TyrThrIleSerLeuAlaArgAlaGlnIleAspDyrAsnAlaProAspCysArgPheIle 40
Db 152 TATACATATTTCTCTGGCTAGTGTCTCAAGAGATTATAAGCCCGGAGCTGTAAATTCATT 211
Qy 41 AspValIysIysGlnGlnIleIleValIYrSerIysLeuValThrIuAsnGlyAla 60
Db 212 AACGTTAAAAAAGGCGCAGCATCTATGTCTACTCAAGCTGTAAAGAAATGAGACT 271
Qy 61 GlyIuPheThrAlaIysSerValIYrGlyAspHisGlnAspGluMetGlyIleValGly 80
Db 272 GGAGATTGGCTGGCAGTGTATGATGGCCAGACGAGATGGAGATGGAGTGGTGGGT 331
Qy 81 TyrPheProSerAsnLeuValIysGluGlnArgValIYrGlnGluAlaThrIysGluIle 100
Db 332 TATTCCCGAGCACTGTGTCAAGAACGCGTGTGTACCAAGAGTACCAAGAGAGT 391
Qy 101 ProThrThrAspIleAspPhePheCysGlu 110
Db 392 CCCACCACGAGATATTGACTTCTTCTGGAG 421

RESULT 6
US-10-219-067-71
; Sequence 71, Application US/10219067
; Publication No. US20030187204A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerltsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gueney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC51
; CURRENT APPLICATION NUMBER: US/10/219,067
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-067-71

Alignment Scores:
Pred. No.: 1,48e-76 Length: 521
Score: 547.00 Matches: 99
Percent Similarity: 96.36% Conservative: 7
```

Best Local Similarity: 90.00% Mismatches: 4
 Query Match: 92.55% Indels: 0
 DB: 13 Gaps: 0

US-10-019-455a-26 (1-110) x US-10-219-067-71 (1-521)

```

QY 1 HisGlyValPheMetAspLysLeuSerLysLysLeuCysAlaAspGluGluCysVal 20
DB 92 CATGGAATTTATGACCGCTAGCTTCCAGAAAGCTCTGCGAGATGATGATGCTGTC 151
QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
DB 152 TATACTATTTCTCTGCTAGCTCAAGAAAGATTAAAGCCCGAGCTGATGATTCATT 211
QY 41 AspValLysLysGluGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGluAla 60
DB 212 AACGTTAAAAAGGCGACGACATCTATGTCTCAAAAGCTGTAAAGAAATGGAGCT 271
QY 61 GlyGluPheTyrPalaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
DB 272 GGAAGATTTTGGGCTGCGAGCTTTATGTTATGGCCAGAGACGAGTGGAGTCTGGGT 331
QY 81 TyrPheProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIle 100
DB 332 TATTTCCCGAGAACTTGTCTCAAGAACGCGTGTATCCAGAAAGCTACCAAGAGATT 391
QY 101 ProThrThrAspIleAspPhePheCysGlu 110
DB 392 CCCACCACGGAATTGACTTTCTTCTGCGAG 421

```

RESULT 7
 US-10-219-068-71

```

; Sequence 71, Application US/10219068
; Publication No. US20030187205A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Matanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC31
; CURRENT APPLICATION NUMBER: US/10/219,068
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246

```

SEQ ID NO 71
 LENGTH: 521
 TYPE: DNA
 ORGANISM: Homo Sapien
 US-10-219-068-71

Alignment Scores:

Pred. No.: 1,48e-76 Length: 521
 Score: 547.00 Matches: 99
 Percent Similarity: 96.36% Conservative: 7
 Best Local Similarity: 90.00% Mismatches: 4
 Query Match: 92.55% Indels: 0
 DB: 13 Gaps: 0

US-10-019-455a-26 (1-110) x US-10-219-068-71 (1-521)

```

QY 1 HisGlyValPheMetAspLysLeuSerLysLysLeuCysAlaAspGluGluCysVal 20
DB 92 CATGGAATTTATGACCGCTAGCTTCCAGAAAGCTCTGCGAGATGATGATGCTGTC 151
QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
DB 152 TATACTATTTCTCTGCTAGCTCAAGAAAGATTAAAGCCCGAGCTGATGATTCATT 211
QY 41 AspValLysLysGluGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGluAla 60
DB 212 AACGTTAAAAAGGCGACGACATCTATGTCTCAAAAGCTGTAAAGAAATGGAGCT 271
QY 61 GlyGluPheTyrPalaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
DB 272 GGAAGATTTTGGGCTGCGAGCTTTATGTTATGGCCAGAGACGAGTGGAGTCTGGGT 331
QY 81 TyrPheProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIle 100
DB 332 TATTTCCCGAGAACTTGTCTCAAGAACGCGTGTATCCAGAAAGCTACCAAGAGATT 391
QY 101 ProThrThrAspIleAspPhePheCysGlu 110
DB 392 CCCACCACGGAATTGACTTTCTTCTGCGAG 421

```

RESULT 8
 US-10-219-069-71

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; Sequence 71, Application US/10219069
; Publication No. US20030187206A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Matanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC40
; CURRENT APPLICATION NUMBER: US/10/219,069
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17

```

```

; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-069-71

Alignment Scores:
Pred. No.: 1,48e-76 Length: 521
Score: 547.00 Matches: 99
Percent Similarity: 96.36% Conservative: 7
Best Local Similarity: 90.00% Mismatches: 4
Query Match: 92.55% Indels: 0
DB: 13 Gaps: 0

US-10-019-455a-26 (1-110) x US-10-219-069-71 (1-521)

QY 1 HisGlyValPheMetAspLysLeuSerSerLysLysLeuCYeAlaAspGluGluCysVal 20
DB 92 CATGGAATATTATTTAGACCGCTAGCTTCCAGAAAGCTCTGTGCGAGATGAGTGTCTC 151
QY 21 TyrThrLysSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
DB 152 TATACTATTCTCTGCTAGTCTCAAGAGATTATTAATGCCCGGACTGTAGATTCATT 211
QY 41 AspValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
DB 212 AACGTTAAAAAGGCGACAGATCTATGTCTCAAGAGCTGTAAAGAAATGAGACT 271
QY 61 GlyGluPheTyrAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
DB 272 GGAGAAATTTGGCGTGGCGAGTGTATGTGTATGCGCAGACGAGATGGAGTGGTGGT 331
QY 81 TyrPheProSerAsnLeuValLysGlnArgValTyrGlnGluAlaThrLysGluIle 100
DB 332 TATTTCCTCCAGCACTGTGTCAGACAGCGGTGTGTCAGAGAGCTTACCAAGAGAGTT 391
QY 101 ProThrThrAspLysAspPhePheCysGlu 110
DB 392 CCCACCACGGAATTGACTTCTTCTGCGAG 421

RESULT 9
US-10-219-073-71
; Sequence 71, Application US/10219073
; Publication No. US20030187207A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gueney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Metanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C52
; CURRENT APPLICATION NUMBER: US/10/219,073
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
```

```

; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-073-71

Alignment Scores:
Pred. No.: 1,48e-76 Length: 521
Score: 547.00 Matches: 99
Percent Similarity: 96.36% Conservative: 7
Best Local Similarity: 90.00% Mismatches: 4
Query Match: 92.55% Indels: 0
DB: 13 Gaps: 0

US-10-019-455a-26 (1-110) x US-10-219-073-71 (1-521)

QY 1 HisGlyValPheMetAspLysLeuSerSerLysLysLeuCYeAlaAspGluGluCysVal 20
DB 92 CATGGAATATTATTTAGACCGCTAGCTTCCAGAAAGCTCTGTGCGAGATGAGTGTCTC 151
QY 21 TyrThrLysSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
DB 152 TATACTATTCTCTGCTAGTCTCAAGAGATTATTAATGCCCGGACTGTAGATTCATT 211
QY 41 AspValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
DB 212 AACGTTAAAAAGGCGACAGATCTATGTCTCAAGAGCTGTAAAGAAATGAGACT 271
QY 61 GlyGluPheTyrAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
DB 272 GGAGAAATTTGGCGTGGCGAGTGTATGTGTATGCGCAGACGAGATGGAGTGGTGGT 331
QY 81 TyrPheProSerAsnLeuValLysGlnArgValTyrGlnGluAlaThrLysGluIle 100
DB 332 TATTTCCTCCAGCACTGTGTCAGACAGCGGTGTGTCAGAGAGCTTACCAAGAGAGTT 391
QY 101 ProThrThrAspLysAspPhePheCysGlu 110
DB 392 CCCACCACGGAATTGACTTCTTCTGCGAG 421

RESULT 10
US-10-219-475-71
; Sequence 71, Application US/10219475
; Publication No. US20030187208A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gueney, Austin L.
; APPLICANT: Smith, Victoria
```

```

; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Matanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C38
; CURRENT APPLICATION NUMBER: US/10/219,475
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
;
US-10-019-475-71
;
Alignment Scores:
Pred. No.: 1,48e-76 Length: 521
Score: 547.00 Matches: 99
Percent Similarity: 96.36% Conservative: 7
Best Local Similarity: 90.00% Mismatches: 4
Query Match: 92.55% Indels: 0
DB: 13 Gaps: 0

US-10-019-455a-26 (1-110) x US-10-219-475-71 (1-521)
QY 1 HisGlyValPheMetAspLysSerLysLeuCysAlaAspGluGluCysVal 20
DB 92 CATGGAATATTATGACCGCTAGCTTCCAGAAAGCTCTGTGACATGATGATGCTGTC 151
QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
DB 152 TATACATATTCTCTGGCTAGTCTCAAGAAAGATTATATGCCCCGCACTGTAGATTCAATT 211
QY 41 AspValLysrGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluGlnGlyAla 60
DB 212 AACGTTAAAGGAGGCGACGATCTATGTGACTCAAGCTGGTAAAGAAATGGAGCT 271
QY 61 GlyGluPheTyrAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
DB 272 GGAAGATTTTGGCTGGCAGTGTATTATGTGATGCGCAGAGCAAGATGGAGAGTCTGGGT 331
QY 81 TyrPheProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIle 100
DB 332 TATTTCGCCAGCACTGTGTCAAGAAACAGCGTGTATCCAGAGCTACCAAGAGATT 391
QY 101 ProThrThrAspIleAspPheCysGlu 110
DB 392 CCCACCAAGCAATATGACTTCTTCTGCGAG 421
RESULT 11
US-10-219-480-71
; Sequence 71, Application US/10219480
```

```

; Publication No. US20030187209A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Deanyers, Luc
; APPLICANT: Geritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Matanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C38
; CURRENT APPLICATION NUMBER: US/10/219,480
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
;
US-10-019-480-71
;
Alignment Scores:
Pred. No.: 1,48e-76 Length: 521
Score: 547.00 Matches: 99
Percent Similarity: 96.36% Conservative: 7
Best Local Similarity: 90.00% Mismatches: 4
Query Match: 92.55% Indels: 0
DB: 13 Gaps: 0

US-10-019-455a-26 (1-110) x US-10-219-480-71 (1-521)
QY 1 HisGlyValPheMetAspLysSerLysLeuCysAlaAspGluGluCysVal 20
DB 92 CATGGAATATTATGACCGCTAGCTTCCAGAAAGCTCTGTGACATGATGATGCTGTC 151
QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
DB 152 TATACATATTCTCTGGCTAGTCTCAAGAAAGATTATATGCCCCGCACTGTAGATTCAATT 211
QY 41 AspValLysrGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluGlnGlyAla 60
DB 212 AACGTTAAAGGAGGCGACGATCTATGTGACTCAAGCTGGTAAAGAAATGGAGCT 271
QY 61 GlyGluPheTyrAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
DB 272 GGAAGATTTTGGCTGGCAGTGTATTATGTGATGCGCAGAGCAAGATGGAGAGTCTGGGT 331
QY 81 TyrPheProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIle 100
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DB 332 TATTCCCGAGAACTGTGTCAAGACGCGTGTACCGAAGCTTACCAAGAAATT 391
QY 101 ProThrThraspPheCysGlu 110
DB 392 CCCACCGAGATTTGACTTTCTTCTGCGAG 421

RESULT 12
US-10-219-483-71
; Sequence 71, Application US/10219483
; Publication No. US20030187210A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C43
; CURRENT APPLICATION NUMBER: US/10/219,483
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-483-71

Alignment Scores:
Pred. No.: 1,48e-76 Length: 521
Score: 547.00 Matches: 99
Percent Similarity: 96.36% Conservative: 7
Best Local Similarity: 90.00% Mismatches: 4
Query Match: 92.55% Indels: 0
DB: 13 Gaps: 0

US-10-019-455a-26 (1-110) x US-10-219-483-71 (1-521)

QY 1 HisGlyValPheMetAspLysLeuSerLysLysCysAlaAspGluGluCysVal 20
DB 92 CATGGAATATTATGAGCCGCTAGCTTCCAGAGAGCTGTGAGTAGATGAGTGTGTC 151

QY 21 TyrThrIleSerLeuValAaGAlaGlnGluAspTyrAsnAlaProAspCysAspPheIle 40
DB 152 TATACATTTTCTCTGCTAGTGCCTCAGAGATTATATATCCCGAGCTGTAAATTCATT 211

QY 41 AspValLysLysGlnGlnIleTyrValTyrSerLysLeuValThrGluSngIyAla 60
DB 212 AACGTTAAAAAAGGACGAGATCTATGTACTCAAGCTGTAAAGAAAAATGGAGCT 271

QY 61 GlyGluPheTyrAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
DB 272 GGAGAAATTTGGCGCTGCGAGCTTTATGTGATGCGCAGACGAGATGGAGTCGTGCGGT 331

QY 81 TyrPheProSerAsnLeuValLysGlnGluIleArgValTyrGlnGluAlaThrLysGluIle 100
DB 332 TATTCCCGAGAACTGTGTCAAGACGCGTGTGTACCGAAGCTTACCAAGAAATT 391

QY 101 ProThrThraspPheCysGlu 110
DB 392 CCCACCGAGATTTGACTTTCTTCTGCGAG 421

RESULT 13
US-10-219-525-71
; Sequence 71, Application US/10219525
; Publication No. US20030187211A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C29
; CURRENT APPLICATION NUMBER: US/10/219,525
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-525-71

Alignment Scores:
Pred. No.: 1,48e-76 Length: 521
Score: 547.00 Matches: 99
Percent Similarity: 96.36% Conservative: 7
Best Local Similarity: 90.00% Mismatches: 4
Query Match: 92.55% Indels: 0
DB: 13 Gaps: 0

US-10-019-455A-26 (1-110) x US-10-219-525-71 (1-521)

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QY 1 HisGlyValPheMetAspIleuSerSerIysLeuCyAlaAspGluGluCysVal 20
Db 92 CATGGAATTTTATGACCGCTCTACGCTCCAGAAAGCTCTGGCAGATGATGATGCTC 151
QY 21 TTTTThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
Db 152 TATACATTTCTCTGGCTAGTGTCTCAAGAAATATTAATGCCCCGAGCTGTAGATTCAATT 211
QY 41 AspValIysIleGlyGlnGlnIleTyrValTyrSerIysLeuValThrGluAsnGlyAla 60
Db 212 AACGTTAAAAAGGCGACAGATCTATGTACTCAAAAGCTGTGTAAGAAATGAGACT 271
QY 61 GlyIuPheThrPAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
Db 272 GGAGAAATTTTGGCTGGCTGCTTTATGTGATGGCCAGAGAGATGGAGTCTGGCT 331
QY 81 TyrPheProSerAsnLeuValIysGlnGluArgValTyrGlnGluAlaThrIysGluIle 100
Db 332 TATTTCCCGACGAACTGTGTCAAGAAACGCTGTGTACAGGAAGCTACCAAGAAATT 391
QY 101 ProThrThrAspIleAspPheCysGlu 110
Db 392 CCCACCACGATATGTGACTTTCTTCTGCGAG 421

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RESULT 14

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US-10-219-526-71
Sequence 71, Application US/10219526
Publication No. US20030187212A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C41
CURRENT APPLICATION NUMBER: US/10/219,526
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 71
LENGTH: 521
TYPE: DNA

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ORGANISM: Homo Sapien

US-10-219-526-71

Alignment Scores:

| Pred. No.: | 1,488-76 | Length: | 521 |
|------------------------|----------|---------------|-----|
| Score: | 547.00 | Matches: | 99 |
| Percent Similarity: | 96.36% | Conservative: | 7 |
| Best Local Similarity: | 90.00% | Mismatches: | 4 |
| Query Match: | 92.55% | Indels: | 0 |
| DB: | 13 | Gaps: | 0 |

US-10-019-455A-26 (1-110) x US-10-219-526-71 (1-521)

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QY 1 HisGlyValPheMetAspIleuSerSerIysLeuCyAlaAspGluGluCysVal 20
Db 92 CATGGAATTTTATGACCGCTCTACGCTCCAGAAAGCTCTGGCAGATGATGATGCTGTC 151
QY 21 TTTTThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
Db 152 TATACATTTCTCTGGCTAGTGTCTCAAGAAAGATTATTAATGCCCGAGCTGTAGATTCAATT 211
QY 41 AspValIysIleGlyGlnGlnIleTyrValTyrSerIysLeuValThrGluAsnGlyAla 60
Db 212 AACGTTAAAAAGGCGACAGATCTATGTACTCAAAAGCTGTGTAAGAAATGAGACT 271
QY 61 GlyIuPheThrPAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
Db 272 GGAGAAATTTTGGCTGGCTGCTTTATGTGATGGCCAGAGAGATGGAGTCTGGCT 331
QY 81 TyrPheProSerAsnLeuValIysGlnGluArgValTyrGlnGluAlaThrIysGluIle 100
Db 332 TATTTCCCGACGAACTGTGTCAAGAAACGCTGTGTACAGGAAGCTACCAAGAAATT 391
QY 101 ProThrThrAspIleAspPheCysGlu 110
Db 392 CCCACCACGATATGTGACTTTCTTCTGCGAG 421

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RESULT 15

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US-10-219-530-71
Sequence 71, Application US/10219530
Publication No. US20030187213A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C54
CURRENT APPLICATION NUMBER: US/10/219,530
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294

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;; PRIOR FILING DATE: 1998-03-25
;; PRIOR APPLICATION NUMBER: 60/079656
;; PRIOR FILING DATE: 1998-03-26
;; PRIOR APPLICATION NUMBER: 60/079728
;; PRIOR FILING DATE: 1998-03-27
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 246
;; SEQ ID NO 71
;; LENGTH: 521
;; TYPE: DNA
;; ORGANISM: Homo Sapien
US-10-219-530-71

Alignment Scores:
Pred. No.: 1,48e-76 Length: 521
Score: 547.00 Matches: 99
Percent Similarity: 96.36% Conservative: 7
Best Local Similarity: 90.00% Mismatches: 4
Query Match: 92.55% Indels: 0
DB: 13 Gaps: 0

US-10-019-455A-26 (1-110) x US-10-219-530-71 (1-521)

QY 1 HisGlyValPheMetAspLysLeuSerSerLysLeuCyAlaAspGluGlyVal 20
DB 92 CATGGAAATATTATGACCGCTAGCTTCCAGAAAGCTCTGTGCAGATGATGAGTGTCTC 151
QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
DB 152 TATTAATAATTTCTGCTGCTAGTCTCAAGAAAGTTATTAATGCCCGACTGTAGATTCTT 211
QY 41 AspValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
DB 212 AACGTTAAAGAGGCGACAGATCTATGTACTCAAAAGCTGTAAAGAAATGAGACT 271
QY 61 GlyGluPheTyrAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
DB 272 GGAGAAATTTGGGCTGGCGAGTGTATTATGTGTATGCGCAGAGATGGAGTCTGGGT 331
QY 81 TyrPheProSerAsnLeuValLysGlnGlnArgValTyrGlnGluAlaThrLysGluIle 100
DB 332 TATTTCCCGAGAACTGTGTCAAGSACAGCGTGTGTACCGAAGCTTACCAAGAAATT 391
QY 101 ProThrAspIleAspPhePheCysGlu 110
DB 392 CCCACCACGATATGACTTCTTCGCGAG 421

Search completed: December 30, 2003, 02:01:06
Job time : 248.807 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 29, 2003, 16:24:24 ; Search time 34.972 Seconds
(without alignments)
1388.315 Million cell updates/sec

Title: US-10-019-455a-26

Perfect score: 591
Sequence: 1 HGVFNDRKLSKKLCADEECV.....RVGEATKEIPFTDIDPFCE 110

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-O=/cg2.1/USPTO.spool/US10019455/runat_29122003.160348.277/app.Query.fast_1.1770
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rtm -MINMATCH=0.1 -LOOPEL=0
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-USER=US10019455 @CGN 1.1.142 @runat_29122003.160348.277 -NCPUS=6 -ICPU=3
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:*
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2: /cg2.6/ptodata/2/ina/5B.COMB.seq:*
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5: /cg2.6/ptodata/2/ina/PTUS.COMB.seq:*
6: /cg2.6/ptodata/2/ina/backfiles.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------------------------------|
| 1 | 261.5 | 44.2 | 330 | 1 | US-08-578-649-18 Sequence 18, Appl |
| 2 | 261.5 | 44.2 | 459 | 1 | US-08-578-649-1 Sequence 1, Appl |
| 3 | 241.5 | 40.9 | 581 | 1 | US-08-578-649-4 Sequence 4, Appl |
| 4 | 219.5 | 37.1 | 305 | 1 | US-08-578-649-8 Sequence 8, Appl |
| 5 | 194 | 32.8 | 596 | 1 | US-08-578-649-24 Sequence 24, Appl |
| 6 | 161.5 | 27.3 | 3565 | 1 | US-08-578-649-3 Sequence 3, Appl |
| 7 | 91.5 | 15.5 | 2793 | 1 | US-07-646-537B-1 Sequence 1, Appl |
| 8 | 89.5 | 15.1 | 2757 | 5 | US-08-306-691B-48 Sequence 48, Appl |
| 9 | 88.5 | 15.1 | 2757 | 5 | PCT-US93-06251-79 Sequence 79, Appl |
| 10 | 89.5 | 15.1 | 4762 | 4 | US-09-300-958A-30 Sequence 30, Appl |
| 11 | 82 | 13.9 | 467 | 4 | US-09-300-958A-28 Sequence 28, Appl |
| 12 | 78.5 | 13.3 | 5398 | 3 | US-09-356-952-11 Sequence 11, Appl |

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| 13 | 77 | 13.0 | 2085 | 1 | US-08-164-839-3 Sequence 3, Appl |
| 14 | 77 | 13.0 | 2085 | 1 | US-08-583-799-3 Sequence 3, Appl |
| 15 | 77 | 13.0 | 2520 | 1 | US-08-164-839-5 Sequence 5, Appl |
| 16 | 77 | 13.0 | 2520 | 1 | US-08-583-799-5 Sequence 5, Appl |
| 17 | 71.5 | 12.1 | 2064 | 4 | US-08-630-915A-39 Sequence 39, Appl |
| 18 | 71.5 | 12.1 | 2064 | 1 | US-08-164-839-30 Sequence 30, Appl |
| 19 | 71.5 | 12.1 | 2064 | 1 | US-08-164-839-32 Sequence 32, Appl |
| 20 | 71.5 | 12.1 | 2064 | 1 | US-08-583-799-30 Sequence 30, Appl |
| 21 | 71.5 | 12.1 | 2064 | 1 | US-08-583-799-32 Sequence 32, Appl |
| 22 | 71.5 | 12.1 | 2148 | 1 | US-08-164-839-69 Sequence 69, Appl |
| 23 | 71.5 | 12.1 | 2148 | 1 | US-08-164-839-71 Sequence 71, Appl |
| 24 | 71.5 | 12.1 | 2148 | 1 | US-08-583-799-69 Sequence 69, Appl |
| 25 | 71.5 | 12.1 | 2148 | 1 | US-08-583-799-71 Sequence 71, Appl |
| 26 | 71.5 | 12.1 | 2873 | 4 | US-08-630-915A-13 Sequence 13, Appl |
| 27 | 71 | 12.0 | 1664976 | 4 | US-08-916-421B-1 Sequence 1, Appl |
| 28 | 67.5 | 11.4 | 1593 | 4 | US-09-252-991A-5394 Sequence 5394, Ap |
| 29 | 67 | 11.3 | 3345 | 4 | US-08-630-915A-29 Sequence 29, Appl |
| 30 | 66.5 | 11.3 | 4119 | 4 | US-09-076-259-1 Sequence 1, Appl |
| 31 | 66 | 11.2 | 971 | 4 | US-08-630-915A-197 Sequence 197, Ap |
| 32 | 66 | 11.2 | 1170 | 4 | US-09-252-991A-2073 Sequence 2073, Ap |
| 33 | 66 | 11.2 | 1457 | 3 | US-09-444-053-3 Sequence 3, Appl |
| 34 | 65.5 | 11.1 | 735 | 4 | US-09-252-991A-14239 Sequence 14239, A |
| 35 | 65.5 | 11.1 | 1470 | 4 | US-09-252-991A-14025 Sequence 14025, A |
| 36 | 65 | 11.0 | 840 | 1 | US-08-634-255-7 Sequence 7, Appl |
| 37 | 65 | 11.0 | 840 | 1 | US-08-459-967-7 Sequence 7, Appl |
| 38 | 65 | 11.0 | 840 | 1 | US-08-460-327-7 Sequence 7, Appl |
| 39 | 65 | 11.0 | 840 | 1 | US-08-459-871-7 Sequence 7, Appl |
| 40 | 65 | 11.0 | 840 | 3 | US-09-024-532-1 Sequence 1, Appl |
| 41 | 65 | 11.0 | 840 | 4 | US-09-104-623A-1 Sequence 1, Appl |
| 42 | 65 | 11.0 | 840 | 4 | US-09-019-532-1 Sequence 1, Appl |
| 43 | 65 | 11.0 | 840 | 4 | US-09-417-359A-1 Sequence 1, Appl |
| 44 | 65 | 11.0 | 1110 | 1 | US-08-434-255-5 Sequence 5, Appl |
| 45 | 65 | 11.0 | 1110 | 1 | US-08-459-967-5 Sequence 5, Appl |

ALIGNMENTS

RESULT 1
US-08-578-649-18
; Sequence 18, Application US/08578649
; Patent No. 5770366
; GENERAL INFORMATION:
; APPLICANT: Ulrich Bogdan
; APPLICANT: Reinhard Butner
; APPLICANT: Brigitte Kaluza
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44 MB storage diskette
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/578,649
; FILING DATE: 29-July-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 24 247.2
; FILING DATE: 20-July-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Andrew L. Tiajolofof
; REGISTRATION NUMBER: 31,575
; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3684


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APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA: DE P 43 24 247.2
APPLICATION NUMBER: 1993
FILING DATE: 20-July-1993
ATTORNEY/AGENT INFORMATION:
NAME: Andrew L. TiaJoleff
REGISTRATION NUMBER: 31,575
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 459 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 40..432
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 40..111
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 112..432
US-08-578-649-1
Alignment Scores:
Pred. No.: 1.28e-29 Length: 459
Score: 261.50 Matches: 49
Percent Similarity: 67.53% Conservative: 24
Best Local Similarity: 45.37% Mismatches: 30
Query Match: 44.25% Indels: 5
DB: Gaps: 3
US-10-019-455A-26 (1-110) X US-08-578-649-1 (1-459)
QY 5 MetAspLysLeuSerSerIyrlslyStenuCysAlaSpGlnGluCysValTYrThrIleSer 24
Db 118 ATGCCCAAGCTGGCTGCACCGGAAGCTGTGTGGGACGACGAGTGCACCACCCATTCCTC 177
QY 25 LeuAlaArgAlaGInGlnuAsPTyrAsnaIaProAsPCysArgPheIleAspValLys 44
Db 178 ATGGCTGTGGCCCTTCAGACACTACATGGCCCCCATCTCCGATTCCTGCACATTACACCG 237
QY 45 GlyInGlnIleTyValTySerIySleuValThrgIuaEngIylalagIylu--Phe 63
Db 238 GGCCAGTAGTGATGTCTTCCTCCAAGCTG-----AAGGCGCTGGCGGCTCTTC 288
QY 64 TrpAlaGlySerValTyrcIyAsphIsGlnaspImetGlylle---ValGIlyTyPhe 82
Db 289 TGGGAGGCGAGCGTTCTCAGGAGATTACTATGAGAGTCTGGCTGCTCGCTGGCTATTTC 348
QY 83 ProSerAsnLeuValysGlnGlnuArgValTyrgInguIalThrIysGuIlleProThr 102
Db 349 CCCAGTAGCTTGTCTCCGAAAGCACACAGACCCCTGMAAAGCTGGCAAAGTCGATGTAACA 408
QY 103 ThrAspIleAspPhePheCysGlu 110
Db 409 GACAATGGGATTTCCTACTGCCAG 432
RESULT 3
US-08-578-649-4
; Sequence 4, Application US/08578649
; Patent No. 570366
; GENERAL INFORMATION:
APPLICANT: Ulrich Bogdan
APPLICANT: Reinhard Butner
APPLICANT: Brigitte Kaluza

```

TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 MB storage diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-July-1993
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 581 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 110..499
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 110..178
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 179..499
US-08-578-649-4
Alignment Scores:
Pred. No.: 1,62e-26 Length: 581
Score: 241.50 Matches: 49
Percent Similarity: 64.81% Conservative: 21
Best Local Similarity: 45.37% Mismatches: 33
Query Match: 40.86% Indels: 5
DB: 1 Gaps: 3
US-10-019-455A-26 (1-110) x US-08-578-649-4 (1-581)
QY 5 MetAspLysLeuSerSerLysLysLeuCySaLaaspGluGluCySaValTyrThrIleSer 24
DB 185 ATGCCAAGCTGGCTGACTGTGAGGAGCTGTGCGGACGAGATGAGCATCTATCTCC 244
QY 25 LeuAlaaspGlaGluaspTyrAsnAlaProaspCysaspPheIleaspValLys 44
DB 245 ATGGCTTGGCCCTCCAGACTACTGCGCCCTGATTCCTTGTACTATATAGG 304
QY 45 GlyGlnGlnIleTyrValTyrSerLysLeuValThrGluangLYAlaGlyGlu---Phe 63
DB 305 GGGCAAGGAGGTATGCTCTTCCAAAGTG-----AAGGCCGTGGGCGCTTTC 355
QY 64 TrpAlaGlySerValTyrGlyAspHisGlnaspGluMetGlyIle---ValGlyTyrPhe 82
DB 356 TGGGAGGCGAGGTTCACGGAGGTTACTATGAGACCTGCGACGCCGCGCTGGCTATTC 415
QY 83 ProSerAsnLeuValLysGluGlnAlaGlyValTyrGlnGluAlaThrLysGlnIleProThr 102

DB 416 CCCAGTAGCATTTGCCGGGAGACCTGAACCTGCAAACTGGCAAAATTGATGAGACC 475
QY 103 ThraspLeaspPhePheCyGlu 110
DB 476 GATCAATGGGATTCTACTGCGAG 499
RESULT 4
US-08-578-649-8
Sequence 8, Application US/08578649
Patent No. 5770366
GENERAL INFORMATION:
APPLICANT: Ulrich Bogdan
APPLICANT: Reinhard Butner
APPLICANT: Brigitte Kaluza
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 MB storage diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-July-1993
ATTORNEY/AGENT INFORMATION:
NAME: Andrew L. Tiajoleff
REGISTRATION NUMBER: 31,575
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 305 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: misc RNA
LOCATION: joint1..29, 277..305)
OTHER INFORMATION: /function="Primer"
US-08-578-649-8
Alignment Scores:
Pred. No.: 1,16e-23 Length: 305
Score: 219.50 Matches: 44
Percent Similarity: 64.65% Conservative: 20
Best Local Similarity: 44.44% Mismatches: 30
Query Match: 37.14% Indels: 5
DB: 1 Gaps: 3
US-10-019-455A-26 (1-110) x US-08-578-649-8 (1-305)
QY 12 LysLeuCySaLaaspGluGluCySaValTyrThrIleSerLeuAlaArgLaGlnGluasp 31
DB 7 AAGTTTCGGCGGATGAGGAGTGCGACCAACCCATATCTCATGGCTGTGCGCTTCAGAC 66
QY 32 TyrAsnAlaProaspCysaspPheIleaspValLysGlyGlnGlnIleTyrValTyr 51
DB 67 TACATGGCCCGAGATGCGGATTCCTGACCATTCACCGGGGCCAAGGTGATGATCTTC 126

QY 52 SerLysLeuValThrGluAsnGlyAlaGlyGlu---PheTrpAlaGlySerValTyrGly 70
Db 127 TCACAGCTG-----AAGGCCCGTGGCGGCTCTTCGCGGAGGACGCTTCAGGGA 177
QY 71 AspHisGln---AspGluMetGlyIleValGlyTyrPheProSerAsnLeuValTyrGlu 89
Db 178 GATTACTATGAGATCTGCTGCTCGCTGCTGCTATTTCCCGCAGTACATTCGCGAGAG 237
QY 90 GlnArgValTyrGlnGluAlaThrLysGluIleProThrThrAspIleAspPhe 108
Db 238 GACCAGACCTGAAACCTGGCAAGTCGATGTAGACAGCATTAATGGATTCTTAC 294
RESULT 5
US-08-578-649-24
Sequence 24, Application US/08578649
Patent No. 5770366
GENERAL INFORMATION:
APPLICANT: Ulrich Bogdan
APPLICANT: Reinhard Butner
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-July-1993
ATTORNEY/AGENT INFORMATION:
NAME: Andrew L. TiaJoloff
REGISTRATION NUMBER: 31,575
REFERENCE/DOCKET NUMBER: BOER 1035-PFE/ALT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ. ID NO.: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 596 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: join(40..111, 40..166, 214..347, 393..503, 549
FEATURE: join(40..111, 40..166, 214..347, 393..503, 549
NAME/KEY: sig_peptide
LOCATION: 40..111
FEATURE:
NAME/KEY: exon
LOCATION: 40..166
FEATURE:
NAME/KEY: exon
LOCATION: 214..347
FEATURE:
NAME/KEY: exon
LOCATION: 393..503
FEATURE:

NAME/KEY: exon
LOCATION: 549..569
FEATURE:
NAME/KEY: -
LOCATION: one-of(194, 369, 527)
OTHER INFORMATION: /note="N in positions 194, 369
OTHER INFORMATION: and 527 denotes an indefinite number and sequence
OTHER INFORMATION: of nucleotides "
US-08-578-649-24
Alignment Scores:
Pred. No.: 1.78e-19 Length: 596
Score: 194.00 Matches: 50
Percent Similarity: 47.74% Conservative: 24
Best Local Similarity: 32.26% Mismatches: 28
Query Match: 32.83% Indels: 54
NB: 1 Gaps: 7
US-10-019-455A-26 (1-110) x US-08-578-649-24 (1-596)
QY 5 MetAspLysLeuSerSerLysLysLeuCyAlaAspGluGlyCyValTyr----- 21
Db 118 ATGCCCAAGCTGCTGACCCGAGAGCTGTGTCGACGACGAGTGCCAGCCG-TAAGAAATGG 176
QY 22 -----ThrIleSerLeuAlaArgAla 28
Db 177 GGAGGGTGAATTGGGACCCCTTCTTATTCCTTCCCTAGACCCCTATCTCATGCTGTGGCC 236
QY 29 GlnGluAspTyrAsnAlaProAspCysArgPheIleAspValLysGlyGlnGlnIle 48
Db 237 CTTCAGAGACTACATGAGCCCGGACTGCGCATTCCTGACATTCACCGGGCCAAAGTGCTG 296
QY 49 TyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu---PheTrpAlaGlySer 67
Db 297 TATGCTTCTCCAAAGCTG-----AAGGCCGTGGCGGCTCTTCGCGGAGCGCAGC 347
QY 68 -----ValTyrGlyAspHis 72
Db 348 GTGGGCTTGGGAGAGTGAAAGACCTTTTAACTCTTCCCGGAGGTTACAGAGATTAC 407
QY 73 GlnAspGluMetGlyIle---ValGlyTyrPheProSerAsnLeuValLysGluGlnArg 91
Db 408 TATGAGATCTGCTGCTGCTGCTGCTATTTCCCGCTAGCATTTGCCAGAGAGACAG 467
QY 92 ValTyrGlnGluAlaThrLysGluIleProThrThrAspIle----- 105
Db 468 ACCCTGAACCTGGCAAGTGAATGTG---AAGACAGACGTGAGTGCATGGGGCGCTGG 524
QY 106 -----AspPheheCysGlu 110
Db 525 CANTTCCCTTCTCTTTTTCAGAAATGGGATTTCTACGCGCAG 569
RESULT 6
US-08-578-649-3
Sequence 3, Application US/08578649
Patent No. 5770366
GENERAL INFORMATION:
APPLICANT: Ulrich Bogdan
APPLICANT: Reinhard Butner
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS

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SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-July-1993
ATTORNEY/AGENT INFORMATION:
NAME: Andrew L. Tlaiboloff
REGISTRATION NUMBER: 31,575
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3565 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 1378..1449
FEATURE:
NAME/KEY: exon
LOCATION: 1378..1504
FEATURE:
NAME/KEY: exon
LOCATION: 1586..1719
FEATURE:
NAME/KEY: exon
LOCATION: 2804..2914
FEATURE:
NAME/KEY: exon
LOCATION: 3232..3252
FEATURE:
NAME/KEY:
LOCATION: one-of(2216)
OTHER INFORMATION: /note= "N in position 2216
OTHER INFORMATION: denotes an indefinite number and sequence of
US-08-578-649-3

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| Alignment Scores: | | Pred. No.: | | Length: | | 3565 | |
|------------------------|----------|---------------|----|---------|--|------|--|
| Score: | 1.46e-13 | Matches: | 44 | | | | |
| Percent Similarity: | 161.50 | Conservative: | 12 | | | | |
| Best Local Similarity: | 44.80% | Mismatches: | 24 | | | | |
| Query Match: | 35.20% | Indels: | 45 | | | | |
| DB: | 27.33% | Gaps: | 5 | | | | |

| US-10-019-455A-26 (1-110) x US-08-578-649-3 (1-3565) | |
|---|------|
| QY 5 MetAspLysLeuSerSerLysLeuCyAlaSpHspGluCys----- | 19 |
| 1456 AIGCCCAAGCTGGCTGACCGGAAGCTGTGTGGGACGAGAGTCAGCCGTAGAATGGG | 1515 |
| QY 19 ----- | 19 |
| Db 1516 GAGGGGTGAATTGGGCTGTGAGCTGTAGCTGTGATGTGTCGATTCCTCTATT | 1575 |
| QY 20 -----ValTYrThIeSerLeuAlaArgAlGInGluAspTYrAaAlaProAspCys | 37 |
| 1576 CTTCCCTAGACCCATCTCCATGCTGTGGCCCTTCAGAGCTACATGGCCCCCGACGCG | 1635 |
| QY 38 ArgPheIleAspValLysGlyGInGlnIleTYrValTYrSerLysLeuValThrGlu | 57 |
| 1636 CCAATTCCTGACCATTCACCGGGGCGCAAGTGGTGAATGTCCTTCCCAAGCTG----- | 1686 |
| QY 58 AengIyIaGlyGlu---PheTrpAlaGlySerValTYrGlyAspHisGInAspGluMet | 76 |

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D5 1687 AAGGCGCGGTGGCGCGCTCTCTGGGAGGCGACGCGTG-----CGTCT 1728
QY 77 GlyIleValGlyTyrPheProSerAsnLeuValIleSgluGlnArgValTyrGlnGluAla 96
D6 1729 GCG-----AGAGTGAAGAGGGAAGCGTACAGAGCTGGCGGT 1764
QY 97 ThrIleSgluIlePro 101
D6 1765 AGACTCATTAATCCCC 1779

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1 CLASSIFICATION: 435
2
3 ATTORNEY/AGENT INFORMATION:
4
5 NAME: Gall, Timothy J.
6
7 REGISTRATION NUMBER: 33,111
8
9 REFERENCE/DOCKET NUMBER: DC10
10
11 TELECOMMUNICATION INFORMATION:
12
13 TELEPHONE: (609) 921-5901
14
15 TELEFAX: (609) 921-4526
16
17 INFORMATION FOR SEQ ID NO: 1:
18
19 SEQUENCE CHARACTERISTICS:
20
21 LENGTH: 2793 base pairs
22
23 TYPE: nucleic acid
24
25 STRANDEDNESS: double
26
27 TOPOLOGY: linear
28
29 MOLECULE TYPE: cDNA
30
31 HYPOTHEetical: NO
32
33 FEATURE:
34
35 NAME/KEY: CDS
36
37 LOCATION: 1..2545
38
39
40 US-07-646-537b-1

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| | |
|------------------------|---------|
| Alignment Scores: | |
| Pred. No.: | 0.00233 |
| Score: | 91.50 |
| Percent Similarity: | 55.86% |
| Best Local Similarity: | 33.66% |
| Query Match: | 15.44% |
| DB: | 1 |
| | |
| Length: | 2793 |
| Matches: | 23 |
| Conservative: | 14 |
| Mismatches: | 20 |
| Indels: | 13 |
| Gaps: | 3 |

```

US-10-019-455A-26 (1-110) x US-07-646-537B-1 (1-2793)

QY 26 ALaRGAlaGInGluSpEryrAenAlaProAspCyArGpHeLleAspValLysGly 45
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 2369 GCaAAgCCCGcTAcGAcCTTCTGTGCCGGAGAGAGGTGGAAATGTCCTTAAGAGCGT 2428

QY 46 GInGInLleTyrrValTyrrSerLysLeuValThrGlnAsnGlyAlaGlyGluPheTrrPala 65
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 2429 GATATCATC-----AAGATCCCTCAATMAAGAGGAGCGACGAGCTGTGGCGT 2476

QY 66 GlysErValTyrrGlyAspHisGlnAspGluMetGlyIleValGlyTyrrPheProSerAsn 85

```

DB 2477 GGGAGATCTACGCGCGG-----ATCGGCTGGTTCCTTAC 2515
QY 86 LeuVallysgInArgValTyrgInGlu 95
DB 2516 TATGTGAGAGAGAC-----TATTCCGA 2539

RESULT 8
US-08-306-691B-48
Sequence 48, Application US/08306691B
Patent No. 5734039

GENERAL INFORMATION:
APPLICANT: Calabretta, Bruno
APPLICANT: Skorski, Tomasz
TITLE OF INVENTION: ANTISENSE
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
NUMBER OF SEQUENCES: 55

CORRESPONDENCE ADDRESS:
ADDRESSEE: Seidel, Gonda, Lavoragna & Monaco, P.C.
STREET: Two Penn Center, Suite 1800
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19102

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,691B
FILING DATE: September 15, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-5549
TELEFAX: (215) 568-8383
TELEX: NO. 5734039e
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 2757 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

US-08-306-691B-48

Alignment Scores:
Pred. No.: 0.00451 Length: 2757
Score: 89.50 Matches: 23
Percent Similarity: 52.86% Conservative: 14
Best Local Similarity: 32.86% Mismatches: 20
Query Match: 15.14% Indels: 13
DB: 1 Gaps: 3

US-10-019-455A-26 (1-110) x US-08-306-691B-48 (1-2757)

QY 26 AlaArgAlaGInGluAspTyrrAsnAlaProAspCysArgPheIleAspValLysGly 45
DB 2325 GCCAAAGCCCGATACCTTCGCGCCGCTGACCGCTGACAGCTGCTGCTCAAGAGAGGT 2384

QY 46 GInGInIleTyrrValTyrrSerLysLeuValThrGluAsnGlyAlaGlyGluPheTrpAla 65
DB 2385 GACATCATC-----AAGATCCTTAACAGAGAGAGAGAGAGAGAGGTGCGCA 2432

QY 66 GlySerValTyrgIAspHisGlnAspGluMetGlyIleValGlyTyrrPheProSerAsn 85
DB 2433 GGGAGATCTATGCGCG-----GTGGCTGGTTCCTCCCAAC 2471

QY 86 LeuVallysgInArgValTyrgInGlu 95
DB 2472 TACGTGAGAGAGAT-----TATTCTGAA 2495

RESULT 9
PCT-US93-06251-79
Sequence 79, Application PC/TUS9306251
GENERAL INFORMATION:
APPLICANT: Wickstrom, Eric and Rife, Jason P.
TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: NY
COUNTRY: USA
ZIP: 11530

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06251
FILING DATE: 19930630
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: DIGILIO, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8586
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 2757 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US93-06251-79

Alignment Scores:
Pred. No.: 0.00451 Length: 2757
Score: 89.50 Matches: 23
Percent Similarity: 52.86% Conservative: 14
Best Local Similarity: 32.86% Mismatches: 20
Query Match: 15.14% Indels: 13
DB: 5 Gaps: 3

US-10-019-455A-26 (1-110) x PCT-US93-06251-79 (1-2757)

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DB 2325 GCCAAAGCCCGATACCTTCGCGCCGCTGACCGCTGACAGCTGCTGCTCAAGAGAGGT 2384

QY 46 GInGInIleTyrrValTyrrSerLysLeuValThrGluAsnGlyAlaGlyGluPheTrpAla 65
DB 2385 GACATCATC-----AAGATCCTTAACAGAGAGAGAGAGAGAGAGGTGCGCA 2432

QY 66 GlySerValTyrgIAspHisGlnAspGluMetGlyIleValGlyTyrrPheProSerAsn 85
DB 2433 GGGAGATCTATGCGCG-----GTGGCTGGTTCCTCCCAAC 2471

QY 86 LeuVallysgInArgValTyrgInGlu 95
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RESULT 10


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Db      445 CTTCTCTTCCCTCGACAAAGTGAAGTACCAGACATTCGTCACATTGACTAGTC 504
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Qy      43 LysLYSGlYGlInGlnIleTYrValTYrSerLYSLeuValThrGluAsnGlyAlaGly 62
Db      565 CAACAAGGGGAAACCAATTATATATCTTAACAA-----AACTCATCTGGG--- 609
Qy      63 PheTrAlAGlYserValTYrGlyAspHisGlnAspGluMetGlyIleValGlyTYrPhe 82
Db      610 TGCTGGATGATGATTGATTGACGACAGTATGGGAAAGTTAAC---AGAGCTGCTT 666
Qy      83 ProSerAsnLeuValLYSGlInGlnArg 91
Db      667 CCTCAAAACTTCGCTAGACCTTTAAGA 693

RESULT 13
US-08-164-839-3
; Sequence 3, Application US/08164839
; Patent No. 5514573
; GENERAL INFORMATION:
; APPLICANT: YASUEDA, HISASHI
; APPLICANT: NAKANISHI, KAZUO
; APPLICANT: MOTOKI, MASAO
; APPLICANT: NAGASE, KAZUO
; APPLICANT: MATSUI, HIROSHI
; TITLE OF INVENTION: GENE ENCODING TRANSGLUTAMINASE DERIVED
; FROM FISH
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/164,839
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/004,729
; FILING DATE: 14-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5514573man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-599-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)412-3000
; TELEFAX: (703)413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2085 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE:
; ORGANISM: Pagrus major
; TISSUE TYPE: liver
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2082

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US-08-164-839-3
Alignment Scores:
Pred. No.: 0.214
Score: 77.00
Percent Similarity: 52.50%
Best Local Similarity: 27.50%
Query Match: 13.03%
DB: 1
Caps: 3

US-10-019-455a-26 (1-110) x US-08-164-839-3 (1-2085)
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Db      1225 -----CGAAGATCACAGAGACCATGCTAGTGTGGGAAAGAACATCACACAAAAAGC 1278
Qy      68 ValTYrGlyAspHisGlnAspGluMetGlyIleValGlyTYrPheProSerAsnLeuVal 87
Db      1279 GTTACGGCAACACAGAGAGATGTCCTGCACTACAAATATCTGAAAGCTCCAG 1338
Qy      88 LYSGlInGlnArgValTYrGlnGluAlaThrLYSGluIle-----ProThrAspIle 105
Db      1339 AAGGAGGGAAGTGTACAGAGAGCGGAGCGCGGTCCACAGACCATCCACAGAGATC 1398

RESULT 14
US-08-583-799-3
; Sequence 3, Application US/08583799
; Patent No. 5607849
; GENERAL INFORMATION:
; APPLICANT: YASUEDA, HISASHI
; APPLICANT: NAKANISHI, KAZUO
; APPLICANT: MOTOKI, MASAO
; APPLICANT: NAGASE, KAZUO
; APPLICANT: MATSUI, HIROSHI
; TITLE OF INVENTION: GENE ENCODING TRANSGLUTAMINASE DERIVED
; FROM FISH
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,799
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/004,729
; FILING DATE: 14-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5607849man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-599-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)412-3000
; TELEFAX: (703)413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2085 base pairs
; TYPE: nucleic acid

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STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE: PLAGIUS major
TISSUE TYPE: liver
FEATURE: CDS
LOCATION: 1..2082
US-08-583-799-3

Alignment Scores:
Pred. No.: 0.214 Length: 2085
Score: 77.00 Matches: 22
Percent Similarity: 52.50% Conservative: 20
Best Local Similarity: 27.50% Mismatches: 28
Query Match: 13.03% Indels: 10
Gaps: 3
DB: 1

US-10-019-455a-26 (1-110) x US-08-583-799-3 (1-2085)

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DB 1174 GAGGTGAACCTTACACCATCTGATGCTCCAAAAGATGCCAAGCA----- 1224
QY 51 TySerLysLeuValThrgLysnglyAglY-----GluPheTrpAlaGlySer 67
DB 1225 -----CGAAGATCACAGAGACCATGCTAGTGGGAGAGAACATCAGCAAAAAGC 1278
QY 68 ValTYGlyAspHisGlnAspGluMetGlyIleValGlyTyRheProSerAsnLeuVal 87
DB 1279 GTTACCGGCAACACAGAGAGATGTCATCTGCACTACAAATATCTTGAAGCTCCAG 1338
QY 88 LysGluGlnArgValTYGlnGlnAlaThrlYsgluIle-----ProThrThraspile 105
DB 1339 AAGGAGAGGAAAGTGTACAGAGAGCGCGGAGGTCTCAGAGCATCCAGAGATC 1398

RESULT 15
US-08-164-839-5
Sequence 5' Application US/08164839
Patent No. 5514573
GENERAL INFORMATION:
APPLICANT: YASUEDA, HISASHI
APPLICANT: NAKANISHI, KAZUO
APPLICANT: MOTOKI, MASAO
APPLICANT: NAGASE, KAZUO
APPLICANT: MATSUI, HIROSHI
TITLE OF INVENTION: GENE ENCODING TRANSGLUTAMINASE DERIVED
FROM FISH
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/164,839
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/004,729
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5514573man F.
REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 10-599-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 412-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2520 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE: PLAGIUS major
TISSUE TYPE: liver
FEATURE: CDS
LOCATION: 34..2121
US-08-164-839-5

Alignment Scores:
Pred. No.: 0.28 Length: 2520
Score: 77.00 Matches: 22
Percent Similarity: 52.50% Conservative: 20
Best Local Similarity: 27.50% Mismatches: 28
Query Match: 13.03% Indels: 10
Gaps: 3
DB: 1

US-10-019-455a-26 (1-110) x US-08-164-839-5 (1-2520)

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DB 1210 GAGGTGAACCTTACACCATCTGATGCTCCAAAAGATGCCAAGCA----- 1260
QY 51 TySerLysLeuValThrgLysnglyAglY-----GluPheTrpAlaGlySer 67
DB 1261 -----CGAAGATCACAGAGACCATGCTAGTGGGAGAGAACATCAGCAAAAAGC 1314
QY 68 ValTYGlyAspHisGlnAspGluMetGlyIleValGlyTyRheProSerAsnLeuVal 87
DB 1315 GTTACCGGCAACACAGAGAGATGTCATCTGCACTACAAATATCTTGAAGCTCCAG 1374
QY 88 LysGluGlnArgValTYGlnGlnAlaThrlYsgluIle-----ProThrThraspile 105
DB 1375 AAGGAGAGGAAAGTGTACAGAGAGCGCGGAGGTCTCAGAGCATCCAGAGATC 1434

Search completed: December 29, 2003, 22:08:08
Job time: 39.972 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd

OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 22:08:26 ; Search time 1216 Seconds
(without alignments)

12918.830 Million cell updates/sec

Title: US-10-019-455A-46

Perfect score: 384
Sequence: 1 atgccaagaatatctgattct.....atatgactctctctgaa 384

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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| Post-processing: | Minimum Match | 0% |
| | Maximum Match | 100% |

Listing first 45 summaries

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29:  em_vt:*
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31:  em_hcg_inv:*
32:  em_hcg_other:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
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| 1 | 384 | 100.0 | 384 | 6 | BD010835 | BD010835 Novel pol |
| 2 | 384 | 100.0 | 384 | 6 | BD093316 | BD093316 Novel pol |
| 3 | 344 | 89.6 | 384 | 6 | BD010805 | BD010805 Novel pol |
| 4 | 344 | 89.6 | 384 | 6 | BD093106 | BD093106 Novel pol |
| 5 | 344 | 89.6 | 929 | 10 | AF243504 | AF243504 Mus muscu |
| 6 | 344 | 89.6 | 947 | 6 | BD010821 | BD010821 Novel pol |
| 7 | 344 | 89.6 | 947 | 6 | BD093122 | BD093122 Novel pol |
| 8 | 344 | 89.6 | 958 | 10 | MM249339 | AF243339 Mus muscu |
| 9 | 344 | 89.6 | 1054 | 10 | AF233333 | AF233333 Mus muscu |
| 10 | 330 | 85.9 | 330 | 6 | BD010836 | BD010836 Novel pol |
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| 13 | 294.8 | 76.8 | 330 | 6 | BD093118 | BD093118 Novel pol |
| 14 | 287.6 | 74.9 | 307 | 6 | BD010830 | BD010830 Novel pol |
| 15 | 287.6 | 74.9 | 307 | 6 | BD093131 | BD093131 Novel pol |
| 16 | 285.4 | 74.3 | 384 | 6 | BD010802 | BD010802 Novel pol |
| 17 | 285.4 | 74.3 | 384 | 6 | BD093103 | BD093103 Novel pol |
| 18 | 285.4 | 74.3 | 521 | 6 | AX356818 | AX356818 Sequence |
| 19 | 285.4 | 74.3 | 521 | 6 | AX362311 | AX362311 Sequence |
| 20 | 285.4 | 74.3 | 521 | 6 | AX454774 | AX454774 Sequence |
| 21 | 285.4 | 74.3 | 521 | 6 | AX491252 | AX491252 Sequence |
| 22 | 285.4 | 74.3 | 846 | 9 | AF233261 | AF233261 Homo sapi |
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| 24 | 285.4 | 74.3 | 923 | 6 | BD010820 | BD010820 Novel pol |
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| 28 | 261 | 68.0 | 261 | 6 | BD093130 | BD093130 Novel pol |
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| 30 | 249 | 64.8 | 330 | 6 | BD093117 | BD093117 Novel pol |
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| 32 | 142 | 37.0 | 21581 | 2 | ACT06161 | ACT06161 Rattus no |
| 33 | 130.8 | 34.1 | 466 | 2 | AF233819 | AF233819 Rana cate |
| 34 | 126.4 | 32.9 | 14475 | 2 | BSX10362 | BSX10362 Mus muscu |
| 35 | 111.6 | 29.1 | 232 | 9 | HS253325 | AF252925 Homo sapi |
| 36 | 111.6 | 29.1 | 12151 | 9 | HS705D16 | ALU34428 Human DNA |
| 37 | 80.2 | 20.9 | 259 | 9 | HS253326 | AF252926 Homo sapi |
| 38 | 79.6 | 20.7 | 358 | 9 | HS253324 | AF252924 Homo sapi |
| 39 | 71.8 | 18.7 | 545 | 10 | RNU67884 | U67884 Rattus norv |
| 40 | 64 | 16.7 | 580 | 10 | MM1A | X94332 M.musculus |
| 41 | 64 | 16.7 | 581 | 6 | A42945 | A42945 Sequence 4 |
| 42 | 64 | 16.7 | 581 | 6 | AX016788 | AX016788 Sequence |
| 43 | 63.4 | 16.5 | 396 | 6 | BT007044 | BT007044 Homo sapi |
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| BD010835 | BD010835 | 384 bp | DNA |
| LOCUS | BD010835 | | linear |
| DEFINITION | Novel polypeptide and DNA thereof. | | |
| ACCESSION | BD010835 | | |
| VERSION | BD010835.1 GI:18639208 | | |
| KEYWORDS | UP 2001060994-A/36. | | |
| SOURCE | Rattus sp. | | |
| ORGANISM | Rattus sp. | | |

REFERENCE
AUTHORS
1 (bases 1 to 384)
Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
Yoshimura, K. and Tanaka, H.

REFERENCE 1 (bases 1 to 384)
AUTHORS Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y., Yoshimura, K. and Tanaka, H.
TITLE Novel polypeptide and DNA thereof
JOURNAL Patent: JP 2001069994-A 6 21-MAR-2001;
TAKEDA CHEMICAL INDUSTRIES LTD
COMMENT OS Mus sp. (mouse)
PN JP 2001069994-A/6
PD 21-MAR-2001
PF 29-JUN-2000 JP 2000195911
PR YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI SHINICHI MOGI,
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/03, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC A61P19/08,
PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC G01N33/53//
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CC
FH Key Location/Qualifiers
FT source 1..384
FT /organism="Mus sp. (mouse)"
FT Location/Qualifiers
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/organism="Mus sp."
/mol_type="genomic DNA"
/db_xref="taxon:10095"

BASE COUNT 98 a 68 c 111 g 107 t

ORIGIN

Query Match 89.6%; Score 344; DB 6; Length 384;
Best Local Similarity 93.5%; Pred. No. 3e-93;
Matches 359; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1 ATGGCAAGATATGATCTTTCTGCGGGGCGCTTGCTCTCTGCGCGGCGATGGC 60
DB 1 ATGGCAAGATATGATCTTTCTGCGGGGCGCTTGCTCTCTGCGCGGCGATGGT 60
QY 61 ATGTTTATGATAAATCTTCTCTAGAGAGTGTGTGAGATGAGAGTGTCTATACC 120
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QY 121 ATTTCTCTGGCAAGAGCAGAGAGACTACATGCCCCGAGCTGTAGCTTCATCATGTC 180
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QY 181 AAGAAAGGGGACAGATCTATGTTTATTCAGAGCTGTAAACGAAATGAGAGTGGGGCA 240
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QY 361 ACGGATATTGACTTCTCTGTGAA 384
DB 361 ACGGATATTGACTTCTCTGTGAA 384

RESULT 4
BD093106 384 bp DNA linear PAT 27-AUG-2002
LOCUS BD093106
DEFINITION Novel polypeptide and its DNA.
ACCESSION BD093106.1 GI:22638694
VERSION
KEYWORDS WO 0102564-A/6.

SOURCE Mus sp.
ORGANISM Mus sp.
REFERENCE 1 (bases 1 to 384)
AUTHORS Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y., Yoshimura, K. and Tanaka, H.
TITLE Novel polypeptide and its DNA
JOURNAL Patent: WO 0102564-A 6 11-JAN-2001;
TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
COMMENT OS Mus sp. (mouse)
PN WO 0102564-A/6
PD 11-JAN-2001
PF 29-JUN-2000 WO 2000JP004278
PI 30-JUN-1999 JP 99P 186718
PR YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI MOGI,
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/12, C12N5/10, C12P21/02, C07K14/47, C07K16/18, A61K45/00, PC A61K38/17,
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CC
FH Key Location/Qualifiers
FT source 1..384
FT /organism="Mus sp."
FT /mol_type="genomic DNA"
FT /db_xref="taxon:10095"

BASE COUNT 98 a 68 c 111 g 107 t

ORIGIN

Query Match 89.6%; Score 344; DB 6; Length 384;
Best Local Similarity 93.5%; Pred. No. 3e-93;
Matches 359; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1 ATGGCAAGATATGATCTTTCTGCGGGGCGCTTGCTCTCTGCGCGGCGATGGC 60
DB 1 ATGGCAAGATATGATCTTTCTGCGGGGCGCTTGCTCTCTGCGCGGCGATGGT 60
QY 61 ATGTTTATGATAAATCTTCTCTAGAGAGTGTGTGAGATGAGAGTGTCTATACC 120
DB 61 GATTATTAGATAAATCTTCTCTAGAGAGTGTGTGAGATGAGAGTGTCTATACC 120
QY 121 ATTTCTCTGGCAAGAGCAGAGAGACTACATGCCCCGAGCTGTAGCTTCATCATGTC 180
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QY 121 ATTTCTCTGGCAAGAGCAGAGAGACTACATGCCCCGAGCTGTAGCTTCATCATGTC 180
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QY 181 AAGAAAGGGGACAGATCTATGTTTATTCAGAGCTGTAAACGAAATGAGAGTGGGGCA 240
DB 181 AAGAAAGGGGACAGATCTATGTTTATTCAGAGCTGTAAACGAAATGAGAGTGGAG 240
QY 241 TTCTGGGCTGGCAGAGTTTATGAGTACACAGAGATGAGATGGGAATTTGGGTTATTTCC 300
DB 241 TTCTGGGCTGGCAGAGTTTATGAGTACACAGAGATGAGATGGGAATTTGGGTTATTTCC 300
QY 301 CCCAGCAACTTGGTTAGAGAGCAAGAGTGTACAGAGAGCCACCAAGAGATTTCCAAAC 360
DB 301 CCCAGCAACTTGGTTAGAGAGCAAGAGTGTACAGAGAGCCACCAAGAGATTTCCAAAC 360
QY 361 ACGGATATTGACTTCTCTGTGAA 384
DB 361 ACGGATATTGACTTCTCTGTGAA 384

RESULT 5
AF243504 929 bp mRNA linear ROD 26-DEC-2000
LOCUS AF243504
DEFINITION Mus musculus fibrocyte-derived protein (fdp) mRNA, complete cds.
ACCESSION AF243504

VERSION AF243504.1 GI:11991841
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 929)
 AUTHORS Cohen-Salmon, M., Frenzy, D., Liu, W., Verpy, E., Voegelting, S. and Petic, C.
 TITLE Fdp, a new fibrocyte-derived protein related to MIA/CD-RAP, has an in vitro effect on the early differentiation of the inner ear mesenchyme
 JOURNAL J. Biol. Chem. 275 (51), 40036-40041 (2000)
 MEDLINE 20568254
 PUBMED 10998416
 REFERENCE 2 (bases 1 to 929)
 AUTHORS Cohen-Salmon, M., Frenzy, D., Verpy, E., Voegelting, S. and Petic, C.
 TITLE Direct Submission
 JOURNAL Submitted (09-MAR-2000) Biotechnologies, Institut Pasteur, 25 rue du Dr. Roux, Paris 75015, France
 FEATURES
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 BASE COUNT 260 a 156 c 220 g 293 t
 ORIGIN
 Query Match 89.6%; Score 344; DB 10; Length 929;
 Best Local Similarity 93.5%; Pred. No. 3e-93;
 Matches 359; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

RESULT 6
 BD010821 947 bp DNA linear PAT 31-JUN-2002
 LOCUS Novel polypeptide and DNA thereof.
 DEFINITION BD010821
 ACCESSION BD010821.1 GI:18639194
 VERSION JP 2001069994-A/22.
 KEYWORDS Mus sp.
 SOURCE Mus sp.
 ORGANISM Mus sp.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 947)
 AUTHORS Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y., Yoshimura, K. and Tanaka, H.
 TITLE Novel polypeptide and DNA thereof
 JOURNAL Patent: JP 2001069994-A 22 21-MAR-2001;
 COMMENT TAKEDA CHEMICAL INDUSTRIES LTD
 OS Mus sp. (mouse)
 PN JP 2001069994-A/22
 PD 21-MAR-2001
 PF 29-JUN-2000 JP 2000195911
 PR
 PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI SHINICHI MOGI,
 PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
 PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC A61P19/08,
 PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC G01N33/53//
 PC C12P21/08, C12N15/00, A61K37/02, C12N5/00
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 FH Key Location/Qualifiers
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 BASE COUNT 279 a 158 c 221 g 289 t
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 Query Match 89.6%; Score 344; DB 6; Length 947;
 Best Local Similarity 93.5%; Pred. No. 3e-93;
 Matches 359; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Db 371 ACGGATATTGACTTCTGTGAA 394

RESULT 7
BD093122
LOCUS BD093122 947 bp DNA linear PAT 27-AUG-2002
DEFINITION Novel polypeptide and its DNA.
ACCESSION BD093122.1 GI:22638710
VERSION BD093122.1
KEYWORDS WO 0102564-A/22.
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 947)
Ito, Y., Nishii, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y., Yoshimura, K. and Tanaka, H.
Novel polypeptide and its DNA
Patent: WO 0102564-A 22 11-JAN-2001.
TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHII, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
HIDEYUKI TANAKA
COMMENT OS Mus sp. (mouse)
PN WO 0102564-A/22
PD 11-JAN-2001
PF 29-JUN-2000 WO 2000JP004278
PR 30-JUN-1999 JP 99P 186718
PI YASUAKI ITO, KAZUNORI NISHII, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/12, C12N5/10, C12P21/02, C07K14/47, C07K16/18, A61K45/00, PC A61K38/17, A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/7088// (C12P21/PC A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/7088// (C12P21/PC 02, C12R1:19)
CC
PC
FH Key Location/Qualifiers.
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BASE COUNT 279 a 158 c 221 g 289 t
ORIGIN
Query Match 89.6%; Score 344; DB 6; Length 947;
Best Local Similarity 93.5%; Pred. No. 3e-93;
Matches 359; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 361 ACGGATATTGACTTCTGTGAA 384
Db 371 ACGGATATTGACTTCTGTGAA 394

RESULT 8
MMU243939
LOCUS MMU243939 958 bp mRNA linear ROD 29-JAN-2001
DEFINITION Mus musculus mRNA for melanoma inhibitory activity-like protein (Mial gene).
ACCESSION AJ243939.1 GI:12619174
VERSION AJ243939
KEYWORDS melanoma inhibitory activity-like protein; Mial gene.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 Rendtorff, N.D., Frodin, M., Attie-Bitach, T., Vekemans, M. and Tommerup, N.
Identification and characterization of an inner ear-expressed human melanoma inhibitory activity (MIA)-like gene (MIAL) with a frequent polymorphism that abolishes translation
Genomics 71 (1), 40-52 (2001)
JOURNAL MEDLINE 21100875
PUBMED 1161796
REFERENCE 2 (bases 1 to 958)
Rendtorff, N.D.
TITLE Direct Submission
SUBMITTED (20-JUN-1999) Rendtorff N.D., Department of Medical Genetics, Institute of Medical Biochemistry and Genetics, Blegdamevej 3, 2200 Copenhagen N, DENMARK
COMMENT Related sequence: AJ242552
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/mol_type="mRNA"
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BASE COUNT 273 a 161 c 225 g 299 t
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Best Local Similarity 93.5%; Pred. No. 3e-93;
Matches 359; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 121 ATTCTCTGGCAAGACACAGAGACTACAAATGCCCGGACTGTAGTTCATCATGTC 180
 DB 144 ATTTCTCTGGCAAGACACAGAGACTACAAATGCCCGGACTGTAGTTCATCATGTC 203
 QY 131 AAGAAAGGGCAGACATCTATTTTATTCAGAGCTGTATACAGAAATGAGAGCTGGGCA 240
 DB 204 AAGAAAGGGCAGACATCTATTTTATTCAGAGCTGTATACAGAAATGAGAGCTGGGCA 263
 QY 241 TTCTGGGCTGGCAGGTGTATGTATGACCAACAGATGAGATGGGATTTGGTATTTTC 300
 DB 264 TTTTGGGCTGGCAGGTGTATGTATGACCAACAGATGAGATGGGATTTGGTATTTTC 323
 QY 301 CCCAGCACTTGTGTAGAGACACAGATGTATACAGAGGCGCCAGCAAGATTCACAC 360
 DB 324 CCCAGCACTTGTGTAGAGACACAGATGTATACAGAGGCGCCAGCAAGATTCACAC 383
 QY 361 ACGGATATTGACTTCTTCTGTGAA 384
 DB 384 ACGGATATTGACTTCTTCTGTGAA 407

RESULT 9
 AF233333 1054 bp mRNA linear ROD 06-JUL-2000
 LOCUS AF233333 Mus musculus otoraplin mRNA, complete cds.
 DEFINITION AF233333
 ACCESSION AF233333.1 GI:8927429
 VERSION
 KEYWORDS
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 1054)
 Roberton, N.G., Heller, S., Lin, J.S., Resendes, B.L., Weremowicz, S., Denis, C.S., Bell, A.M., Hudspeth, A.J., and Morton, C.C.
 A novel conserved cochlear gene, OTOR: identification, expression analysis, and chromosomal mapping
 Genomics 66 (3), 242-248 (2000)
 JOURNAL 2034619
 MEDLINE 10873378
 PUBMED 2 (bases 1 to 1054)
 Roberton, N.G., Heller, S., Lin, J.S., Resendes, B.L., Weremowicz, S., Denis, C.S., Bell, A.M., Hudspeth, A.J., and Morton, C.C.
 Direct Submission
 Submitted (10-FEB-2000) Pathology, Brigham and Women's Hospital, 75 Francis Street, Boston, MA 02115, USA
 FEATURES
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 /db_xref="GI:8927430"
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 NLVEQRYVQEAETKEIPTDIDPFCE"
 BASE COUNT 296 a 183 c 265 g 310 t
 ORIGIN

Query Match 89.6%; Score 344; DB 10; Length 1054;
 Best Local Similarity 93.5%; Pred. No. 3e-93;
 Matches 359; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1 ATGGCAAAATATGATCTTTTGGTGGGGCTTGTGGCTCTCTGTGCGGCGCATGCG 60
 DB 18 ATGGCAAAATATGATCTTTTGGTGGGGCTTGTGGCTCTCTGTGCGGCGCATGCG 77
 QY 61 ATGTTAATGATAAATCTTCTTAAGAGTTGTGTGAGATGAGAGTGTGTATACC 120

DB 78 GTAATTAATGATAAATCTTCTTAAGAGTTGTGTGAGATGAGAGTGTGTATACT 137
 QY 121 ATTTCTCTGGCAAGACACAGAGACTACAAATGCCCGGACTGTAGTTCATCATGTC 180
 DB 138 ATTTCTCTGGCAAGACACAGAGACTACAAATGCCCGGACTGTAGTTCATCATGTC 197
 QY 181 AAGAAAGGGCAGACATCTATTTTATTCAGAGCTGTATACAGAAATGAGAGCTGGGCA 240
 DB 198 AAGAAAGGGCAGACATCTATTTTATTCAGAGCTGTATACAGAAATGAGAGCTGGGCA 257
 QY 241 TTCTGGGCTGGCAGGTGTATGTATGACCAACAGATGAGATGGGATTTGGTATTTTC 300
 DB 258 TTTTGGGCTGGCAGGTGTATGTATGACCAACAGATGAGATGGGATTTGGTATTTTC 317
 QY 301 CCCAGCACTTGTGTAGAGACACAGATGTATACAGAGGCGCCAGCAAGATTCACAC 360
 DB 318 CCCAGCACTTGTGTAGAGACACAGATGTATACAGAGGCGCCAGCAAGATTCACAC 377
 QY 361 ACGGATATTGACTTCTTCTGTGAA 384
 DB 378 ACGGATATTGACTTCTTCTGTGAA 401

RESULT 10
 BD010836 330 bp DNA linear PAT 31-JUN-2002
 LOCUS BD010836
 DEFINITION Novel polypeptide and DNA thereof.
 ACCESSION BD010836
 VERSION BD010836.1 GI:18639209
 KEYWORDS JP 2001069994-A/37.
 SOURCE Rattus sp.
 ORGANISM Rattus sp.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 1 (bases 1 to 330)
 Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y., Yoshimura, K., and Tanaka, H.
 Novel polypeptide and DNA thereof
 Patent: JP 2001069994-A 37 21-MAR-2001;
 TAKEDA CHEMICAL INDUSTRIES LTD
 OS Rattus sp. (rat)
 PN JP 2001069994-A/37
 PD 21-MAR-2001
 PF 29-JUN-2000 JP 2000195911
 PR

PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI
 SHINICHI MOGI,
 PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
 PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC
 A61P19/08,
 PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC
 G01N33/53//
 PC C12P21/08, C12N15/00, A61K37/02, C12N5/00
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 CC Key Location/Qualifiers
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 FT /organism="Rattus sp. (rat)"
 FT Location/Qualifiers
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 /db_xref="taxon:10118"
 BASE COUNT 91 a 62 c 91 g 86 t
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Query Match 85.9%; Score 330; DB 6; Length 330;
 Best Local Similarity 100.0%; Pred. No. 5.4e-89;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 CATGGCAGCTTATGATAAATCTTCTTAAGAGTTGTGTGAGATGAGAGTGTGTCTC 114

Db 1 CATGCGATGTTATGATATAAATTCTTCTTAAGAAGTGTGTGAGATGAGAGTGTCTC 60
QY 115 TATACCATTTCTCTGGCAAGAGCAGAGAACTCAATGCCCGCATGTAGTTCATC 174
Db 61 TATACCATTTCTCTGGCAAGAGCAGAGAACTCAATGCCCGCATGTAGTTCATC 120
QY 175 AATGTCAGAAAGGGGAGCAGATCTATGTTTATTCAGCTGTGTACAGAAATGAGCT 234
Db 121 AATGTCAGAAAGGGGAGCAGATCTATGTTTATTCAGCTGTGTACAGAAATGAGCT 180
QY 235 GGGGCAATTCGGGCTGGCAGTGTATGTTATGTTACCAAGATGAGATGGAAATTTGGGT 294
Db 181 GGGGCAATTCGGGCTGGCAGTGTATGTTATGTTACCAAGATGAGATGGAAATTTGGGT 240
QY 295 TATTTCCCGCAACTTGGTTAGAGAGCAACGAGTGTACAGAGGCCCAAGAGATT 354
Db 241 TATTTCCCGCAACTTGGTTAGAGAGCAACGAGTGTACAGAGGCCCAAGAGATT 300
QY 355 CCAACCAAGGATATGACTTCTCTGTGAA 384
Db 301 CCAACCAAGGATATGACTTCTCTGTGAA 330

RESULT 11
BD093137 330 bp DNA linear PAT 27-AUG-2002
LOCUS BD093137
DEFINITION Novel polypeptide and its DNA.
ACCESSION BD093137.1 GI:22638725
VERSION WO 0102564-A/37.
KEYWORDS Rattus sp.
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 330)
AUTHORS Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
Yoshimura, K. and Tanaka, H.
TITLE Novel polypeptide and its DNA
JOURNAL Patent: WO 0102564-A 37 11-JAN-2001;
TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO
OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,
HIDEYUKI TANAKA

COMMENT

OS Rattus sp. (rat)
PN WO 0102564-A/37
PD 11-JAN-2001
PF 29-JUN-2000 WO 2000JP04278
PR 30-JUN-1999 JP 99P 186718
PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI
MOGI,
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/12, C12N5/10, C12P21/02, C07K14/47, C07K16/18, A61K45/00, PC
A61K38/17
PC A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/7088// (C12P21/
PC 02, C12R1:19)
CC
FH Key Location/Qualifiers.
FT /organism="Rattus sp."
/mol_type="genomic DNA"
/db_xref="taxon:10118"

FEATURES

source 1..330 Location/Qualifiers
BASE COUNT 91 a 62 c 91 g 86 t
ORIGIN

Query Match 85.9%; Score 330; DB 6; Length 330;
Best Local Similarity 100.0%; Pred. No. 5.4e-89;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 CATGCGATGTTATGATATAAATTCTTCTTAAGAAGTGTGTGAGATGAGAGTGTCTC 114
Db 1 CATGCGATGTTATGATATAAATTCTTCTTAAGAAGTGTGTGAGATGAGAGTGTCTC 60

QY 115 TATACCATTTCTCTGGCAAGAGCAGAGAACTCAATGCCCGCATGTAGTTCATC 174
Db 61 TATACCATTTCTCTGGCAAGAGCAGAGAACTCAATGCCCGCATGTAGTTCATC 120
QY 175 AATGTCAGAAAGGGGAGCAGATCTATGTTTATTCAGCTGTGTACAGAAATGAGCT 234
Db 121 AATGTCAGAAAGGGGAGCAGATCTATGTTTATTCAGCTGTGTACAGAAATGAGCT 180
QY 235 GGGGCAATTCGGGCTGGCAGTGTATGTTATGTTACCAAGATGAGATGGAAATTTGGGT 294
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QY 295 TATTTCCCGCAACTTGGTTAGAGAGCAACGAGTGTACAGAGGCCCAAGAGATT 354
Db 241 TATTTCCCGCAACTTGGTTAGAGAGCAACGAGTGTACAGAGGCCCAAGAGATT 300
QY 355 CCAACCAAGGATATGACTTCTCTGTGAA 384
Db 301 CCAACCAAGGATATGACTTCTCTGTGAA 330

RESULT 12
BD010817 330 bp DNA linear PAT 31-JAN-2002
LOCUS BD010817
DEFINITION Novel polypeptide and DNA thereof.
ACCESSION BD010817.1 GI:18639190
VERSION JP 2001069994-A/18.
KEYWORDS Mus sp.
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 330)
AUTHORS Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
Yoshimura, K. and Tanaka, H.
TITLE Novel polypeptide and DNA thereof
JOURNAL Patent: JP 2001069994-A 18 21-MAR-2001;
TAKEDA CHEMICAL INDUSTRIES LTD
OS Mus sp. (mouse)
PN JP 2001069994-A/18
PD 21-MAR-2001
PF 29-JUN-2000 JP 2000195911
PR

COMMENT

PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI
SHINICHI MOGI,
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/09, A61K38/00, A61K45/00, A61P19/00, A61P19/02, PC
A61P19/08,
PC C07K14/47, C07K16/18, C12N1/22, C12N5/10, G01N33/15, G01N33/50, PC
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PC C12P21/08, C12N15/00, A61K37/02, C12N5/00
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FH Key Location/Qualifiers
FT /organism="Mus sp. (mouse)"

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BASE COUNT 91 a 60 c 92 g 87 t
ORIGIN

Query Match 76.8%; Score 294.8; DB 6; Length 330;
Best Local Similarity 93.3%; Pred. No. 2.6e-78;
Matches 308; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 55 CATGCGATGTTATGATATAAATTCTTCTTAAGAAGTGTGTGAGATGAGAGTGTCTC 114
Db 1 CATGCGATGTTATGATATAAATTCTTCTTAAGAAGTGTGTGAGATGAGAGTGTCTC 60
QY 115 TATACCATTTCTCTGGCAAGAGCAGAGAACTCAATGCCCGCATGTAGTTCATC 174

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Db      61 TATACATTTCTCTGGCAAGAGACAGAAAGTTTCATGCCCCAGACTGTAGTTCATC 120
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Qy      235 GGGGCAATCTGGGCTGGCAGTGTATGTTATGTTACACACAGATGAGATGGAAATTTGGCT 294
Db      181 GGAGAGTTTGGGCTGGCAGTGTATGTTATGTTACACACAGATGAGATGGAAATTTAGCT 240
Qy      295 TATTTCCCAAGCAACTTGTGTAGAGCAACAGATGACAGAGGCCCAAGAGAGAT 354
Db      241 TATTTCCCAAGCAACTTGTGTAGAGCAACAGATGACAGAGGCCCAAGAGAGATC 300
Qy      355 CCAACCAAGGATATTGACTTCTTCTGTGAA 384
Db      301 CCAACCAAGGATATTGACTTCTTCTGTGAA 330

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RESULT 13
BD093118 330 bp DNA linear PAT 27-ANG-2002

LOCUS BD093118 Novel polypeptide and its DNA.
DEFINITION BD093118
ACCESSION BD093118.1 GI:22638706
VERSION MO 0102564-A/18.
KEYWORDS Mus sp.
SOURCE Mus sp.
ORGANISM Mus sp.

REFERENCE 1 (bases 1 to 330)
AUTHORS Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y.,
Yoshimura,K. and Tanaka,H.
TITLE Novel polypeptide and its DNA
JOURNAL Patent: WO 0102564-A 18 11-JAN-2001;
TAKEDA CHEMICAL INDUSTRIES LTD,YASUAKI ITO,KAZUNORI NISHI,KAZUHIRO
OGI,SHOICHI OKUBO,SHINICHI MOGI,YUKO NOGUCHI,KOJI YOSHIMURA,
HIDEYUKI TANAKA

COMMENT OS Mus sp. (mouse)
PN MO 0102564-A/18
PD 11-JAN-2001
PF 29-JUN-2000 WO 2000JP004278
PR 30-JUN-1999 JP 99P 186718
PI YASUAKI ITO,KAZUNORI NISHI,KAZUHIRO OGI,SHOICHI OKUBO,SHINICHI

PI MOGI,
PI YUKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA
PC C12N15/12,C12N5/10,C07K14/47,C07K16/18,A61K45/00,PC
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PC A61K39/395,A61K49/16,A61P19/02,A61P19/08,A61K31/7088//C12P21/
PC 02,C12R1:19)
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FH Key Location/Qualifiers.
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BASE COUNT 91 a 60 c 92 g 87 t
ORIGIN

Query Match 76.8%; Score 294.8; DB 6; Length 330;
Best Local Similarity 93.3%; Pred. No. 2.6e-78;
Matches 308; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Qy 55 CATGCACTGTTATGATTAACCTTTCTTCTAGAGAGTTGTGCAGATGAGAGTGTGC 114
Db 1 CATGCTATTTATTAAGTAACCTTTCTTCTAGAGAGTTGTGTGCAGATGAGAGTGTGC 60
Qy 115 TATACCACTTTCTGTGGCAAGACACAGAAAGATCAATGCCCCGAGCTAGATTCATC 174
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DEFINITION BD010830 Novel polypeptide and DNA thereof.
ACCESSION BD010830
VERSION BD010830.1 GI:18639203
KEYWORDS JP 2001069994-A/31.
SOURCE Rattus sp.
ORGANISM Rattus sp.

REFERENCE 1 (bases 1 to 307)
AUTHORS Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y.,
Yoshimura,K. and Tanaka,H.
TITLE Novel polypeptide and DNA thereof
JOURNAL Patent: JP 2001069994-A 31 21-MAR-2001;
TAKEDA CHEMICAL INDUSTRIES LTD

COMMENT OS Rattus sp. (rat)
PN JP 2001069994-A/31
PD 21-MAR-2001
PF 29-JUN-2000 JP 2000195911
PR

PI YASUAKI ITO,KAZUNORI NISHI,KAZUHIRO OGI,SHOICHI OKUBO,PI
SHINICHI MOGI,
PI YUKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA
PC C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P9/00,A61P19/02,PC
A61P19/08,
PC C07K14/47,C07K16/18,C12N1/21,C12N5/10,G01N33/15,G01N33/50,PC
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Matches 301; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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DB 301 GGAGAT 306

RESULT 15
BD093131
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DEFINITION Novel polypeptide and its DNA.
ACCESSION BD093131.1 GI:22638719
VERSION WO 0102564-A/31.
KEYWORDS Rattus sp.
SOURCE Rattus sp.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 307)
Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
Yoshimura, K. and Tanaka, H.
Novel polypeptide and its DNA
Patent: WO 0102564-A 31.11-JAN-2001;
TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO
OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,
HIDEYUKI TANAKA
OS Rattus sp. (rat)
PN WO 0102564-A/31
PD 11-JUN-2001
PF 29-JUN-2000 WO 2000JP004278
PR 30-JUN-1999 JP 99P 186718
PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI
MOGI.
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
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Query Match 74.9%; Score 287.6; DB 6; Length 307;
Best Local Similarity 98.4%; Pred. No. 4, 1e-76;
Matches 301; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 49 GCCGGGCGATGGCGATGTTAGATTAACCTTCTTCTAAGAAAGTTGTGCGAGATGAGAG 108
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QY 109 TGTGCTTATACATTTCTCTGGCAAGACACAGAAAGATCAATGCCCCGACTGTAGG 168
DB 61 TGTGCTTATACATTTCTCTGGCAAGACACAGAAAGATCAATGCCCCGACTGTAGG 120
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QY 229 GGAGCTGGGGCAATTCCTGGCTGGCAGTGTATGATGACACAGATGAGATGGGAAT 288
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QY 289 GTGGGTTATTTCCCGACCACTTGTGTTAGAGAGCAAGATGTAACAGGA-GGCCACCA 347
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Search completed: December 30, 2003, 04:08:00
Job time : 1217 secs

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/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (p) day 5; 72 from p6; 60 from p7; 46 from p8; 18 from p9; 20 from p10; 14 from p12 and 24 from p13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the modiolus. epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211; Stratagene) and Uni-Zap XR Gigaapak III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly, 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5'-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigaapak III Gold and upon titration on XL1 Blue MR⁺ cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's Exassist interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAAACAGTATACAC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in Genbank and have know function; 23% have hits in Genbank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT
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| Query Match | 89.6% | Score 344; | DB 13; | Length 398; |
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| Matches 359; | Conservative 0; | Mismatches 25; | Indels 0; | Gaps 0 |

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| Qy | 181 | AAGAAAGGCGACAGATCTTATGTTTATTCGAACGTGTACAGAAATGAGCTGGGCGCA | 240 |
| Db | 193 | AAGAAAGGCGACAGATCTTATGTTTATTCGAAGTGTACAGAAACGAGCTGGAGAG | 252 |
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| LOCUS | BO564607 | | | | |
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| ACCESSION | BO564607 | | | | |
| VERSION | BO564607.1 | GI:21467924 | | | |
| KEYWORDS | EST. | | | | |
| SOURCE | Mus musculus (house mouse) | | | | |
| ORGANISM | Mus musculus | | | | |
| | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | | |
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FEATURES
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epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro FastTrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on X1 Blue MRF⁺ cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's Exassist interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAAACGCTACGAC) and 25x strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in Genbank and have known function; 23% have hits in Genbank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT
ORIGIN

143 a 83 c 135 g 127 t

Query Match 89.6%; Score 344; DB 13; Length 488;
Best Local Similarity 93.5%; Pred. No. 2.5e-95;

Matches 359; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1 ATGGCAAGATTTATTTGCTTGGGGCCCTTGCGCTCTGCGCGGCGATGCG 60
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DB 367 ACCGATTTGACTTCTTCTGTGAA 390

RESULT 3
B0568498
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE

JOURNAL
COMMENT

FEATURES
source

1. 514 bp mRNA linear EST 19-JUN-2002
g1109c02.y1 Mouse Organ of Corti cDNA plibuescript Mus musculus cDNA
clone g1109c02 5', mRNA sequence.
B0568498
B0568498.1 GI:21471815
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 514)
EST analysis of gene expression in the mouse Organ of Corti at the
onset of hearing
Unpublished
Contact: Kachar, B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: Kachar@nidcd.nih.gov
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Location/Qualifiers

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organ of Corti (OC) was fine dissected from a total of 386
OC as follows: 102 samples from post-natal (P) day 5, 72
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
14 from P12 and 24 from P13. After killing animals by
cervical dislocation followed by decapitation, the bulla
was removed and opened in Leibowitz medium. The bony
capsule of the cochlea was clipped away, serial vascularis
and spiral ligament were removed and the sensory
epithelium was carefully dissected out of the modiolus.
Total RNA was extracted using the micro FastTrack kit
(catalog # K1593-02; Invitrogen, Carlsbad, CA), according
to manufacturer's instructions. Reverse transcription and
library construction were carried out with the Uni-Zap XR
vector kit (catalog # 237211, Stratagene) and Uni-Zap XR
Gigapack III Gold Cloning kit (catalog # 237612), both
from Stratagene (La Jolla, CA, USA), according to
manufacturer's instructions. Briefly: 1.5 ug mRNA was
reverse transcribed using a hybrid oligo(dT) linker-primer
that contains an Xho I site. First strand synthesis was
primed with the linker-primer and transcribed using
Moloney murine leukemia virus reverse transcriptase
(MMLV-RT) and 5-methyl dCTP. The second strand was
synthesized with DNA polymerase and RNase H. Complementary
DNA was blunt ended with Pfu DNA polymerase, ligated with
EcoR I adapters in the presence of ligase and digested
with Xho I. The cDNA was sequentially size fractionated

over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XL1 Blue MRF⁺ cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's EXassist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert6(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACGCTATGACC) and 25% strength M13 dye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Watham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified.

BASE COUNT
ORIGIN

147 a 85 c 143 g 139 t

Query Match 89.6%; Score 344; DB 13; Length 514;
Best Local Similarity 93.5%; Pred. No. 2.6e-95;
Matches 359; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1 ATGGCAGCAATATGATCTTTGCTGGGGGCTTGTGCTCTGTCGCGGATGAC 60
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DB 365 ACGGATATGAGCTTCTCTGTGAA 388

RESULT 4
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DEFINITION gi11d01.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA
ACCESSION BO564134
VERSION BO564134.1 GI:21467451
KEYWORDS EST.

SOURCE
ORGANISM Mus musculus (house mouse)

REFERENCE
AUTHORS Kachar, B.
TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
JOURNAL Unpublished

COMMENT

Contract: Kachar B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765

FEATURES
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Email: kacharbenidcd.nih.gov
Plate: 11 row: d column: 01
Seq primer: M13Rpl reverse primer (ABI).
Location/Qualifiers

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/clone_id="Mouse Organ of Corti cDNA pBluescript"

/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Lebowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus.

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Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dt) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker primer and transcribed using

Moloney murine leukemia virus reverse transcriptase (MMuLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested

with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with

EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XL1 Blue MRF⁺ cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's EXassist Interference resistance helper phage (catalogue # 211203) was adopted

to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert6(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from

the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACGCTATGACC) and 25%

universal M13 reverse primer (CAGGAACGCTATGACC) and 25%

strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT

155 a 87 c 148 g 144 t

ORIGIN

Query Match 89.6%; Score 344; DB 13; Length 534;
Best Local Similarity 93.5%; Pred. No. 2.7e-95;
Matches 359; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

1 ATGCGAAGATATGATCTTTGCTTGGGGGCTTGTGCTCTGTGCGGCGATGGC 60
3 ATGCGAAGATATGATCTTTGCTTGGGGGCTTGTGCTCTGTGCGGCGATGGT 62
61 ATGTTATGATGATTAACCTTCTCTAAGAGTTGTGCGAGATGAGTGTCTATACC 120
63 GATTTATGATGATTAACCTTCTCTAAGAGTTGTGCGAGATGAGTGTCTATACC 122
121 ATTTCTGCGAAGACAGACAGAGAGTCAATGCGGAGCTGTAGTTCATGATGTC 180
123 ATTTCTGCGAAGACAGACAGAGAGTCAATGCGGAGCTGTAGTTCATGATGTC 182
181 AAGAAAGGCGACAGATCTATGTTTATTCAGCTGTGTAAGAAATGAGAGCTGGGCA 240
183 AAGAAAGGCGACAGATCTATGTTTATTCAGCTGTGTAAGAAATGAGAGCTGGAGAG 242
241 TTCTGGCGCTGAGCTGTTTATGATGACCAAGATGATGAGGATGTTGGTATATTC 300
243 TTTTGGCGCTGAGCTGTTTATGATGACCAAGATGATGAGGATGTTGGTATATTC 302
301 CCAGCACTTGTGATAGAGACAGAGTGTACAGAGAGCCACCAAGAGATTCACACC 360
303 CCAGCACTTGTGATAGAGACAGAGTGTACAGAGAGCCACCAAGAGATTCACACC 362
361 ACGGATATGACTTCTTCTGTGAA 384
363 ACGGATATGACTTCTTCTGTGAA 386

RESULT 5 560 bp mRNA linear EST 19-JUN-2002
B0569741
LOCUS g1135f01.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA
DEFINITION
Accession B0569741 GI:21473058
VERSION B0569741
KEYWORDS
SOURCE EST.
ORGANISM Mus musculus (house mouse)
MUS musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 560)
Kachar.B.
EST analysis of gene expression in the mouse Organ of Corti at the
onset of hearing
Unpublished
Contact: Kachar.B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-6027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: kachar@nidcd.nih.gov
Plate: 135 row: f column: 01
Seq primer: M13RPI reverse primer (ABI).

FEATURES

source

Location/Qualifiers

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/organism="Mus musculus"
/mol_type="mRNA"
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/db_xref="taxon:10090"
/clone="g1135f01"
/sex="male and female"
/dev_stage="postnatal day 5 to 13"
/clone_1ib="Mouse Organ of Corti cDNA pBluescript"
/note="Organ: Organ of Corti. Vector: pBluescript. The
OC as follows: 102 samples from post-natal (P) day 5; 72
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
14 from P12 and 24 from P13. After killing animals by
cervical dislocation followed by decapitation, the bulla
was removed and opened in Leibovitz medium. The bony
capsule of the cochlea was clipped away, stria vascularis
and spiral ligament were removed and the sensory
epithelium was carefully dissected out of the modiolus.
Total RNA was extracted using the micro Fasttrack kit
(catalog # K1593-02, Invitrogen, Carlsbad, CA), according
to manufacturer's instructions. Reverse transcription and
library construction were carried out with the Uni-Zap XR
vector kit (catalog # 237211, Stratagene) and Uni-Zap XR
Gigapack III Gold Cloning kit (catalog # 237612), both
from Stratagene (La Jolla, CA, USA), according to
manufacturer's instructions. Briefly: 1.5 ug mRNA was
reverse transcribed using a hybrid oligo(dT) linker-primer
that contains an Xho I site. First strand synthesis was
primed with the linker-primer and transcribed using
Moloney murine leukemia virus reverse transcriptase
(MMLV-RT) and 5-methyl dCTP. The second strand was
synthesized with DNA polymerase and RNase H. Complementary
DNA was blunt ended with Pfu DNA polymerase, ligated with
EcoR I adapters in the presence of ligase and digested
with Xho I. The cDNA was sequentially size fractionated
over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden)
and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA)
columns to enrich for cDNAs greater than 400bp and 1000 bp
columns. The cDNA was then directionally ligated to
the Uni-Zap XR vector, which had been pre-digested with
EcoR I and Xho I. The phagemid was packaged with Gigapack
III Gold and, upon titration on XLI Blue MRF⁺ cells, the
yield of the phage library was estimated to be 11,100,000
recombinants. Stratagene's Exsist Interference
resistance helper phage (catalogue # 211203) was adopted
to rescue plasmid DNA from the phages. Upon plating of the
rescued library, individual cDNA clones were selected and
grown in 96-well, 2 ml growth plate. Plasmid DNA was
purified from 200 ul of saturated culture with the
Concert96(TM) plasmid purification kit (Invitrogen,
Carlsbad, CA) as instructed by the manufacturer. ESTs from
the 5' end of the cDNA clones were generated with the
universal M13 reverse primer (CACGACACGCTAGACC) and 25
strength BigDye terminator sequencing chemistry (Applied
Biosystems, Foster City, CA). Sequencing reactions were
performed on MJ Tetrad thermal cyclers (MJ Research,
Waltham, MA), and analyzed on 3700 automated capillary
sequencers using POPs polymer (Applied Biosystems, Foster
City, CA). The frequency distribution of the library is
as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10;
1.4% 11-50 and 0.1% 51-150. As to gene function, 23%
genes are present in GenBank and have known function; 23%
have hits in GenBank, but do not have assigned function;
12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT

160 a 92 c 154 g 153 t

ORIGIN

Query Match 89.6%; Score 344; DB 13; Length 560;
Best Local Similarity 93.5%; Pred. No. 2.8e-95;
Matches 359; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1 ATGGCAAGATATGATCTTTGCTGGGGGCTTGTGCTCTGTGCGGCGATGCG 60
 DB 6 ATGGCAAGATATGATCTTTGCTGGGGGCTTGTGCTCTGTGCGGCGATGCG 65
 QY 61 ATGTTATGATTAACCTTCTTCTAAGAAAGTTGTGTGAGATGAGAGTGTCTATACC 120
 DB 66 GATTTATGATTAACCTTCTTCTAAGAAAGTTGTGTGAGATGAGAGTGTCTATACC 125
 QY 121 ATTTCTCTGGCAAGACACAGAAAGCTCAATGCCCGGAGTGTAGTTCAATGTC 180
 DB 126 ATTTCTCTGGCAAGACACAGAAAGTTCAATGCCCGGAGTGTAGTTCAATGTC 185
 QY 181 AAGAAAGGCGACAGATCTATGTTTATGCAAGCTGTGTACAGAAATGAGCTGGGCA 240
 DB 186 AAGAAAGGCGACAGATCTATGTTTATGCAAGCTGTGTACAGAAATGAGCTGGGCA 245
 QY 241 TTCTGGGCTGGCAGTCTTATGCTGACACACAGATGAGATGGAATGTGGGTTATTC 300
 DB 246 TTTTGGGCTGGCAGTCTTATGCTGACACACAGATGAGATGGAATGTGGGTTATTC 305
 QY 301 CCCAGCACTGTGTGTAAGACAGACAGTGTACAGAGAGCCACCAAGAGATTCACACC 360
 DB 306 CCCAGCACTGTGTGTAAGACAGACAGTGTATACAGAGAGCCACCAAGAGATTCACACC 365
 QY 361 ACGGATATGACTCTTCTCTGTGAA 384
 DB 366 ACGGATATGACTCTTCTCTGTGAA 389

RESULT 6
 BQ564944
 LOCUS
 DEFINITION
 608 bp mRNA linear EST 19-JUN-2002
 g127909.y1 Mouse Organ of Corti cDNA Bluescript Mus musculus cDNA
 clone g127909 5', mRNA sequence.

ACCESSION
 BQ564944
 VERSION
 BQ564944.1 GI:21468261
 KEYWORDS
 EST.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 1 (bases 1 to 608)
 EST analysis of gene expression in the mouse Organ of Corti at the
 onset of hearing

JOURNAL
 Unpublished

COMMENT
 Contact: Kachar, B.
 Structural Cell Biology
 National Institute of Deafness and other Communication Disorders
 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
 Tel: 301-402-1599
 Fax: 301-402-1765
 Email: kachar@nidcd.nih.gov
 Plate: 27 row: 9 column: 09
 Seq primer: M13RPI reverse primer (ABI).
 Location/Qualifiers

FEATURES
 Source
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 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="BALB/c"
 /db_xref="taxon:10090"
 /clone="g127909"
 /sex="male and female"
 /dev_stage="Post natal day 5 to 13"
 /clone_lib="Postnatal Organ of Corti cDNA Bluescript"
 /note="Organ: Organ of Corti; Vector: pBluescript; The
 Organ of Corti (OC) was fine dissected from a total of 386
 OC as follows: 102 samples from post-natal (P) day 5; 72
 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
 14 from P12 and 24 from P13. After killing animals by
 cervical dislocation followed by decapitation, the bulla
 was removed and opened in Leibowitz medium. The bony
 capsule of the cochlea was chipped away, stria vascularis

BASE COUNT
 169 a 107 c 166 g 166 t

Query Match 89.6%; Score 344; DB 13; Length 608;
 Best Local Similarity 93.5%; Pred. No. 2.9e-95;
 Matches 359; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1 ATGGCAAGATATGATCTTTGCTGGGGGCTTGTGCTCTGTGCGGCGATGCG 60
 DB 13 ATGGCAAGATATGATCTTTGCTGGGGGCTTGTGCTCTGTGCGGCGATGCG 72
 QY 61 ATGTTATGATTAACCTTCTTCTAAGAAAGTTGTGTGAGATGAGAGTGTCTATACC 120
 DB 73 GATTTATGATTAACCTTCTTCTAAGAAAGTTGTGTGAGATGAGAGTGTCTATACC 132
 QY 121 ATTTCTCTGGCAAGACACAGAAAGCTCAATGCCCGGAGTGTAGTTCAATGTC 180
 DB 133 ATTTCTCTGGCAAGACACAGAAAGTTCAATGCCCGGAGTGTAGTTCAATGTC 192
 QY 181 AAGAAAGGCGACAGATCTATGTTTATGCAAGCTGTGTACAGAAATGAGCTGGGCA 240
 DB 193 AAGAAAGGCGACAGATCTATGTTTATGCAAGCTGTGTACAGAAATGAGCTGGGCA 252
 QY 241 TTCTGGGCTGGCAGTCTTATGCTGACACACAGATGAGATGGAATGTGGGTTATTC 300

and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro FastTrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR vector kit (catalog # 237612), both according to manufacturer's instructions. Briefly: 1.5 ug RNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XL1 Blue MRF⁺ cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's Exsist interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAAACAGCTATGACC) and 254 strong hairpin terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

Db 253 TTTTGGCTGGACAGTGTATTATGTGACCAACGAGATGATGGATTTGATGTTATTC 312

QY 301 CCCGACCACTGGTTAGAGCAACGAGTACCAAGGAGCCACCAAGAGATTCACACC 360

Db 313 CCCAGCACTTGGTGAAGAGCAGCTGTATATACAGAGAGGCCACCAAGAGATCCCAACC 372

QY 361 ACGGATATTGACTTCTTCTGTGAA 384

Db 373 ACGGATATTGACTTCTTCTGTGAA 396

RESULT 7
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LOCUS B0568471
DEFINITION g1108904.Y1 Mouse Organ of Corti cDNA pluscript Mus musculus cDNA
clone g1108904 5', mRNA sequence.
ACCESSION B0568471
VERSION B0568471.1 GI:21471788
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Kachar, B.
1 (bases 1 to 630)
EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
Unpublished
Contact: Kachar, B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: kacharbenidcd.nih.gov
Plate: 108 row: 9 column: 04
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
1. 630
/organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
/db_xref="taxon:10090"
/clone="g1108904"
/sex="male and female"
/dev_stage="Post natal day 5 to 13"
/clone_1db="Mouse Organ of Corti cDNA pluscript". The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR GigaPack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMuV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested

with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been preligated with EcoR I and Xho I. The phagemid was packaged with GigaPack III Gold and, upon titration on XL1 Blue MRF⁺ cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExSist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAAGGAAACAGTATGAC) and 25⁺ strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 178 a 111 c 167 g 174 t
ORIGIN
Query Match 89.6%; Score 344; DB 13; Length 630;
Best Local Similarity 93.5%; Pred. No. 3e-95;
Matches 359; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
QY 1 ATGGCAAGATATGATTTCTTTCTGGGCGCTTGTGCTCTCTGCGCGGCATGGC 60
Db 13 ATGGCAAGATATGATTTCTTTCTGGGCGCTTGTGCTCTCTGCGCGGCATGGT 72
QY 61 ATGTTATGATTAACCTTCTTAAAGATGTGTGACATGAGATGTCTATACC 120
Db 73 GATTTATGATTAACCTTCTTAAAGATGTGTGACATGAGATGTCTATACT 132
QY 121 ATTTCTGCGAAGACACAGAAAGTCAATGCGCCGAGCTGAGTTCATCATGTC 180
Db 133 ATTTCTGCGAAGACACAGAAAGTCAATGCGCCGAGCTGAGTTCATCATGTC 192
QY 181 AAGAAAGGCGACAGATCTATGTTTATTCAGCTGTAAAGAAATGAGCTGGGCA 240
Db 193 AAGAAAGGCGACAGATCTATGTTTATTCAGCTGTAAAGAAATGAGCTGGGAG 252
QY 241 TTTGGGCTGGACAGTGTATTATGTATGACCAAGATGAGTGGGATTTATTC 300
Db 253 TTTGGGCTGGACAGTGTATTATGTATGACCAAGATGAGTGGGATTTATTTTC 312
QY 301 CCCACCACTGGTTAGAGCAACGAGTACCAAGGAGCCACCAAGAGATTCACACC 360
Db 313 CCCAGCACTTGGTGAAGAGCAGCTGTATATACAGAGAGGCCACCAAGAGATCCCAACC 372
QY 361 ACGGATATTGACTTCTTCTGTGAA 384
Db 373 ACGGATATTGACTTCTTCTGTGAA 396
RESULT 8
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LOCUS BB611549
DEFINITION BB611549 RIKEN full-length enriched, 13 days embryo head Mus musculus cDNA clone 311008J012 5', mRNA sequence.
ACCESSION BB611549
VERSION BB611549.1 GI:15393547

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10

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/clone_1lb="Mouse Organ of Corti cDNA pluescript"
 /note="Organ: Organ of Corti; Vector: pluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the modiolus epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR vector kit (catalog # 237612), both according to from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMuLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adaptors in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on X11 Blue MRF⁺ cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concerted (TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAAACGCTATGACC) and 25x strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in Genbank and have known function; 23% have hits in Genbank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT
 ORIGIN

Query Match 89.2%; Score 342.4; DB 13; Length 474;
 Best Local Similarity 93.2%; Pred. No. 7.8e-95;
 Matches 358; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

1 ATGGCAAGATATGATCTTTGCTGGGGCCCTTGTGCTCTCTGCGCGGCATGCG 60
 14 ATGGCAAGATATGATCTTTGCTGGGGCCCTTGTGCTCTCTGCGCGGCATGCG 73
 61 ATGTTATGATTAACCTTTCTTAAAGAGTTGTGTGAGATGAGAGTGTCTATACC 120
 74 GATTTTATGATTAACCTTTCTTAAAGAGTTGTGTGAGATGAGAGTGTCTATACC 133
 121 ATTCTCTGGCAAGACAGAGACTATGCGCCGCACTGTAGTTCATCAATGTC 180

Db 134 ATTTCTCTGGCAAGACAGAGACTATGCGCCGCACTGTAGTTCATCAATGTC 193
 Oy 181 AAGAAAGGCGAGAGATCTATGTTTATTCAGAGCTGGTAACAGAAATGAGAGTGGGCA 240
 Db 194 AAGAAAGGCGAGAGATCTATGTTTATTCAGAGCTGGTAACAGAAATGAGAGTGGGCA 253
 Oy 241 TTCTGGGCTGGCGAGTGTATATGCTGACACACAGAGATGAGTGGAAATTTGGGTTATTC 300
 Db 254 TTTTGGGCTGGCGAGTGTATATGCTGACACACAGAGATGAGTGGAAATTTGGGTTATTC 313
 Oy 301 CCCGCAACTTGTGTTAGAGAGCAACGAGTATACAGAGCCCAAGAGATTCACACC 360
 Db 314 CCCGCAACTTGTGTTAGAGAGCAACGAGTATACAGAGCCCAAGAGATTCACACC 373
 Oy 361 ACGGATATGACTTCTTCTGTGAA 384
 Db 374 ACGGATATGACTTCTTCTGTGAA 397

RESULT 10
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 LOCUS B0563768
 DEFINITION clone gi06c09.5, mRNA sequence.

ACCESSION B0563768
 VERSION B0563768.1 GI:21466749
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE
 AUTHORS Kachar,B.
 TITLE 1 (bases 1 to 684)
 JOURNAL
 COMMENT
 Unpublished
 Contact: Kachar,B.
 Structural Cell Biology
 National Institute of Deafness and other Communication Disorders
 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
 Tel: 301-402-1599
 Fax: 301-402-1765
 Email: kachar@nidcd.nih.gov
 Plate: 06 row: c column: 09
 Seq primer: M13R1 reverse primer (ABI).
 Location/Qualifiers

FEATURES
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 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="BALB/c"
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 /clone="gi06c09"
 /sex="male and female"
 /dev_stage="post natal day 5 to 13"
 /note="Organ: Organ of Corti; Vector: pluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR vector kit (catalog # 237612), both according to from Stratagene (La Jolla, CA, USA), according to

manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XL1 Blue MRF⁺ cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stragene's Exasist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert 6(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAAACAGTATAC) and 25x strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in Genbank and have known function; 23% have hits in Genbank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 194 a 120 c 178 g 192 t

Query Match 89.2%; Score 342.4; DB 13; Length 684;
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Matches 358; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

1 ATGGCAAGATATATGATCTTTGCTGGGGCTTGAGGCTCTGTCGGCGGATGAGC 60
13 ATGGCAGGATATGATCTTTGCTGGGGCTTGAGGCTCTGTCGGCGGATGAGT 72
61 ATGTTATGATATATGATCTTTGCTGGGGCTTGAGGCTCTGTCGGCGGATGAGT 120
73 GATTTATGATATATGATCTTTGCTGGGGCTTGAGGCTCTGTCGGCGGATGAGT 132
121 ATTTCTCTGGCAAGACAGAGAACTATGCTGCGGAGCTGATGCTTCAATGTC 180
133 ATTTCTCTGGCAAGACAGAGAACTATGCTGCGGAGCTGATGCTTCAATGTC 192
181 AAGAAAGGCGACAGATCTATGTTATTCAGAGCTGTATACAGAAATGAGAGCTGGGCA 240
193 AAGAAAGGCGACAGATCTATGTTATTCAGAGCTGTATACAGAAATGAGAGCTGGGAG 252
241 TTCTGGCTGGCAAGTGTATGATGACCAACAGATGAGATGGAATGTTGGTATTTTC 300
253 TTTGGCTGGCAAGTGTATGATGACCAACAGATGAGATGGAATGTTGGTATTTTC 312
301 CCAGCAATTTGGTTAGAGACCAAGAGTTTCCAGAGGCCACCAAGAGATTCCAAAC 360
313 CCAGCAATTTGGTTAGAGACCAAGAGTTTCCAGAGGCCACCAAGAGATTCCAAAC 372
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373 ACGGATATGATCTTCTCTGTA 396

RESULT 11

LOCUS B0566932

DEFINITION

B0566932 409 bp mRNA linear EST 19-JUN-2002
g173909.y1 Mouse Organ of Corti cDNA bluescript Mus musculus cDNA
clone g173909 5', mRNA sequence.

ACCESSION

B0566932
B0566932.1 GI:21470249

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: kachar@nidcd.nih.gov
Plate: 73 row: g column: 09
Seq primer: M13RP1 reverse primer (AB1).
Location/Qualifiers

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/clone="g173909"

/sex="male and female"

/dev_stage="post natal day 5 to 13"

/clone_id="Mouse Organ of Corti cDNA bluescript"

/note="Organ: Organ of Corti; Vector: bluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (p) day 5; 72 from p6; 60 from p7; 46 from p8; 18 from p9; 20 from p10; 14 from p12 and 24 from p13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Lebowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fastrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stragene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stragene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XL1 Blue MRF⁺ cells, the yield of the phage library was estimated to be 11,100,000

recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 µl of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAAACAGCTATGACC) and 25X strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 102 a 75 c 121 g 111 t

Query Match 85.4%; Score 327.8; DB 13; Length 409;

Best Local Similarity 92.7%; Pred. No. 2.4e-90;

Matches 355; Conservative 0; Mismatches 27; Indels 1; Gaps 1;

1 ATGGCAGAAATATGATCTTTGCTGGGGGCTTGTGCTCTGTGCGGGGATGAC 60
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 61 ATGTTTATGATTAATCTTTCTTAAGAAGTTGTGTC-AGATAGAGAGTGTCTTATAC 119
 87 GTATTATAGATAAATCTTTCTTAAGAAGTTGTGTCAGATAGAGAGTGTCTTATAC 146
 120 CATTTCTGTGCAAGAGCAGAGAAAGTAACTAATGCCCCGAGCTAGGTTCAATCATGT 179
 147 TATTTCTGTGCAAGAGCAGAGAAAGTAAATGCCCCGAGCTAGGTTCAATCATGT 206
 180 CAGAAGAGGAGCAGAGATCTATGTTTATTCAGAGCTGTATACAGAAATGAGCTGGGCG 239
 207 CAGAAGAGGAGCAGAGATCTATGTTTATTCAGAGCTGTATACAGAAATGAGCTGGGCG 266
 240 ATTCTGGGCTGCGAGTGTATATGTTGACACACAGAGATGAGATGGAATGTGGTTATTT 299
 267 GTTTTGGGCTGCGAGTGTATATGTTGACACACAGAGATGAGATGGAATGTGGTTATTT 326
 300 CCCCAGCACTGGTTAGAGCAAGAGTGTACAGAGAGCCCAAGAGAGATTCACAC 359
 327 CCCCAGCACTGGTTAGAGCAAGAGTGTATACAGAGAGCCCAAGAGAGATTCACAC 386
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 387 CACGAGATATGACTTCTTCTGTG 409

RESULT 12
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 LOCUS g137b12.1 Mouse Organ of Corti cDNA pluescript Mus musculus cDNA
 DEFINITION g137b12.1 5', mRNA sequence.
 ACCESSION B0565411
 VERSION B0565411.1 GI:21468728
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 490)
 AUTHORS Kachar,B.
 TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing

JOURNAL COMMENT

Unpublished
 Contact: Kachar,B.
 Structural Cell Biology
 National Institute of Deafness and other Communication Disorders
 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
 Tel: 301-402-1599
 Fax: 301-402-1765
 Email: KacharB@nidcd.nih.gov
 Plate: 37 row b column: 12
 Seq primer: M13R1 reverse primer (AB1).
 Location/Qualifiers

FEATURES

source

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 /organism="Mus musculus"
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 /db_xref="taxon:10090"
 /clone="g137b12"
 /sex="male and female"
 /dev_stage="Post natal day 5 to 13"
 /clone_11b="Mouse Organ of Corti cDNA pluescript"
 /note="Organ of Corti; Vector: pluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (p) day 5; 72 from p6; 60 from p7; 46 from p8; 18 from p9; 20 from p10; 14 from p12 and 24 from p13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR GigaPack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 µg mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with GigaPack III Gold and, upon titration on XL1 Blue MRF⁻ cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 µl of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAAACAGCTATGACC) and 25X strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of

Genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 191 a 77 c 109 g 112 t 1 others

Query Match 81.4%; Score 312.6; DB 13; Length 490;
Best Local Similarity 88.5%; Pred. No. 1.3e-85;
Matches 339; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 2 TGGCAGAAATGATTTCTTTGCTTGGGGGCTTGTGGCTCTGTGCGGGCATGCA 61
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QY 62 TGTATATGATTAACCTTTCTTCTAGAGTTGTGTCAGATAGAGTGTGTATACCA 121
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QY 122 TTTCTCTGGCAGAGACAGAAAGCTACATGATGCTGTAGTTCATCATGTCA 181
DB TTTCTCTGGCAGAGACAGAAATTTACATGCCCCCAACTGTGTTTCATCATGTCA 267
QY 182 AGAAAGGAGCAGATCTATGTTTATTCAGCTGTAAACAGAAATGAGCTGGGAGT 241
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QY 362 CGGATATGACTTCTTCTGTGAA 384
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RESULT 13 365 bp mRNA linear EST 10-DEC-2002
BY232622 RIKEN full-length enriched, adult inner ear Mus musculus
CDNA clone F930026J20 5', mRNA sequence.

ACCESSION BY232622
VERSION BY232622.1 GI:26413732
KEYWORDS EST
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 365)
AUTHORS Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Oosato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schombach, C., Gojibori, T., Baldarelli, R., Hill, D. P., Bull, C., Hume, D. A., Quackenbush, J., Schiraldi, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Brad, D., Brust, V., Chochia, C., Corbani, L. E., Cousins, S., Dalia, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Fraser, K. S., Gasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustavich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawai, H., Kawasawa, Y., Kedzielski, R. M., King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Pereira, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wymshaw-Boris, A., Yamada, M., Yang, I., Yang, L., Yuan, Z., Zavalan, M., Zhu, Y., Zimmer, A., Carmine, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura

TITLE
JOURNAL MEDLINE
PUBMED
Contact: Yoshinori Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Saitama-cho, Tsukuba-shi, Ibaraki, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.go.jp,
url: http://genome.res.riken.go.jp/
Aizawa, K., Akimura, T., Arakawa, T., Carmine, P., Fukuda, S., Hirozane
, T., Imoto, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A.,
Murata, M., Nakamura, M., Nomura, K., Numata, R., Ohno, M., Sakai, K.,
Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shizaki, T., Tagami,
M., Waki, K., Watanabe, A., Muramatsu, M. and Hayashizaki, Y. Direct
Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multipipillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Tissues were provided by Kirk W. Beisel (Boys Town National
Research Hospital 555 North 30th Street Omaha, NE 68131 USA) whose
assistance we gratefully acknowledge. Please visit our web site
(http://genome.res.riken.go.jp) for further details.
Location/Qualifiers

FEATURES

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Matches 317; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

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DB ATTTCTTGGCAGAGACAGAAAGCTACATGCCCCGAGCTGTAGTTCATCATGTGC 203

REFERENCE 1 (bases 1 to 280)
 AUTHORS Kachar, B.
 TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
 JOURNAL Unpublished
 COMMENT Contact: Kachar, B.
 Structural Cell Biology
 National Institute of Deafness and other Communication Disorders
 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
 Tel: 301-402-1599
 Fax: 301-402-1765
 Email: kacharb@nidcd.nih.gov
 Plate: 114 row: f column: 04
 Seq primer: M13P1 reverse primer (ABI).
 Location/Qualifiers

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 /note="Organ: Organ of Corti; Vector: pBluescript; The Organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack Kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's EXASist interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert36 (TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. Esrs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAAACAGCTTACAC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary

BASE COUNT 72 a 44 c 85 g 73 t
 ORIGIN

Query Match 60.6%; Score 232.8; DB 13; Length 280;
 Best Local Similarity 93.5%; Pred. No. 5e-61;
 Matches 243; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1 ATGGCAAGATATGATTTCTTTGCTGGGGGCTTGCGCTCTGTCGGCGGATGCG 60
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 QY 61 ATGTTATGATTAACCTTTCTTAAAGAGTGTGCGAGATGAGAGTGTCTATAC 120
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 Db 261 TTCTGGGCTGGCAGTGTGTTA 280

Search completed: December 30, 2003, 06:07:17
 Job time : 1279.36 secs

sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Run on:      December 29, 2003, 22:01:01 ; Search time 127.462 Seconds
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Perfect score: 384
Sequence: 1 atggcaagaatatgtatctt.....atatgacttcttctgtgaa 384
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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| Post-processing: | Minimum Match | 0% |
| | Maximum Match | 100% |
| | Listing first | 45 summaries |

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6: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
7: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
8: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
9: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
10: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
11: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
12: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
13: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
14: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
15: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
16: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
17: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.*
18: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
19: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
20: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
21: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*
25: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|----------|----------------------|
| 1 | 384 | 100.0 | 384 | 22 | AAFS9098 | Rat MLP nucleotide |
| 2 | 344 | 89.6 | 384 | 22 | AAFS9068 | Mouse MLP nucleotide |
| 3 | 344 | 89.6 | 947 | 22 | AAFS9084 | Mouse MLP nucleotide |
| 4 | 330 | 85.9 | 330 | 22 | AAFS9099 | Rat MLP nucleotide |
| 5 | 294.8 | 76.8 | 330 | 22 | AAFS9080 | Mouse MLP nucleotide |
| 6 | 287.6 | 74.9 | 307 | 22 | AAFS9933 | Rat MLP nucleotide |
| 7 | 285.4 | 74.3 | 384 | 22 | AAFS9665 | Human MLP nucleotide |
| 8 | 285.4 | 74.3 | 387 | 24 | AAST583 | DNA encoding novel |

| | | | | | | |
|----|-------|------|------|----|----------|---------------------|
| 9 | 285.4 | 74.3 | 426 | 22 | AAH26341 | Human growth regul |
| 10 | 285.4 | 74.3 | 521 | 24 | ABL95730 | Human angiogenesis |
| 11 | 285.4 | 74.3 | 521 | 24 | ABL88251 | Human PRO9873 cDNA |
| 12 | 285.4 | 74.3 | 521 | 24 | ABX33571 | cDNA encoding human |
| 13 | 285.4 | 74.3 | 891 | 22 | AAH98288 | Human EST-derived |
| 14 | 285.4 | 74.3 | 891 | 22 | AAH26342 | Human growth regul |
| 15 | 285.4 | 74.3 | 923 | 22 | AAE59083 | Human MLP nucleoti |
| 16 | 285.4 | 74.3 | 1201 | 22 | AAH26343 | Human growth regul |
| 17 | 261 | 68.0 | 261 | 22 | AAE59082 | Rat MLP nucleotide |
| 18 | 249 | 64.8 | 330 | 22 | AAE59079 | Human MLP nucleoti |
| 19 | 64 | 16.7 | 581 | 16 | AAO84052 | Sequence encoding |
| 20 | 63.4 | 16.5 | 433 | 22 | AAH47783 | Recombinant human |
| 21 | 63.4 | 16.5 | 459 | 16 | AAO84050 | Sequence encoding |
| 22 | 63.4 | 16.5 | 459 | 22 | AAI70083 | Melanoma inhibitor |
| 23 | 63.4 | 16.5 | 459 | 22 | AAH18732 | Human antisease ol |
| 24 | 63.4 | 16.5 | 555 | 23 | ABV95229 | Human prostate exp |
| 25 | 62.4 | 16.2 | 330 | 16 | AAO84061 | Sequence encoding |
| 26 | 61.6 | 16.1 | 442 | 24 | ABL63602 | Breast cancer rela |
| 27 | 61.8 | 16.1 | 442 | 24 | ABL64012 | Breast cancer rela |
| 28 | 57.4 | 14.9 | 305 | 16 | AAO84055 | Amplified fragment |
| 29 | 47.2 | 12.3 | 1060 | 22 | AAE92140 | Human PRO19670 cDN |
| 30 | 47.2 | 12.3 | 1060 | 24 | ABE74460 | Human cDNA encodin |
| 31 | 47.2 | 12.3 | 1060 | 24 | ABL95738 | Human angiogenesis |
| 32 | 47.2 | 12.3 | 1060 | 24 | ABL88249 | Human PRO19670 cDN |
| 33 | 47.2 | 12.3 | 1060 | 25 | ACA57963 | Human PRO19670 cDN |
| 34 | 47.2 | 12.3 | 1060 | 25 | ACA58892 | cDNA encoding human |
| 35 | 47.2 | 12.3 | 1060 | 25 | ACA60445 | Novel human secret |
| 36 | 47.2 | 12.3 | 1060 | 25 | ACA63455 | cDNA encoding huma |
| 37 | 47.2 | 12.3 | 1060 | 25 | ABX98443 | Human cDNA encodin |
| 38 | 47.2 | 12.3 | 1060 | 25 | ABX98935 | Novel human secret |
| 39 | 47.2 | 12.3 | 1060 | 25 | ACA05960 | Human secreted/tra |
| 40 | 47.2 | 12.3 | 1060 | 25 | ABX98024 | Human PRO polynuci |
| 41 | 47.2 | 12.3 | 1060 | 25 | ABX78808 | Human PRO polynuci |
| 42 | 47.2 | 12.3 | 1060 | 25 | ABX75821 | Human cDNA encodin |
| 43 | 47.2 | 12.3 | 1060 | 25 | ABX77026 | Human PRO polynuci |
| 44 | 47.2 | 12.3 | 1060 | 25 | ABX16866 | Human cDNA encodin |
| 45 | 47.2 | 12.3 | 1061 | 22 | AAE46205 | Human DNA encoding |

ALIGNMENTS

| | |
|----------|---|
| RESULT 1 | |
| AAFS9098 | |
| ID | AAFS9098 standard; DNA; 384 BP. |
| AC | AAFS9098; |
| XX | |
| DT | 23-APR-2001 (first entry) |
| XX | |
| DE | Rat MLP nucleotide sequence SEQ ID NO:46. |
| XX | |
| XX | MLP; MIA; melanoma inhibitory activity; cancer; bone disease; joint disease; pathologic angiogenesis; diagnosis; antiinflammatory; cardiant; gene therapy; secretory cell function regulator; promoter; inhibitor; ds. |
| XX | |
| OS | Rattus sp. |
| XX | |
| FN | W0200102564-A1. |
| XX | |
| PD | 11-JAN-2001. |
| XX | |
| PF | 29-JUN-2000; 2000MO-JP04278. |
| XX | |
| PR | 30-JUN-1999; 99JP-0186718. |
| XX | |
| PA | (TAKE) TAKEDA CHEM IND LTD. |
| XX | |
| PI | Itoh Y, Nishi K, Ogi K, Okubo S, Mogi S, Noguchi Y, Yoshimura K, Tataka H; |
| XX | |
| WI | WI; 2001-159271/16. |

DR P-PSDB; AAB69130.

XX Safe, low-toxicity secretory cell function-regulatory protein and
 PT encoded DNA, applicable as drugs, in diagnosis and development of
 PT promoters and inhibitors for preventing or treating e.g. bone and joint
 diseases -

XX Claim 13; Page 105-106; 111pp; Japanese.

XX The present invention describes novel MLP proteins and their encoding
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
 CC activities, and can be used in gene therapy and as secretory cell
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in
 CC the diagnosis and development of promoters and inhibitors for preventing
 CC or treating bone and joint diseases as well as pathologic angiogenesis.
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
 CC in the exemplification of the present invention.

XX Sequence 384 BP; 98 A; 72 C; 109 G; 105 T; 0 other;

SQ

Query Match 100.0%; Score 384; DB 22; Length 384;
 Best Local Similarity 100.0%; Pred. No. 3.2e-118; Mismatches 0; Gaps 0;
 Matches 384; Conservative 0; Indels 0;

QY 1 ATGGCAAGATATATTTCTTTGCTTGGGGCTTGTGGCTCTCTGCGGGCATGCG 60
 DB 1 ATGGCAAGATATTTCTTTGCTTGGGGCTTGTGGCTCTCTGCGGGCATGCG 60

QY 61 ATGTTATGATATACTTTCTTCTAAGAACTGTGTGAGATGAGAGTGTCTATACC 120
 DB 61 ATGTTATGATATACTTTCTTCTAAGAACTGTGTGAGATGAGAGTGTCTATACC 120

QY 121 ATTCTCTGGCAGAGCAGAGAGAGATGAGATGAGAGTGTGTATGATCAATGTC 180
 DB 121 ATTCTCTGGCAGAGCAGAGAGAGATGAGATGAGAGTGTGTATGATCAATGTC 180

QY 121 ATTTCTCTGGCAGAGCAGAGAGATGAGATGAGAGTGTGTATGATCAATGTC 180
 DB 121 ATTTCTCTGGCAGAGCAGAGAGATGAGATGAGAGTGTGTATGATCAATGTC 180

QY 181 AAGAAAGGGCAGACAGATCTATGTTTATTCAGAGTGTATACAGAAATGAGAGTGGGCA 240
 DB 181 AAGAAAGGGCAGACAGATCTATGTTTATTCAGAGTGTATACAGAAATGAGAGTGGGCA 240

QY 241 TTCTGGGCTGGCAGAGTGTATGTTATGAGCAGCAGATGAGATGAGATGAGTGTATTC 300
 DB 241 TTCTGGGCTGGCAGAGTGTATGTTATGAGCAGCAGATGAGATGAGATGAGTGTATTC 300

QY 301 CCCAGCACTTGTGTAGAGCAGAGAGTGTACAGAGGCGCCACAGAGATTTCCAAAC 360
 DB 301 CCCAGCACTTGTGTAGAGCAGAGAGTGTACAGAGGCGCCACAGAGATTTCCAAAC 360

QY 361 ACGGATATGACTTCTTCTGTGAA 384
 DB 361 ACGGATATGACTTCTTCTGTGAA 384

Db 361 ACGGATATGACTTCTTCTGTGAA 384

RESULT 2
 ID AAF59068 standard; DNA; 384 BP.
 XX AAF59068;
 AC
 XX 23-APR-2001 (first entry)
 DT
 XX Mouse MLP nucleotide sequence SEQ ID NO:10.
 DE
 XX MLP; MTA; melanoma inhibitory activity; cancer; bone disease;
 KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
 KW cardiant; gene therapy; secretory cell function regulator; promoter;
 KW inhibitor; ds.
 XX Mus musculus.
 OS
 XX WO200102564-A1.
 PN
 XX 11-JAN-2001.

XX 29-JUN-2000; 2000MO-JP04278.
 PF
 XX 30-JUN-1999; 99JP-0186718.
 PR
 XX (TAKE) TAKEDA CHEM IND LTD.
 PA
 XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
 PI Tanaka H;
 PI
 XX NPI; 2001-159271/16.
 DR
 XX P-PSDB; AAB69125.
 DR
 XX Safe, low-toxicity secretory cell function-regulatory protein and
 PT encoded DNA, applicable as drugs, in diagnosis and development of
 PT promoters and inhibitors for preventing or treating e.g. bone and joint
 PT diseases -

XX Claim 11; Page 93; 111pp; Japanese.

PS

XX The present invention describes novel MLP proteins and their encoding
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
 CC activities, and can be used in gene therapy and as secretory cell
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in
 CC the diagnosis and development of promoters and inhibitors for preventing
 CC or treating bone and joint diseases as well as pathologic angiogenesis.
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
 CC in the exemplification of the present invention.

XX Sequence 384 BP; 98 A; 68 C; 111 G; 107 T; 0 other;

SQ

Query Match 89.6%; Score 344; DB 22; Length 384;
 Best Local Similarity 93.5%; Pred. No. 8.1e-105; Mismatches 25; Indels 0; Gaps 0;
 Matches 359; Conservative 0; Mismatches 25; Indels 0;

QY 1 ATGGCAAGATATGATTTCTTTGCTTGGGGCTTGTGGCTCTCTGCGGGCATGCG 60
 DB 1 ATGGCAAGATATGATTTCTTTGCTTGGGGCTTGTGGCTCTCTGCGGGCATGCG 60

QY 61 ATGTTATGATATACTTTCTTCTAAGAACTGTGTGAGATGAGAGTGTCTATACC 120
 DB 61 ATGTTATGATATACTTTCTTCTAAGAACTGTGTGAGATGAGAGTGTCTATACC 120

QY 121 ATTCTCTGGCAGAGCAGAGAGATGAGATGAGAGTGTGTATGATCAATGTC 180
 DB 121 ATTCTCTGGCAGAGCAGAGAGATGAGATGAGAGTGTGTATGATCAATGTC 180

QY 121 ATTTCTCTGGCAGAGCAGAGAGATGAGATGAGAGTGTGTATGATCAATGTC 180
 DB 121 ATTTCTCTGGCAGAGCAGAGAGATGAGATGAGAGTGTGTATGATCAATGTC 180

QY 181 AAGAAAGGGCAGACAGATCTATGTTTATTCAGAGTGTATACAGAAATGAGAGTGGGCA 240
 DB 181 AAGAAAGGGCAGACAGATCTATGTTTATTCAGAGTGTATACAGAAATGAGAGTGGGCA 240

QY 241 TTCTGGGCTGGCAGAGTGTATGTTATGAGCAGCAGATGAGATGAGATGAGTGTATTC 300
 DB 241 TTCTGGGCTGGCAGAGTGTATGTTATGAGCAGCAGATGAGATGAGATGAGTGTATTC 300

QY 301 CCCAGCACTTGTGTAGAGCAGAGAGTGTACAGAGGCGCCACAGAGATTTCCAAAC 360
 DB 301 CCCAGCACTTGTGTAGAGCAGAGAGTGTACAGAGGCGCCACAGAGATTTCCAAAC 360

QY 361 ACGGATATGACTTCTTCTGTGAA 384
 DB 361 ACGGATATGACTTCTTCTGTGAA 384

Db 361 ACGGATATGACTTCTTCTGTGAA 384

RESULT 3
 ID AAF59084 standard; DNA; 947 BP.
 XX AAF59084;
 AC
 XX 23-APR-2001 (first entry)
 DT
 XX Mouse MLP nucleotide sequence SEQ ID NO:30.
 DE

XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
 KM joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
 KM cardiant; gene therapy; secretory cell function regulator; promoter;
 KM inhibitor; ds.
 XX Mus musculus.
 OS
 XX MO200102564-A1.
 FN
 XX 11-JAN-2001.
 PD
 XX 29-JUN-2000; 2000MO-JP04278.
 PE
 XX 30-JUN-1999; 99JP-0186718.
 PR
 XX (TAKE) TAKEDA CHEM IND LTD.
 PA
 XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
 PI Tanaka H;
 PI
 XX WPI; 2001-159271/16.
 DR
 XX Safe, low-toxicity secretory cell function-regulatory protein and
 PT encoded DNA, applicable as drugs, in diagnosis and development of
 PT promoters and inhibitors for preventing or treating e.g. bone and joint
 PT diseases -
 XX
 XX Example 2; Page 100-101; 11pp; Japanese.
 XX
 CC The present invention describes novel MLP proteins and their encoding
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
 CC activities, and can be used in gene therapy and as secretory cell
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in
 CC the diagnosis and development of promoters and inhibitors for preventing
 CC or treating bone and joint diseases as well as pathologic angiogenesis.
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
 CC in the exemplification of the present invention.
 CC
 XX
 SQ Sequence 947 BP; 279 A; 158 C; 221 G; 289 T; 0 other;

Query Match 89.6%; Score 344; DB 22; Length 947;
 Best Local Similarity 93.5%; Pred. No. 1.3e-104;
 Matches 359; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1 ATGCAAGAATATGATTTCTTCTGCGGCGCTTGCTGCTGCTGCTGCGGCGCATGGC 60
 DB 11 ATGCAAGAATATGATTTCTTCTGCGGCGCTTGCTGCTGCTGCTGCGGCGCATGGT 70
 QY 61 ATGTTTATGATATAAATCTTCTTCTAGAGTGTGTGAGATGAGAGTGTCTATAC 120
 DB 71 GTATTATGATATAAATCTTCTTCTAGAGTGTGTGAGATGAGAGTGTCTATAC 130
 QY 121 ATTCTCTGCGAAGACACAGAGACTACATGCCCCGAGCTGTAGCTTCATCATGTC 180
 DB 131 ATTCTCTGCGAAGACACAGAGACTACATGCCCCGAGCTGTAGCTTCATCATGTC 190
 QY 181 AAGAAAGGCGAGCATCTATGTTTATTCAGAGTGTGTAAGAAATGAGAGCTGAGGCA 240
 DB 191 AAGAAAGGCGAGCATCTATGTTTATTCAGAGTGTGTAAGAAATGAGAGCTGAGGAG 250
 QY 241 TTCTGGCTGCGACATGTTTATGTTGACACAGAGATGAGATGGAATGTGGTTATTTTC 300
 DB 251 TTCTGGCTGCGACATGTTTATGTTGACACAGAGATGAGATGGAATGTGGTTATTTTC 310
 QY 301 CCCGCAACTTGTGTTAAGAGACACAGAGTGTACAGAGGCCACCAAGAGATCCAAACC 360
 DB 311 CCCGCAACTTGTGTTAAGAGACACAGAGTGTATACAGAGGCCACCAAGAGATCCAAACC 370
 QY 361 ACGGATATGACTTCTCTGAGAA 384
 DB 371 ACGGATATGACTTCTCTGAGAA 394

RESULT 4
 AAF59099
 ID AAF59099 standard; DNA; 330 BP.
 XX
 AC AAF59099;
 XX
 DT 23-APR-2001 (first entry)

XX Rat MLP nucleotide sequence SEQ ID NO:48.
 DE
 XX
 KM MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
 KM joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
 KM cardiant; gene therapy; secretory cell function regulator; promoter;
 KM inhibitor; ds.
 XX
 OS Rattus sp.
 XX
 XX MO200102564-A1.
 PN
 XX 11-JAN-2001.
 PD
 XX 29-JUN-2000; 2000MO-JP04278.
 PF
 XX 30-JUN-1999; 99JP-0186718.
 PR
 XX (TAKE) TAKEDA CHEM IND LTD.
 PA
 XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
 PI Tanaka H;
 PI
 XX WPI; 2001-159271/16.
 DR
 XX P-PSDB; AAB69131.

PT Safe, low-toxicity secretory cell function-regulatory protein and
 PT encoded DNA, applicable as drugs, in diagnosis and development of
 PT promoters and inhibitors for preventing or treating e.g. bone and joint
 PT diseases -
 XX
 XX
 XX Claim 12; Page 107; 11pp; Japanese.

CC The present invention describes novel MLP proteins and their encoding
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
 CC activities, and can be used in gene therapy and as secretory cell
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in
 CC the diagnosis and development of promoters and inhibitors for preventing
 CC or treating bone and joint diseases as well as pathologic angiogenesis.
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
 CC in the exemplification of the present invention.
 CC
 XX
 SQ Sequence 330 BP; 91 A; 62 C; 91 G; 86 T; 0 other;

Query Match 85.9%; Score 330; DB 22; Length 330;
 Best Local Similarity 100.0%; Pred. No. 3.7e-100;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 CATGGCAGTTTATGATATAAATCTTCTTCTAGAGTGTGTGCGAGATGAGAGTGTGC 114
 DB 1 CATGGCAGTTTATGATATAAATCTTCTTCTAGAGTGTGTGCGAGATGAGAGTGTGC 60
 QY 115 TATACCATTTCTCTGGCAAGACACAGAGACTACATGCCCCGAGCTGTAGTTCATC 174
 DB 61 TATACCATTTCTCTGGCAAGACACAGAGACTACATGCCCCGAGCTGTAGTTCATC 120
 QY 175 AATGTCAGAAAGGCGACAGATCTATGTTTATTCAGAGCTGTGTAACAGAAATGAGACT 234
 DB 121 AATGTCAGAAAGGCGACAGATCTATGTTTATTCAGAGCTGTGTAACAGAAATGAGACT 180
 QY 235 GGGGCAATTCGGGCTGGCAGAGTGTATGTTGACCAACAGATGAGATGGAAATGTGGGT 294
 DB 181 GGGGCAATTCGGGCTGGCAGAGTGTATGTTGACCAACAGATGAGATGGAAATGTGGGT 240
 QY 295 TATTTCCAGCAACTGTGTAGAGACAGAGTGTACAGAGGAGCCACCAAGAGATT 354

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Db      241 TATTTCCCGCACTTGTGTTAGAGCAGATGTAACGAGGCCACCAAGAAATT 300
Qy      355 CCAACCGAGATATTGACTTCTTCTGTGAA 384
        |||
        |||
        |||
Db      301 CCAACCGAGATATTGACTTCTTCTGTGAA 330

RESULT 5
AAF59080
ID      AAF59080 standard; DNA; 330 BP.
AC      AAF59080;
XX      23-APR-2001 (first entry)
DE      Mouse MLP nucleotide sequence SEQ ID NO:25.
XX      MLP, MIA; melanoma inhibitory activity; cancer; bone disease;
XX      joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
XX      cardiant; gene therapy; secretory cell function regulator; promoter;
XX      inhibitor; ds.
XX      Mus musculus.
XX      WO200102564-A1.
XX      11-JAN-2001.
XX      29-JUN-2000; 2000MO-JP04278.
XX      30-JUN-1999; 99JP-0186718.
XX      (TAKE ) TAKEDA CHEM IND LTD.
XX      Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
XX      Tanaka H;
XX      WPI; 2001-159271/16.
XX      P-PSDB; AAB69127.
XX      Safe, low-toxicity secretory cell function-regulatory protein and
XX      encoded DNA, applicable as drugs, in diagnosis and development of
XX      promoters and inhibitors for preventing or treating e.g. bone and joint
XX      diseases -
XX      Claim 10; Page 98; 11pp; Japanese.
XX      The present invention describes novel MLP proteins and their encoding
XX      DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
XX      activities, and can be used in gene therapy and as secretory cell
XX      function regulators. The MLP proteins and DNAs can be used in drugs, in
XX      the diagnosis and development of promoters and inhibitors for preventing
XX      or treating bone and joint diseases as well as pathologic angiogenesis.
XX      AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
XX      in the exemplification of the present invention.
XX      Sequence 330 BP; 91 A; 60 C; 92 G; 87 T; 0 other;
SQ      Query Match      76.8%; Score 294.8; DB 22; Length 330;
        Best Local Similarity 93.3%; Pred. No. 2.3e-88;
        Matches 308; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
Qy      55 CATGGCAGTGTATGATATAAATTCTTCTAAGACTGTGGCAGATGAGAGTGTCT 114
        |||
        |||
        |||
Db      1 CATGTGATATTAATGATTAACCTTCTTCTAAGAGTGTGGCAGATGAGAGTGTCT 60
Qy      115 TATACCATTTCTCTGCGAAGACACAGAGACTACATGCCCGGACTGTAGTTATC 174
        |||
        |||
        |||
Db      61 TATATCTATTTCTCTGCGAAGACACAGAGATTAATGATGCCCGGACTGTAGTTATC 120
        |||
        |||
        |||
Qy      175 AATGTCAAGAAAGGCGACGATCTATGTTTATTCGAAGCTGTGTACAGAAATGGAAGCT 234
        |||
        |||
        |||

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Db      121 GATGTCAAGAAAGGCGACAGATCTATGTTTACTCCCAAGCTGTGTACAGAAAAAGAGCT 180
Qy      235 GGGGCATTTCTGGGCTGCGAGTGTTTATGCTGACCCACAGATGAGATGGGAATTGGGT 294
        |||
        |||
        |||
Db      181 GGAGAGTTTGGGCTGCGAGTGTTTATGTTGACACACAGATGAGATGGGAATTGGGT 240
Qy      295 TATTTCCCGCACTTGTGTTAGAGCAGATGTAACGAGGCCACCAAGAAATT 354
        |||
        |||
        |||
Db      241 TATTTCCCGCACTTGTGTTAGAGCAGATGTAACGAGGCCACCAAGAAATT 300
Qy      355 CCAACCGAGATATTGACTTCTTCTGTGAA 384
        |||
        |||
        |||
Db      301 CCAACCGAGATATTGACTTCTTCTGTGAA 330

RESULT 6
AAF59093
ID      AAF59093 standard; DNA; 307 BP.
AC      AAF59093;
XX      23-APR-2001 (first entry)
DE      Rat MLP nucleotide sequence SEQ ID NO:41.
XX      MLP, MIA; melanoma inhibitory activity; cancer; bone disease;
XX      joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
XX      cardiant; gene therapy; secretory cell function regulator; promoter;
XX      inhibitor; ds.
XX      Rattus sp.
XX      WO200102564-A1.
XX      11-JAN-2001.
XX      29-JUN-2000; 2000MO-JP04278.
XX      30-JUN-1999; 99JP-0186718.
XX      (TAKE ) TAKEDA CHEM IND LTD.
XX      Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
XX      Tanaka H;
XX      WPI; 2001-159271/16.
XX      Safe, low-toxicity secretory cell function-regulatory protein and
XX      encoded DNA, applicable as drugs, in diagnosis and development of
XX      promoters and inhibitors for preventing or treating e.g. bone and joint
XX      diseases -
XX      Example 9; Page 104; 11pp; Japanese.
XX      The present invention describes novel MLP proteins and their encoding
XX      DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
XX      activities, and can be used in gene therapy and as secretory cell
XX      function regulators. The MLP proteins and DNAs can be used in drugs, in
XX      the diagnosis and development of promoters and inhibitors for preventing
XX      or treating bone and joint diseases as well as pathologic angiogenesis.
XX      AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
XX      in the exemplification of the present invention.
XX      Sequence 307 BP; 84 A; 56 C; 90 G; 77 T; 0 other;
SQ      Query Match      74.9%; Score 287.6; DB 22; Length 307;
        Best Local Similarity 98.4%; Pred. No. 5.7e-86;
        Matches 301; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
Qy      49 GCGGGGCGATGCGATGTTATGATTAACCTTCTTCTAAGAGTGTGTGCAATGAGAG 108
        |||
        |||
        |||
Db      1 GCGGGGCGATGCGATGTTATGATTAACCTTCTTCTAAGAGTGTGTGCAATGAGAG 60

```

QY 109 TGTGCTATACCATTTCTCTGGCAGAGCAGGAGACTCAATGCCCGGACTGAGG 168
 Db 61 TGTGCTATACCATTTCTCTGGCAGAGCAGGAGACTCAATGCCCGGACTGAGG 120
 QY 169 TTATCATATGTCAGAAAGGCGACAGATCTATGTTATCCAAAGCTGTGAACAGAAAT 228
 Db 121 TTATCATATGTCAGAAAGGCGACAGATCTATGTTATCCAAAGCTGTGAACAGAAAT 180
 QY 229 GGAAGCTGGGCGATTCTGGGCTGGCAGTGTATGTATGATGACCAAGATGATGAGAT 288
 Db 181 GGAAGCTGGGCGATTCTGGGCTGGCAGTGTATGTATGATGACCAAGATGATGAGAT 240
 QY 289 GTGGGTTATTTCCCGCAGCACTTGTTAGAGAGCAAGATGTACCAAGA-GGCCACCA 347
 Db 241 GTGGGTTATTTCCCGCAGCACTTGTTAGAGAGCAAGATGTACCAAGAAGGCGCCACCA 300
 QY 348 GGAGAT 353
 Db 301 GGAGAT 306

RESULT 7

AAFS9065 standard; DNA; 384 BP.

AAFS9065;

23-APR-2001 (first entry)

Human MLP nucleotide sequence SEQ ID NO:4.

MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
 joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
 cardiac; gene therapy; secretory cell function regulator; promoter;
 inhibitor; ds.

Homo sapiens.

WO200102564-A1.

11-JAN-2001.

29-JUN-2000; 2000WO-JP04278.

30-JUN-1999; 99JP-0186718.

(TAKE) TAKEDA CHEM IND LTD.

Itch Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
 Tanaka H;

WPI; 2001-159271/16.

P-PSDB; AAB69123.

Safe, low-toxicity secretory cell function-regulatory protein and
 encoded DNA, applicable as drugs, in diagnosis and development of
 promoters and inhibitors for preventing or treating e.g. bone and joint
 diseases

Example 1; Page 91; 11pp; Japanese.

The present invention describes novel MLP proteins and their encoding
 DNAs. The MLP proteins and DNAs have antiinflammatory and cardiac
 activities, and can be used in gene therapy and as secretory cell
 function regulators. The MLP proteins and DNAs can be used in drugs, in
 the diagnosis and development of promoters and inhibitors for preventing
 or treating bone and joint diseases as well as pathologic angiogenesis.
 AAFS9063 to AAFS9099 and AAB69122 to AAB69132 represent sequences used
 in the exemplification of the present invention.

Sequence 384 BP; 99 A; 70 C; 106 G; 109 T; 0 other;

Query Match 74.3%; Score 285.4; DB 22; Length 384;

Best Local Similarity 84.1%; Pred. No. 3.5e-85;
 Matches 322; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 1 ATGGCAGAAATATTATCTTTGCTGGGCGCTTGAGCTCTGAGCCGGCATGAC 60
 Db 1 ATGGCAGAAATATTATCTTTGCTTTCTCCCGGCTTGGCTGTATGTGCTGATGA 60
 QY 61 ATGTTATGATTAACCTTCTTCTAAGAAAGTTGTGTGAGATGAGAGTGTCTATACC 120
 Db 61 ATATTATGACCGCTAGCTTCCAGAAAGCTGTGAGATGATGAGTGTCTATACT 120
 QY 121 ATTTCTCTGCAAGACAGCAGAGACTCAATGCCCCGACTGTAGTTCAATGTC 180
 Db 121 ATTTCTCTGCTAGTGTCAAGAAAGATTAATGCCCGACTGTAGATTCAATGCTT 180
 QY 181 AAGAAAGGCGACAGATCTATGTTATTTCCAAAGCTGTGAACAGAAAGTGGAGGCA 240
 Db 181 AAAAAAGGCGACAGATCTATGTTACTCAAGAGCTGTGAAGAAAGTGGAGGCA 240
 QY 241 TTCTGGGCTGGCAGTGTATGATGACCAAGATGATGAGATGAGATGATGATTTTC 300
 Db 241 TTTGGGCTGGCAGTGTATGATGATGACCAAGATGAGATGAGATGATGATTTTC 300
 QY 301 CCCAGCACTTGTTAGAGAGCAAGAGTGTACCAAGAGGCCACCAAGAGATTTCAAC 360
 Db 301 CCCAGCACTTGTTAGAGAGCAAGAGTGTGTACCAAGAGGATACCAAGAGAGTTCCACC 360
 QY 361 ACGGATTTGACTTTCTCTGTGA 383
 Db 361 ACGGATTTGACTTTCTCTGTGA 383

RESULT 8

AAFS17583 standard; CDNA; 387 BP.

AAFS17583;

26-FEB-2002 (first entry)

DNA encoding novel secreted protein #12.

Secreted protein; cytoprotic; immunosuppressive; vulnary; vaccine;
 antiinflammatory; neuroprotective; nephroprotective; cardiovascular;
 human; cancer; autoimmune disease; wound healing disorder; infection;
 haematopoietic disorder; inflammatory disorder; infertility;
 neurological disease; psychiatric disease; cardiovascular disease;
 respiratory disease; renal; gastrointestinal; ss.

Homo sapiens.

WO200179454-A1.

25-OCT-2001.

11-APR-2001; 2001WO-US11797.

13-APR-2000; 2000US-196603P.

24-APR-2000; 2000US-199417P.

(SMK) SMITHKLINE BEECHAM CORP.

(SMK) SMITHKLINE BEECHAM PLC.

Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;

WPI; 2002-061975/08.

P-PSDB; AAU09871.

Key Location/Qualifiers

CDS 1..387

FT /*tag= a

FT /product= "Human secreted protein"

PT New secreted proteins or polypeptides, useful for treating e.g. cancer,
 PT autoimmune diseases, wound healing disorder, infections, haematopoietic
 PT disorders, inflammatory disorders, infertility, cancer -
 XX
 XX
 PS Claim 2; Page 44; 92pp; English.

XX The invention relates to an isolated novel secreted polypeptide (I) and
 CC polynucleotide (II). (I) and (II) are useful for treating cancer,
 CC autoimmune diseases, wound healing disorder, infections, haematopoietic
 CC disorders, inflammatory disorders, infertility, neurological and
 CC psychiatric diseases, cardiovascular diseases, respiratory diseases,
 CC renal diseases, or gastrointestinal diseases. These may also be used to
 CC treat diseases, abnormalities and disorders caused by abnormal
 CC expression, production, function and/or metabolism of the genes, as
 CC vaccines for inducing immunological response in a mammal, and in
 CC screening methods for detecting the effect of added compounds on the
 CC production of mRNA and polypeptide in cells. The polypeptides can be used
 CC as immunogens to produce antibodies immunospecific for the polypeptides,
 CC and to identify membrane-bound or soluble receptors. The polynucleotides
 CC may be used as diagnostic reagents, in chromosome localisation studies,
 CC and in tissue expression studies. The present sequence represents the
 CC coding sequence of novel human secreted protein #12.

XX Sequence 387 BP; 101 A; 70 C; 106 G; 110 T; 0 other;

Query Match 74.3%; Score 285.4; DB 24; Length 387;
 Best Local Similarity 84.1%; Pred. No. 3.5e-85;
 Matches 322; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 1 AAGGCAAGATATTTGATCTTTGCTGGGGGCTTGAGCTCTGTCGGGGATGCG 60
 DB 1 ATGGCAAGATATTTGATCTTTGCTGGGGGCTTGAGCTCTGTCGGGGATGCG 60
 QY 61 ATGTTATGATTAACCTTTCTTAAGAAGTTGTGAGATGAGAGATGATATACC 120
 DB 61 ATATTATGACCGCTGACCTTCCAGAAAGCTGTGAGATGAGATGATGATATCT 120
 QY 121 ATTTCTGGCAAGACAGCAAGAGATGATGCTGGGGCTGAGGTTATCATGTC 180
 DB 121 ATTTCTGGCAAGACAGCAAGAGATGATGCTGGGGCTGAGGTTATCATGTC 180
 QY 181 AAGAAAGGGCAGCAGATCTATTTATTCAGAGCTGTAAAGAAATGAGAGTGGGCA 240
 DB 181 AAAAAAGGCGACAGATCTATGTAAGCTGTAAAGAAATGAGAGTGGGCA 240
 QY 241 TTCTGGCTGCGAGTGTATGATGACCAAGAGATGAGATGAGATGAGATGATTC 300
 DB 241 TTCTGGCTGCGAGTGTATGATGATGACCAAGAGATGAGATGAGATGATTC 300
 QY 301 CCCAGCACTTGTGATGAGAGCAAGAGTGTACCAAGAGGCGCAAGAGATTCACAC 360
 DB 301 CCCAGCACTTGTGATGAGAGCAAGAGTGTACCAAGAGGCGCAAGAGATTCACAC 360
 QY 361 ACGGATATGATCTCTTCTGTA 383
 DB 361 ACGGATATGATCTCTTCTGTA 383

RESULT 9
 AAH26341
 ID AAH26341 standard; cDNA; 426 BP.

XX AAH26341;

XX 02-OCT-2001 (first entry)

DE Human growth regulatory-like polypeptide clone 16372272.

XX Growth regulatory-like polypeptide; human; cartilage; melanoma;
 KM neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;
 XX ss.

OS Homo sapiens.

XX PN WO200155332-A2.

XX PD 02-AUG-2001.

XX PF 25-JAN-2001; 2001WO-US02455.

XX PR 25-JAN-2000; 2000US-0491404.

XX PR 02-MAY-2000; 2000US-0563786.

XX PA (HYSE-) HYSEQ INC.

XX PI Mize NK, Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C;

XX PI Dmanac RT;

XX DR WPI; 2001-483233/52.

XX PT Isolated human growth regulatory-like polypeptide useful for treating

XX PT e.g. Alzheimer's disease, cancer, autoimmune disorders,

XX PT hyperproliferative disorders, coagulation disorders, and nervous system

XX PT disorders -

XX PS Example 1; Page 114; 119pp; English.

XX The present sequence is that of Hyseq clone identification number
 CC 16372272, which was obtained from a human thymus cDNA library
 CC using standard PCR with primers specific for vector sequences
 CC flanking the inserts, sequencing by hybridisation sequence
 CC signature analysis, and Sanger sequencing techniques. This
 CC expressed sequence tag was used in the assembly of a full-length
 CC cDNA sequence (see AAH26343) encoding a novel human growth
 CC regulatory-like polypeptide (GRP, see AAB82671). The GRP
 CC belongs to the same protein family as growth regulatory proteins,
 CC growth factors, human melanoma derived growth regulatory protein
 CC precursor (64% similarity and 45% identity over 111 amino acids)
 CC or melanoma inhibitory activity, cattle cartilage-derived
 CC retinoic acid sensitive protein (CD-RAP, 44% identity and 64%
 CC similarity over 126 amino acids) and other retinoic acid-sensitive
 CC proteins. GRP polypeptides and polynucleotides of the invention
 CC can be used in the prophylaxis, treatment (including gene therapy)
 CC and diagnosis of disorders and diseases caused by, or involving,
 CC cartilage development and maintenance, inhibition of melanoma cell
 CC growth and tumours, including neuroectodermal tumours such as
 CC gliomas. The polynucleotides can also be used to design probes
 CC and primers, for chromosome and gene mapping, in the recombinant
 CC production of protein, in the generation of antisense, ribozyme and
 CC peptide-nucleic acid molecules, and to produce transgenic animals.

XX Sequence 426 BP; 119 A; 73 C; 113 G; 120 T; 1 other;

Query Match 74.3%; Score 285.4; DB 22; Length 426;
 Best Local Similarity 84.1%; Pred. No. 3.7e-85;
 Matches 322; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 1 ATGGCAAGATATTTGATCTTTGCTGGGGGCTTGAGCTCTGTCGGGGATGCG 60
 DB 1 ATGGCAAGATATTTGATCTTTGCTGGGGGCTTGAGCTCTGTCGGGGATGCG 60
 QY 61 ATGTTATGATTAACCTTTCTTAAGAAGTTGTGAGATGAGAGTGTGCTATACC 120
 DB 61 ATATTATGACCGCTGACCTTCCAGAAAGCTGTGAGATGAGATGATGATATCT 120
 QY 121 ATTTCTGGCAAGACAGCAAGAGATGATGCTGGGGCTGAGGTTATCATGTC 180
 DB 121 ATTTCTGGCAAGACAGCAAGAGATGATGCTGGGGCTGAGGTTATCATGTC 180
 QY 181 AAGAAAGGGCAGCAGATCTATGTAAGCTGTAAAGAAATGAGAGTGGGCA 240
 DB 181 AAAAAAGGCGACAGATCTATGTAAGCTGTAAAGAAATGAGAGTGGGCA 240
 QY 241 TTCTGGCTGCGAGTGTATGATGACCAAGAGATGAGATGAGATGAGATGATTC 300
 DB 241 TTCTGGCTGCGAGTGTATGATGATGACCAAGAGATGAGATGAGATGATTC 300
 QY 301 CCCAGCACTTGTGATGAGAGCAAGAGTGTACCAAGAGGCGCAAGAGATTCACAC 360
 DB 301 CCCAGCACTTGTGATGAGAGCAAGAGTGTACCAAGAGGCGCAAGAGATTCACAC 360

PD 31-JAN-2002.
XX 29-JUN-2001; 2001WO-US21066.
XX 20-JUL-2000; 2000US-219556P.
XX 25-JUL-2000; 2000US-220585P.
PR 25-JUL-2000; 2000US-220605P.
PR 25-JUL-2000; 2000US-220607P.
PR 25-JUL-2000; 2000US-220624P.
PR 25-JUL-2000; 2000US-220638P.
PR 25-JUL-2000; 2000US-220664P.
PR 25-JUL-2000; 2000US-220666P.
PR 26-JUL-2000; 2000US-220893P.
PR 26-JUL-2000; 2000WO-US20710.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 15-SEP-2000; 2000US-000000P.
PR 10-NOV-2000; 2000WO-US30873.
PR 28-NOV-2000; 2000US-253646P.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000US-0747259.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001WO-US17092.
XX (GENTH) GENENTECH INC.
XX Baker KP, Desnoyers L, Gerritsen MB, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WL;
XX MPI; 2002-172001/22.
DR P-PSDB; AAU83627.
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT useful for treating a PRO related disorder and for diagnosing tumors
PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
PT tumour or liver tumour -
XX Claim 2; Figure 71; 359pp; English.
XX The invention relates to one hundred and twenty two nucleic acids
XX encoding PRO polypeptides. The sequences of the 122 PRO polypeptides
XX encode human secreted proteins. The PRO nucleic acids, polypeptides,
XX agonists and antagonists are useful for treating a PRO related disorder.
XX The PRO polypeptides are useful for diagnosing tumors, especially lung
XX cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
XX liver tumour. The PRO polypeptides are useful for stimulating the
XX proliferation of, or gene expression, in pericyte cells, for stimulating
XX the proliferation or differentiation of chondrocyte cells, for
XX stimulating the release of tumour necrosis factor-alpha from human blood,
XX for stimulating or inhibiting the proliferation of normal human dermal
XX fibroblast cells. The PRO polypeptide may also be used as molecular
XX weight markers and for tissue typing. The PRO nucleic acids have
XX applications in molecular biology, including use as hybridisation probes,
XX and in chromosome and gene mapping. ABK33536-ABK33657 represent human
XX PRO protein coding sequences of the invention.
SQ Sequence 521 BP; 167 A; 86 C; 131 G; 137 T; 0 other;
Query Match 74.3%; Score 285.4; DB 24; Length 521;
Best Local Similarity 84.1%; Pred. No. 4e-85;
Matches 322; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

DB 158 ATTCTCTGCTAGTCTCCAGAGATTATTAATGCCCCGACTGTAGATTCAATTAACGTT 217
QY 181 AAGAAAGGCGACAGATCTATGTTTATTCAGAGCTGTATACAGAAATGAGACTGGGCGCA 240
DB 218 AAAAAAGGCGACAGATCTATGTTTATTCAGAGCTGTATTAAGAAATGAGACTGGGCGCA 277
QY 241 TTCTGGCTGGCAGATGTTTATGATGACACAGAGATGAGATGGAATTTGGGTTATTTTC 300
DB 278 TTTTGGCTGGCAGATGTTTATGATGATGACACAGAGATGAGATGGAATTTGGGTTATTTTC 337
QY 301 CCCAGCACTGTTGTTAGAGAGCAAGAGTGTACAGAGAGCCACCAAGAGATTCCACCC 360
DB 338 CCCAGCACTGTTGTTAGAGAGCAAGAGTGTGTACAGAGAGCTACCAAGAGATTCCACCC 397
QY 361 ACCGATATTGACTTCTTCTGTGA 383
DB 398 ACCGATATTGACTTCTTCTGTGA 420
RESULT 13
AAH98228
ID AAH98228 standard; cDNA; 891 BP.
XX
AC AAH98228;
XX
DT 12-OCT-2001 (first entry)
DE Human EST-derived coding sequence SEQ ID NO: 85.
XX
XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KM tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KM diagnostics; forensic test; gene mapping; genetic disorder;
KM biodiversity; gene therapy; nutrition; ss.
XX
OS Homo sapiens.
XX
XX WO200154477-A2.
PN
XX 02-AUG-2001.
PD
XX
XX 25-JAN-2001; 2001WO-US02687.
PR
XX 25-JAN-2000; 2000US-0491404.
PR 17-JUL-2000; 2000US-0617746.
PR 03-AUG-2000; 2000US-0631451.
PR 15-SEP-2000; 2000US-0663870.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX
XX MPI; 2001-476164/51.
DR P-PSDB; AAM23569.
XX
PT Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use -
XX
XX
XX Claim 1; Page 236; 1275pp; English.
XX
XX The present invention provides the protein and coding sequences of novel
XX proteins from a variety of organisms, including human, dog, cat, horse,
XX cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
XX urchin and tomato. These were derived from expressed sequence tags (ESTs)
XX from the organism of interest. They can be used in diagnostics,
XX forensic, gene mapping, identification of mutations, to assess
XX biodiversity and for nutritional purposes. The present sequence is a cDNA
XX of the invention.
SQ Sequence 891 BP; 272 A; 146 C; 214 G; 259 T; 0 other;
Query Match 74.3%; Score 285.4; DB 22; Length 891;

Best Local Similarity 84.1%; Pred. No. 5.2e-85;
Matches 322; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

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QY 1 ATGCGAAGATATTGATCTTTGCTGGGGGCTTGTGCTCTCTGTCGCCGGCATGCG 60
DB 19 ATGCGAAGATATTGATCTTTGCTGGGGGCTTGTGCTCTCTGTCGCCGGCATGCG 78
QY 61 ATGTTTATGATTAACCTTCTCTTAAGAAGTTGTGAGATGAGAGTGTCTATACC 120
DB 79 ATATTATGACCGCTGTAGCTTCCAAAGCTGTGTGAGATGATGATGTGTCTATCT 138
QY 121 ATTTCTCTGCGACAGACAGACAGAGACTACATGCCCCGACTGTAGTTCATATGTC 180
DB 139 ATTTCTCTGCGCTAGCTCTCAAGATTTATATGCCCGGACTGTAGTTATTAACGTT 198
QY 181 AAGAAAGGCGACAGATCTATGTTTATTCAGCTGTGTAACGAAATGAGCTGGGCGCA 240
DB 199 AAAAAAGGCGACAGATCTATGTTTATTCAGCTGTGTAAGAAATGAGCTGGGAGAA 258
QY 241 TTCTGGGCTGGCAGTGTATTATGTGACCAACCGAGATGAGATGGGAATGTGGTTATTTC 300
DB 259 TTTTGGGCTGGCAGTGTATTATGTGATGGCCAGACGAGATGGGAGTGTGGTTATTTC 318
QY 301 CCCAGCAACTGTGTTAGAGACAGAGTGTACAGAGGCGCCAGCAAGAGATTCCAAAC 360
DB 319 CCCAGCAACTGTGTTAGAGACAGAGTGTGTACAGAGAGCTACCAAGAAAGTTCCACC 378
QY 361 ACGGATATTGACTTCTTCTGTGA 383
DB 379 ACGGATATTGACTTCTTCTGTGA 401

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RESULT 14
AAH26342
ID AAH26342 standard; cDNA; 891 BP.

AAH26342;

02-OCT-2001 (first entry)

Human growth regulatory-like polypeptide partial cDNA clone.

KM Growth regulatory-like polypeptide; human; cartilage; melanoma;
KM neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;
KM ss.

OS Homo sapiens.

PN WO200155332-A2.

PD 02-AUG-2001.

PF 25-JAN-2001; 2001WO-US02455.

PR 25-JAN-2000; 2000US-0491404.

PR 02-MAY-2000; 2000US-0563786.

PA (HYSE-) HYSEQ INC.

PI Mize NK, Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C;

PI Drmanac RT;

DR WPI; 2001-483233/52.

XX Isolated human growth regulatory-like polypeptide useful for treating
PT e.g. Alzheimer's disease, cancer, autoimmune disorders,
PT hyperproliferative disorders, coagulation disorders, and nervous system
PT disorders -
XX
PS Claim 1, Page 115; 119pp; English.

CC The present sequence is that of a novel nucleic acid that was
CC assembled from human thymus cDNA library-derived Hyseq clone

CC identification number 16372272 (see AAH26341). A recursive
CC algorithm was used to extend the clone by pulling additional
CC sequences from different databases. A full-length sequence (see
CC AAH26341) encoding novel human growth regulatory-like polypeptide
CC (GRP, see AAB2671) was subsequently obtained. Human GRP
CC belongs to the same protein family as growth regulatory proteins,
CC growth factors, human melanoma derived growth regulatory protein
CC precursor (64% similarity and 45% identity over 111 amino acids)
CC or melanoma inhibitory activity, cattle cartilage-derived
CC retinoic acid sensitive protein (CD-RAP, 44% identity and 64%
CC similarity over 126 amino acids) and other retinoic acid-sensitive
CC proteins. GRP polypeptides and polynucleotides of the invention
CC can be used in the prophylaxis, treatment (including gene therapy)
CC and diagnosis of disorders and diseases caused by, or involving,
CC cartilage development and maintenance, inhibition of melanoma cell
CC growth and tumours, including neuroectodermal tumours such as
CC gliomas. The polynucleotides can also be used to design probes
CC and primers, for chromosome and gene mapping, in the recombinant
CC production of protein, in the generation of antisense, ribozyme and
CC peptide-nucleic acid molecules, and to produce transgenic animals.

XX Sequence 891 BP; 272 A; 146 C; 214 G; 259 T; 0 other;

Query Match 74.3%; Score 285.4; DB 22; Length 891;
Best Local Similarity 84.1%; Pred. No. 5.2e-85;
Matches 322; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

```

QY 1 ATGCGAAGATATTGATCTTTGCTGGGGGCTTGTGCTCTCTGTCGCCGGCATGCG 60
DB 19 ATGCGAAGATATTGATCTTTGCTGGGGGCTTGTGCTCTCTGTCGCCGGCATGCG 78
QY 61 ATGTTTATGATTAACCTTCTCTTAAGAAGTTGTGAGATGAGAGTGTCTATACC 120
DB 79 ATATTATGACCGCTGTAGCTTCCAAAGCTGTGTGAGATGATGATGTGTCTATCT 138
QY 121 ATTTCTCTGCGACAGACAGAGACTACATGCCCCGACTGTAGTTCATATGTC 180
DB 139 ATTTCTCTGCGCTAGCTCTCAAGATTTATATGCCCGGACTGTAGTTATTAACGTT 198
QY 181 AAGAAAGGCGACAGATCTATGTTTATTCAGCTGTGTAACGAAATGAGCTGGGCGCA 240
DB 199 AAAAAAGGCGACAGATCTATGTTTATTCAGCTGTGTAAGAAATGAGCTGGGAGAA 258
QY 241 TTCTGGGCTGGCAGTGTATTATGTGACCAACCGAGATGAGATGGGAATGTGGTTATTTC 300
DB 259 TTTTGGGCTGGCAGTGTATTATGTGATGGCCAGACGAGATGGGAGTGTGGTTATTTC 318
QY 301 CCCAGCAACTGTGTTAGAGACAGAGTGTACAGAGGCGCCAGCAAGAGATTCCAAAC 360
DB 319 CCCAGCAACTGTGTTAGAGACAGAGTGTGTACAGAGAGCTACCAAGAAAGTTCCACC 378
QY 361 ACGGATATTGACTTCTTCTGTGA 383
DB 379 ACGGATATTGACTTCTTCTGTGA 401

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RESULT 15
AAF59083
ID AAF59083 standard; DNA; 923 BP.

AAF59083;

23-APR-2001 (first entry)

XX Human MLP nucleotide sequence SEQ ID NO:29.

KM MIP; MIA; melanoma inhibitory activity; cancer; bone disease;
KM joint disease; pathological angiogenesis; diagnosis; antiinflammatory;
KM cardiant; gene therapy; secretory cell function regulator; promoter;
KM inhibitor; ds.

OS Homo sapiens.

PN WO200102564-A1.
XX
PD 11-JAN-2001.
XX
PF 29-JUN-2000; 2000WO-JP04278.
XX
PR 30-JUN-1999; 99JP-0186718.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Itch Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K,
PI Tanaka H;
XX
DR WPI; 2001-159271/16.
XX
PT Safe, low-toxicity secretory cell function-regulatory protein and
PT encoded DNA, applicable as drugs, in diagnosis and development of
PT promoters and inhibitors for preventing or treating e.g. bone and joint
PT diseases -
XX
PS Example 1; Page 99-100; 11pp; Japanese.
XX
CC The present invention describes novel MIP proteins and their encoding
CC DNAs. The MIP proteins and DNAs have antiinflammatory and cardiant
CC activities, and can be used in gene therapy and as secretory cell
CC function regulators. The MIP proteins and DNAs can be used in drugs, in
CC the diagnosis and development of promoters and inhibitors for preventing
CC or treating bone and joint diseases as well as pathologic angiogenesis.
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
CC in the exemplification of the present invention.
XX
SQ Sequence 923 BP; 303 A; 147 C; 213 G; 260 T; 0 other;
Query Match 74.3%; Score 285.4; DB 22; Length 923;
Best Local Similarity 84.1%; Pred. No. 5.3e-85;
Matches 322; Conservative 0; Mismatches 61; Indels 0; Gaps 0;
QY 1 ATGGCAGCAATATTTGATTTTGGTGGGGCTTTGGCTCTCTGTGCCGGGATGGC 60
DB 34 ATGGCAGCAATATTTGATTTTCTCCCGGCTTTGGCTGTATGTCTGTGATGCA 93
QY 61 ATGTTTATGATTAACCTTCTTCTAAGAAAGTTGTGAGATGAGATGCTATACC 120
DB 94 ATATTATGACCGCTTCTAGCTTCCAGAAAGCTCTGTGACATGATGATGATGCTACT 153
QY 121 ATTTCTCTGCAAGACACAGAGACTCAATGCCCCGACTGTAGGTTCAATGTC 180
DB 154 ATTTCTCTGCTAGTGTCTCAAGAGATTAATGCCCGACTGTAGATTCAATTACGTT 213
QY 181 AAGAAAGGGGACAGATCTATGTTTATTTCAAGCTGTGTACAGAAATGAGACTGGGCA 240
DB 214 AAAAAAGGGGACAGATCTATGTATCTCAAGCTGTGTAAAGAAATGAGCTGGAGAA 273
QY 241 TTCTGGGCTGCGAGTGTATGATGACCAACGAGATGATGGAAATGTGGTATTTTC 300
DB 274 TTTTGGGCTGGAGTGTATGATGAGTGGCAGAGAGATGGAGTGTGGTATTTTC 333
QY 301 CCAGCAACTTGTGATGAGACACAGATGTACCAAGAGGACCAAGAGATTTCCAAC 360
DB 334 CCCAGCACTTGTGATGAGACACAGATGTGTACCAAGAGATTTCCAAGAGATTTCCAAC 393
QY 361 ACGGATATGACTTCTTCTGTGA 383
DB 394 ACGGATATGACTTCTTCTGTGA 416

Search completed: December 30, 2003, 02:14:34
Job time : 128.462 secs


```

; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-216-163-71
Query Match      74.3%; Score 285.4; DB 13; Length 521;
Best Local Similarity 84.1%; Pred. No. 2.9e-88;
Matches 322; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

1  ATGGCAAGATATTTGATTTCTTTGCTTGGGCGCTTGCTCTCTGTCGCCGCGCATGCG 60
19  ATGGCAAGATATTTGATTTCTTTGCTTGGGCGCTTGCTCTCTGTCGCCGCGCATGCG 78
61  ATGTTATGATTAACCTTTCTTCTTAAGAGTGTGTGCGAGATGAGAGTGTCTTATACC 120
79  ATATTTATGACCGCTAGCTTCCAGAGCTCTGTGCGAGATGATGATGATGATCTTACT 138
121  ATTTCTTGGCAGACACACAGAGAGCTCAATGCCCGGACGTGAGTTCAATGATGTC 180
139  ATTTCTGCTGCTAGCTCAAGAGATTAATGATGATGATGATGATGATGATGATGAT 198
181  AAGAAAGGCGACAGATCTATGTTTATTCAGAGCTGTTAAAGAAATGAGCTGGGCGA 240
199  AAAAAAGGCGACAGATCTATGTTTATTCAGAGCTGTTAAAGAAATGAGCTGGGCGA 258
241  TTCTGGGCTGGCAGTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 300
259  TTTGGGCTGGCAGTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 318
301  CCCAGCACTTGTGTAGAGCAACGAGTGTACAGAGAGCGCCAGAGAGATTCACAAC 360
319  CCCAGCACTTGTGTAGAGCAACGAGTGTGTACAGAGAGCTTCAAGAGAGTTCCACC 378
361  ACGGATATTGACTTCTCTGTGA 383
379  ACGGATATTGACTTCTCTGTGA 401

RESULT 2
US-10-216-163-71
; Sequence 71, Application US/10216163
; Publication No. US20030149239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C3
; CURRENT APPLICATION NUMBER: US/10/216,163
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079234
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246

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; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-216-163-71
Query Match      74.3%; Score 285.4; DB 13; Length 521;
Best Local Similarity 84.1%; Pred. No. 2.9e-88;
Matches 322; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

1  ATGGCAAGATATTTGATTTCTTTGCTTGGGCGCTTGCTCTCTGTCGCCGCGCATGCG 60
38  ATGGCAAGATATTTGATTTCTTTGCTTGGGCGCTTGCTCTCTGTCGCCGCGCATGCG 97
61  ATGTTATGATTAACCTTTCTTCTTAAGAGTGTGTGCGAGATGAGAGTGTCTTATACC 120
98  ATATTTATGACCGCTAGCTTCCAGAGCTCTGTGCGAGATGATGATGATGATGATGAT 157
121  ATTTCTTGGCAGACACACAGAGAGCTCAATGCCCGGACGTGAGTTCAATGATGTC 180
158  ATTTCTGCTGCTAGCTCAAGAGATTAATGATGATGATGATGATGATGATGATGATGAT 217
181  AAGAAAGGCGACAGATCTATGTTTATTCAGAGCTGTTAAAGAAATGAGCTGGGCGA 240
218  AAAAAAGGCGACAGATCTATGTTTATTCAGAGCTGTTAAAGAAATGAGCTGGGCGA 277
241  TTCTGGGCTGGCAGTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 300
278  TTTGGGCTGGCAGTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 337
301  CCCAGCACTTGTGTAGAGCAACGAGTGTACAGAGAGCGCCAGAGAGATTCACAAC 360
338  CCCAGCACTTGTGTAGAGCAACGAGTGTGTACAGAGAGCTTCAAGAGAGTTCCACC 397
361  ACGGATATTGACTTCTCTGTGA 383
398  ACGGATATTGACTTCTCTGTGA 420

RESULT 3
US-10-216-765-71
; Sequence 71, Application US/10218765
; Publication No. US20030187201A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C19
; CURRENT APPLICATION NUMBER: US/10/218,765
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910

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Page 3

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PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/086392
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089905
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
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PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090691
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/095302
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/095318
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/095916
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/096146
PRIOR FILING DATE: 1998-08-11
PRIOR APPLICATION NUMBER: 60/096791
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 60/097986
PRIOR FILING DATE: 1998-08-26
PRIOR APPLICATION NUMBER: 60/098544
PRIOR FILING DATE: 1998-08-31
PRIOR APPLICATION NUMBER: 60/099596
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099598
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099803
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099811
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099812
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099816
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/100038
PRIOR FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: 60/100385
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100390
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100627
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100848
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/100919
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/101477
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101738
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101741
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101786
PRIOR FILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: 60/101916
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101922
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/106178
PRIOR FILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: 60/106248
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 60/106464
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 60/106905
PRIOR FILING DATE: 1998-11-03
PRIOR APPLICATION NUMBER: 60/108787
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/108801
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/108849
PRIOR FILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: 60/112422
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/113296
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/113605
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113621
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/115558
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115565
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115733
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/119549
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/123618
PRIOR FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: 60/125259
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 60/125775
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 60/126773
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: 60/127887
PRIOR FILING DATE: 1999-04-05
PRIOR APPLICATION NUMBER: 60/130232
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/131022
PRIOR FILING DATE: 1999-04-26
PRIOR APPLICATION NUMBER: 60/131270
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131291
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131445
PRIOR FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 60/134287
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/140650
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/140723
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/141037
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 60/144758
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; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/145698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 60/146222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 60/146963
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/149320
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/149638
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/151733
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/164418
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: 60/166361
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/169445
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835

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Query Match 74.3%; Score 285.4; DB 13; Length 521;
Best Local Similarity 84.1%; Pred. No. 2.9e-88;
Matches 322; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

```

```

QY 1 ATGGCAAGATATTGATCTTTTGGGCGCTTGCTCTCTGCGCGCATGCG 60
DB 38 ATGGCAAGATATTGATCTTTTCCCGGCTTGCTCTGCTGCTGCTGCTG 97
QY 61 ATGTTATGATTAACCTTTTCTAAGAGTGTGTGAGAGAGAGTGTATAC 120
DB 98 ATATTATGACCGCTAGCTTCCAGAGCTGTGCGAGATGATGATGATTA 157
QY 121 ATTCTCTGCGAAGAGCAGAGACTACATGCCCCGAGCTGTGATTCATCAT 180
DB 158 ATTTCTGTGCTAGTGTGCTCAAGAGATTAATGCCCGGAGCTGTGATTA 217
QY 181 AAGAAAGGCGAGAGATCTATGTTTATTCAGCTGTGTAACAGAAAATGAG 240
DB 218 AAAAAAGGCGAGAGATCTATGTTTACTCAAGCTGTGTAAGAAAATGAG 277
QY 241 TTCTGGGCTGCGAGTGTGTTATGAGCAACAGAGATGAGATGAGTTGG 300
DB 278 TTTTGGGCTGCGAGTGTGTTATGAGTGTGCGAGAGAGTGTGAGTTTTC 337
QY 301 CCCAGCAACTTGTGTTAGAGCAACGAGTGTACAGAGGCGCCAGAGAGAT 360
DB 338 CCCAGCAACTTGTGTTAGAGCAACGAGTGTGTACAGAGAGATGAGTT 397
QY 361 ACGGATATTGACTTCTTCTGGA 383
DB 398 ACGGATATTGACTTCTTCTGGA 420

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RESULT 4

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US-10-219-063-71
; Sequence 71, Application US/10219063
; Publication No. US20030187202A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William J.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

```

```

; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC24
; CURRENT APPLICATION NUMBER: US/10/219,063
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien

```

```

Query Match 74.3%; Score 285.4; DB 13; Length 521;
Best Local Similarity 84.1%; Pred. No. 2.9e-88;
Matches 322; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

```

```

QY 1 ATGGCAAGATATTGATCTTTTGGGCGCTTGCTCTCTGCGCGCATGCG 60
DB 38 ATGGCAAGATATTGATCTTTTCCCGGCTTGCTCTGCTGCTGCTGCTG 97
QY 61 ATGTTATGATTAACCTTTTCTAAGAGTGTGTGAGAGAGTGTATAC 120
DB 98 ATATTATGACCGCTAGCTTCCAGAGCTGTGCGAGATGATGATGATTA 157
QY 121 ATTCTCTGCGAAGAGCAGAGACTACATGCCCCGAGCTGTGATTCATCAT 180
DB 158 ATTTCTGTGCTAGTGTGCTCAAGAGATTAATGCCCGGAGCTGTGATTA 217
QY 181 AAGAAAGGCGAGAGATCTATGTTTATTCAGAGTGTGTAACAGAAAATGAG 240
DB 218 AAAAAAGGCGAGAGATCTATGTTTACTCAAGCTGTGTAAGAAAATGAG 277
QY 241 TTCTGGGCTGCGAGTGTGTTATGAGCAACAGAGATGAGATGAGTTGG 300
DB 278 TTTTGGGCTGCGAGTGTGTTATGAGTGTGCGAGAGAGTGTGAGTTTTC 337
QY 301 CCCAGCAACTTGTGTTAGAGCAACGAGTGTACAGAGGCGCCAGAGAGAT 360
DB 338 CCCAGCAACTTGTGTTAGAGCAACGAGTGTGTACAGAGAGATGAGTT 397
QY 361 ACGGATATTGACTTCTTCTGGA 383
DB 398 ACGGATATTGACTTCTTCTGGA 420

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RESULT 5

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US-10-219-066-71
; Sequence 71, Application US/10219066
; Publication No. US20030187203A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary

```

```

APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C27
CURRENT APPLICATION NUMBER: US/10/219,066
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 71
LENGTH: 521
TYPE: DNA
ORGANISM: Homo Sapien
US-10-219-066-71

```

| Query Match | 74.3% | Score 285.4 | DB 13 | Length 521 |
|-----------------------|----------------|---|----------|------------|
| Best Local Similarity | 84.1% | Pred. 2.9e-88 | | |
| Matches 322 | Conservative 0 | Mismatches 61 | Indels 0 | Gaps 0 |
| QY | 1 | ATGGCAGAAATATGATTCCTTTTCTGGGGCCCTTGTGCTCTGTGTCGGGAGTGGC | 60 | |
| Db | 38 | ATGGCAGAAATATGATTCCTTTCTGGGGCTTGTGCTGTATGTCGTGCATGGA | 97 | |
| QY | 61 | ATGTTATATGATAAATCTTCTCTTAGAAGATGTGTGCAGATAGAGAGTGTCTATAC | 120 | |
| Db | 98 | ATATTTATGACCGCTTAGCTTAGCTTCCAGAGAGCTCTGTGAGATGATGAGTGTCTATACT | 157 | |
| QY | 121 | ATTTCCTGGCAGAGACACAGAAAGCTACACATGCCCGAGCTGTAGGTTCAATCATGTC | 180 | |
| Db | 158 | ATTTCCTGGCTAGTGTCTCAGAAAGATTATATGCCCGGACGTGATTCATTAACGTT | 217 | |
| QY | 181 | AAGAAAGGCGACAGATCTATGTTTATTCCAAGCTGGTAAACAGAAATGGAGCTGGGGCA | 240 | |
| Db | 218 | AAAAAAGGCGACACATCTATGTGTACTCAAAAGCTGTAAAGAAATGGAGCTGGAGAA | 277 | |
| QY | 241 | TTCTGGGCTGGAGTGTATATGTGTATGCACACAGAGATAGATGGGAAATTTGGGTTATTC | 300 | |
| Db | 278 | TTTTGGGCTGGAGTGTATATGTGTATGCGCCAGACAGATGGGAGTCTGTGGTTATTTTC | 337 | |
| QY | 301 | CCGAGCAATTTGGTTAGAGCAACGAGTGTATCCAGAGAGGCCAACAGAGATTTCCACCC | 360 | |
| Db | 338 | CCGAGCAATTTGTCAGAGAAACAGAGGTGTGTATCCAGAGAACTTCAAGAGAGTTCCACCC | 397 | |
| QY | 361 | ACGGATATATGACTTTCTTCTGTGA | 383 | |
| Db | 398 | ACGGATATGACTTTCTTCTGTGA | 420 | |

```

1      RESULT 6
2      US-10-219-067-71
3      ; Sequence 71, Application US/10219067
4      ; Publication No. US20030187204A1
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Baker, Kevin P.
7      ; APPLICANT: Desnoyers, Luc
8      ; APPLICANT: Gerritsen, Mary
9      ; APPLICANT: Goddard, Audrey
10     ; APPLICANT: Godowski, Paul J.
11     ; APPLICANT: Grimaldi, J. Christopher
12     ; APPLICANT: Gurney, Austin L.
13     ; APPLICANT: Smith, Victoria
14     ; APPLICANT: Stephan, Jean-Philippe F.
15     ; APPLICANT: Watanabe, Colin L.
16     ; APPLICANT: Wood, William T.
17     ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
18     ; FILE REFERENCE: P3530P1C51
19     ; CURRENT APPLICATION NUMBER: US/10/219,067
20     ; CURRENT FILING DATE: 2002-08-14
21     ; PRIOR APPLICATION NUMBER: 10/119,480
22     ; PRIOR FILING DATE: 2002-04-09
23     ; PRIOR APPLICATION NUMBER: 60/059113
24     ; PRIOR FILING DATE: 1997-09-17
25     ; PRIOR APPLICATION NUMBER: 60/062287
26     ; PRIOR FILING DATE: 1997-10-17
27     ; PRIOR APPLICATION NUMBER: 60/063549
28     ; PRIOR FILING DATE: 1997-10-28
29     ; PRIOR APPLICATION NUMBER: 60/064103
30     ; PRIOR FILING DATE: 1997-10-31
31     ; PRIOR APPLICATION NUMBER: 60/068873
32     ; PRIOR FILING DATE: 1997-12-17
33     ; PRIOR APPLICATION NUMBER: 60/078910
34     ; PRIOR FILING DATE: 1998-03-20
35     ; PRIOR APPLICATION NUMBER: 60/079294
36     ; PRIOR FILING DATE: 1998-03-25
37     ; PRIOR APPLICATION NUMBER: 60/079656
38     ; PRIOR FILING DATE: 1998-03-26
39     ; PRIOR APPLICATION NUMBER: 60/079728
40     ; PRIOR FILING DATE: 1998-03-27
41     ; Remaining Seq Application data removed - See File Wrapper or PALM.
42     ; NUMBER OF SEQ ID NOS: 246
43     ; SEQ ID NO 71
44     ; LENGTH: 521
45     ; TYPE: DNA
46     ; ORGANISM: Homo Sapien
47     ; US-10-219-067-71

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| | Query Match | Similarity | 74.3% | Score | 285.4 | DB | 13 | Length | 521 | |
|----|-------------|---|--------------|-------|------------|------|--------|--------|------|---|
| | Best Local | Similarity | 84.1% | Pred. | No. | 2.9e | DB | | | |
| | Matches | 322 | Conservative | 0 | Mismatches | 61 | Indels | 0 | Gaps | 0 |
| QY | 1 | ATGGCAAGAAATATTGATCTCTTTCTGCGGGCCCTTGCGCTCTCTGTGCGGGAGATGCG | 60 | | | | | | | |
| Db | 38 | ATGGCAAGAAATATTGATCTCTTTCTCTCCGGGCTTTGTGCGCTGTATGCGCTGTGATGGA | 97 | | | | | | | |
| QY | 61 | ATGTTTATGATATAACTTTCTCTTAAGAAGTGTGTGCAGATGTGAAGTGTGTATACG | 120 | | | | | | | |
| Db | 98 | ATATTTATGACCGCTACGCTTCCAAAGCTCTGTGCAGATGTGAAGTGTGTATACG | 157 | | | | | | | |
| QY | 121 | ATTTCCTGCGAAGAGCACAAGGAAGCTACATGCCCGGACTGTAGCTTCATCATATGC | 180 | | | | | | | |
| Db | 158 | ATTTCCTGCGCTAGTGTCTCAAGAGATTATATAGCCCCGGACTGTAGCTTCATTAACGTT | 217 | | | | | | | |
| QY | 181 | AAGAAAGGAGAGAGATCTATGTTTATTTCGAAGCTGTGAACAGAAATGAGAGCTGGGCA | 240 | | | | | | | |
| Db | 218 | AAAAAGGAGCAGATCTATGTGTACTCAAGCTGTAAAGAAATGAGAGCTGGAGAA | 277 | | | | | | | |
| QY | 241 | TTCTGGGCTGGCAGTGTTTATGTGTACCAACAGAGATGAGATGGAAATGTGTGATTATTC | 300 | | | | | | | |
| Db | 278 | TTTTGGGCTGGCAGTGTTTATGTGTAGAGGACAGATGGAGAGCTGGGATTAATTC | 337 | | | | | | | |

QY 301 CCCAGCACTTGGTTAGAGACAGATGTACACGAGGCCACCAAGATTTCCACC 360
DB 338 CCAGAGACTTGGTCAAGAGACGCGTGTGTACAGAGAGCTCAAGAGAGTTCCAC 397
QY 361 ACGGATATTGACTTCTTGTGA 383
DB 398 ACGGATATTGACTTCTTGTGCA 420

RESULT 7

US-10-219-068-71
; Sequence 71, Application US/10219068
; Publication No. US20030187205A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerltsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gueney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C31
; CURRENT APPLICATION NUMBER: US/10/219,068
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-068-71

Query Match 74.3%; Score 285.4; DB 13; Length 521;
Best Local Similarity 84.1%; Pred. No. 2.9e-88;
Matches 322; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 1 ATGGCAAGATATTGATCTTTTGGGCGCTTGTCCTCTCTGTCGGGCGCATGGC 60
DB 38 ATGGCAAGATATTGATCTTTTCTCCGGGCTTGTGCTGTATGTGCTGTCATGGA 97
QY 61 ATGTTTATGATAAATCTTCTCTAAGAGTTGTGTGCAATAGAGAGTGTCTATAC 120
DB 98 ATATTATGAGCCCTTGAAGCTTCCAAAGAGCTGTGCAATATGATGTGTCTATAC 157
QY 121 ATTCTCTGCAAGAGCAGAGAAAGATACATGCCCCGAGCTAGTTCATCAATGTC 180

DB 158 ATTCTCTGCTAGTCTCTCAAGAAATTTATATGCCCCGAGCTGTACATTCATACGTT 217
QY 181 AAGAAAGGCGAGCAGATCTATGTTATTCAGCTGTGTAAAGAAAATGAGCTGGGCA 240
DB 218 AAAAAAGGCGAGCAGATCTATGTTATCTCAAGCTGTGTAAAGAAAATGAGCTGGAGAA 277
QY 241 TTCTGGGCTGGAGTGTATTATGTGTGACCAAGATGATGGAAATTTGTGGTTATTTTC 300
DB 278 TTTGGGCTGGAGTGTATTATGTGTGATGCGCAGAGCAGATGGAGTGTGTGGTTATTTTC 337
QY 301 CCCAGCACTTGGTTAGAGACAGATGTACACGAGGCCACCAAGATTTCCACC 360
DB 338 CCAGAGACTTGGTCAAGAGACGCGTGTGTACAGAGAGCTCAAGAGAGTTCCAC 397
QY 361 ACGGATATTGACTTCTTGTGA 383
DB 398 ACGGATATTGACTTCTTGTGCA 420

RESULT 8

US-10-219-069-71
; Sequence 71, Application US/10219069
; Publication No. US20030187206A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerltsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gueney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C40
; CURRENT APPLICATION NUMBER: US/10/219,069
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-069-71

Query Match 74.3%; Score 285.4; DB 13; Length 521;
Best Local Similarity 84.1%; Pred. No. 2.9e-88;
Matches 322; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 1 ATGGCAAGATATTGATCTTTTGGGCGCTTGTCCTCTCTGTCGGGCGCATGGC 60

PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 71
LENGTH: 521
TYPE: DNA
ORGANISM: Homo Sapien
US-10-219-475-71

Query Match 74.3%; Score 285.4; DB 13; Length 521;
Best Local Similarity 84.1%; Pred. No. 2.9e-88;
Matches 322; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 1 ATGGCAAGATATTTGATTTCTTTGCTGGGGGCTTGTGGCTCTGTGCGGGCATGGC 60
DB 38 ATGGCAAGATATTTGATTTCTTTCTCTCCGGGCTTGTGGCTGTATGCTGTGATGCA 97
QY 61 ATGTTATGATTAACCTTTCTTCTAAGAAATGTGTGCAATGAGAGTGTCTATATACC 120
DB 98 ATATTTATGACCGCTCAGCTTCCAGAAAGCTCTGTGCAAGATGATGATGATGCTATACT 157
QY 121 ATTCTCTGCAAGACAGACAGAAAGCTACATATGCCCCGAGCTGTAGTTTCATCATGTC 180
DB 158 ATTCTCTGCTAGTGTCTCAAGAAAGATTAATATGCCCCGAGCTGTAGTTTCATTAAGCTT 217
QY 181 AAGAAAGGAGAGAGATCTATGTTTATTCAGAGCTGTAAAGAAATGAGCTGGAGCA 240
DB 218 AAAAAAGGAGAGAGATCTATGTTTCTCAAGAGCTGTAAAGAAATGAGCTGGAGCA 277
QY 241 TTCTGGGCTGCAAGTGTATGTTATGTTGACCAAGAGATGAGATGGAAATTTGGGTTATTTTC 300
DB 278 TTTTGGGCTGCAAGTGTATGTTATGTTATGTTGACCAAGAGATGAGATGGAAATTTGGGTTATTTTC 337
QY 301 CCCAGCAACTGTGTTAAGAGCAAGAGTGTACAGAGGCGCCACCAAGAGATTTCCAAAC 360
DB 338 CCCAGCAACTGTGTTAAGAGCAAGAGTGTGTACCAAGAGATTTCCAAAGAGATTTCCCAAC 397
QY 361 ACGGATATTGACTTTCTTCTGTGA 383
DB 398 ACGGATATTGACTTTCTTCTGTGA 420

RESULT 11
US-10-219-480-71

Sequence 71, Application US/10219480
Publication No. US20030187209A1
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerltisen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P9530P1C38
CURRENT APPLICATION NUMBER: US/10/219,480

CURRENT FILING DATE: 2002-08-13

PRIOR APPLICATION NUMBER: 10/119,480

PRIOR FILING DATE: 2002-04-09

PRIOR APPLICATION NUMBER: 60/059113

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/062287

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 71
LENGTH: 521
TYPE: DNA
ORGANISM: Homo Sapien
US-10-219-480-71

Query Match 74.3%; Score 285.4; DB 13; Length 521;
Best Local Similarity 84.1%; Pred. No. 2.9e-88;
Matches 322; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 1 ATGGCAAGATATTTGATTTCTTTGCTGGGGGCTTGTGGCTCTGTGCGGGCATGGC 60
DB 38 ATGGCAAGATATTTGATTTCTTTCTCTCCGGGCTTGTGGCTGTATGCTGTGATGCA 97
QY 61 ATGTTATGATTAACCTTTCTTCTAAGAAATGTGTGCAATGAGAGTGTCTATATACC 120
DB 98 ATATTTATGACCGCTCAGCTTCCAGAAAGCTCTGTGCAAGATGATGATGATGCTATACT 157
QY 121 ATTCTCTGCAAGACAGACAGAAAGCTACATATGCCCCGAGCTGTAGTTTCATCATGTC 180
DB 158 ATTCTCTGCTAGTGTCTCAAGAAAGATTAATATGCCCCGAGCTGTAGTTTCATTAAGCTT 217
QY 181 AAGAAAGGAGAGAGATCTATGTTTATTCAGAGCTGTAAAGAAATGAGCTGGAGCA 240
DB 218 AAAAAAGGAGAGAGATCTATGTTTCTCAAGAGCTGTAAAGAAATGAGCTGGAGCA 277
QY 241 TTCTGGGCTGCAAGTGTATGTTATGTTGACCAAGAGATGAGATGGAAATTTGGGTTATTTTC 300
DB 278 TTTTGGGCTGCAAGTGTATGTTATGTTATGTTGACCAAGAGATGAGATGGAAATTTGGGTTATTTTC 337
QY 301 CCCAGCAACTGTGTTAAGAGCAAGAGTGTACAGAGGCGCCACCAAGAGATTTCCAAAC 360
DB 338 CCCAGCAACTGTGTTAAGAGCAAGAGTGTGTACCAAGAGATTTCCAAAGAGATTTCCCAAC 397
QY 361 ACGGATATTGACTTTCTTCTGTGA 383
DB 398 ACGGATATTGACTTTCTTCTGTGA 420

RESULT 12
US-10-219-483-71

Sequence 71, Application US/10219483
Publication No. US20030187210A1
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerltisen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME

```

FILE REFERENCE: P3530P1C43
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 71
LENGTH: 521
TYPE: DNA
ORGANISM: Homo Sapien
US-10-219-483-71

Query Match      74.3%; Score 285.4; DB 13; Length 521;
Best Local Similarity 84.1%; Pred. No. 2.9e-88;
Matches 322; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

1 ATGGCAGATATTTGATTTCTTTGCTGGGGGCTTTGGGCTCTGTGCGGGCATGCG 60
38 ATGGCAGATATTTGATTTCTTTGCTGGGGGCTTTGGGCTCTGTGCGGGCATGCG 97
61 ATGGTATGATTAACCTTTCTTAAGAAAGTGTGAGATGAGAGTGTCTATACC 120
98 ATATTTATGACCGCTGTAGCTTCCAAAGAGCTCTGTGAGATGATGATGTCTATACC 157
121 ATTTCTGTGCAAGAGCAGCAGAGATCAATGCCCCGAGCTGTAGTTCATCATGTC 180
158 ATTTCTGTGCAAGAGCAGCAGATCAATGCCCCGAGCTGTAGTTCATCATGTC 217
181 AAGAAAGGGCAGCAGATCTATGTTTATTCAGAGCTGTGTAACAGAAATGAGCTGGGCA 240
218 AAAAAAGGGCAGCAGATCTATGTTTATTCAGAGCTGTGTAACAGAAATGAGCTGGGCA 277
241 TTCTGGCTGGCAGAGTGTATGTTATGTCACCAAGATGAGATGAGATGAGTATTC 300
278 TTTTGGCTGGCAGAGTGTATGTTATGTTATGTCACCAAGATGAGATGAGTATTC 337
301 CCAGCAACTTGTGTAGAGCAGAGTGTACCAAGAGCTGTGTAACAGAAATGAGCTGGGCA 360
338 CCAGCAACTTGTGTAGAGCAGAGTGTGTACCAAGAGCTGTGTAACAGAAATGAGCTGGGCA 397
361 ACGATATTTGACTTCTTCTGTGA 383
398 ACGATATTTGACTTCTTCTGTGA 420

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APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C29
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 71
LENGTH: 521
TYPE: DNA
ORGANISM: Homo Sapien
US-10-219-525-71

Query Match      74.3%; Score 285.4; DB 13; Length 521;
Best Local Similarity 84.1%; Pred. No. 2.9e-88;
Matches 322; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

1 ATGGCAGATATTTGATTTCTTTGCTGGGGGCTTTGGGCTCTGTGCGGGCATGCG 60
38 ATGGCAGATATTTGATTTCTTTGCTGGGGGCTTTGGGCTCTGTGCGGGCATGCG 97
61 ATGGTATGATTAACCTTTCTTAAGAAAGTGTGAGATGAGAGTGTCTATACC 120
98 ATATTTATGACCGCTGTAGCTTCCAAAGAGCTCTGTGAGATGATGATGTCTATACC 157
121 ATTTCTGTGCAAGAGCAGCAGAGATCAATGCCCCGAGCTGTAGTTCATCATGTC 180
158 ATTTCTGTGCAAGAGCAGCAGATCAATGCCCCGAGCTGTAGTTCATCATGTC 217
181 AAGAAAGGGCAGCAGATCTATGTTTATTCAGAGCTGTGTAACAGAAATGAGCTGGGCA 240
218 AAAAAAGGGCAGCAGATCTATGTTTATTCAGAGCTGTGTAACAGAAATGAGCTGGGCA 277
241 TTCTGGCTGGCAGAGTGTATGTTATGTCACCAAGATGAGATGAGATGAGTATTC 300
278 TTTTGGCTGGCAGAGTGTATGTTATGTTATGTCACCAAGATGAGATGAGTATTC 337
301 CCAGCAACTTGTGTAGAGCAGAGTGTACCAAGAGCTGTGTAACAGAAATGAGCTGGGCA 360
338 CCAGCAACTTGTGTAGAGCAGAGTGTGTACCAAGAGCTGTGTAACAGAAATGAGCTGGGCA 397
361 ACGATATTTGACTTCTTCTGTGA 383
398 ACGATATTTGACTTCTTCTGTGA 420

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RESULT 13
US-10-219-525-71
Sequence 71, Application US/10219525
Publication No. US20030187211A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Geritsen, Mary
APPLICANT: Goddard, Audrey

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| | | | |
|----|-----|--|-----|
| Qy | 181 | AAAGAGGGGAGAGAGATCTATGTTATTTCCAAAGCTGGTAAACAGAAATATGAGCTGGGGCA | 240 |
| Db | 218 | AAAAAAAAAGGCGACAGATCTATGTGTACTCAAGCTGGTAAAGAAATATGAGCTGGAGAA | 277 |
| Qy | 241 | TTCTGGGCTGGCAGTGTTTATGTGTGACCAACGAGTAGATGGAAATTTGGGTTATTC | 300 |
| Db | 278 | TTTTGGGCTGGCAGTGTTTATGTGTGTGGCCAGGACGAGATGGGAGTGTGGGTTATTC | 337 |
| Qy | 301 | CCGACGAATCTGGTTTAGAAGCAAGAGGTATCCAGAGGCGACCAAGAGATTTCCAAC | 360 |
| Db | 338 | CCGAGGAATCTGGTCAAGGAACAGCGGTGTGTACCCAGGAAGTTACCAAGAGATTTCCACC | 397 |
| Qy | 361 | ACCGATATTGACTTCTTCTGTGA | 383 |
| Db | 398 | ACCGATATTGACTTCTTCTGTGCA | 420 |

Search completed: December 30, 2003, 10:03:03
Job time : 315.339 secs

FEATURE

ALIGNMENTS

TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 330 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: mat peptide
LOCATION: 7..327
NAME/KEY: misc RNA
LOCATION: 4..6
OTHER INFORMATION: /function= "Startcodon Met"
US-08-578-649-18

Query Match 16.2%; Score 62.4; DB 1; Length 330;
Best Local Similarity 58.0%; Pred. No. 2.6e-11;
Matches 152; Conservative 0; Mismatches 101; Indels 9; Gaps 2;

QY 67 ATGCATTAATCTTCTTCTAAGAGTTGTGTGAGATGAGAGTGTGTCTATATACCATTTCT 126
DB 13 ATGCCAAATTAAGCAGATCTGTAATTAATGATGAGATCAGAGTGCAGCCACCTATCTCC 72
QY 127 CTGGCAGAGCAGCAGAACACTACATGATGCGCCGAGCTGATGATCATATGTCAGAAA 186
DB 73 ATGGCTGTGCGCTTCAGACTACATGCGCCGAGCTGCGCATTTCTTACCATTTACCGG 132
QY 187 GGAGCAGCAGATCTATGTTTATTCAGCTGTGTACAGAAAATGAGCTGGGGCATTTGG 246
DB 133 GGGCAGAGTGTATGCTCTTCTTCCAAAGCTG-----AAGGCCGTGGCGGCTCTTCTGG 186
QY 247 GCTGAGCTGTTTATGATGATCAGCAGAGATGAGAGAAAT---GTGGTATTTTCCCG 303
DB 187 GGAGGAGCGCTTCAGAGGATTAATGAGATCTGGCTGCGCTGGGCTATTTTCCCG 246
QY 304 AGCAACTTGTAGAGAGCAAC 325
DB 247 AGTACATGCTCCGAGAGGACC 268

RESULT 4
US-08-578-649-8
Sequence 8, Application US/08578649
Patent No. 5770366

GENERAL INFORMATION:
APPLICANT: Ulrich Bogdan
APPLICANT: Reinhard Butner
APPLICANT: Brigitte Kaluza
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 MB storage diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-July-1993
ATTORNEY/AGENT INFORMATION:

NAME: Andrew L. Tiajoleff
REGISTRATION NUMBER: 31,575
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 305 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: misc RNA
LOCATION: join(1..29, 277..305)
OTHER INFORMATION: /function= "Primer"
US-08-578-649-8

Query Match 14.9%; Score 57.4; DB 1; Length 305;
Best Local Similarity 58.5%; Pred. No. 1.2e-09;
Matches 141; Conservative 0; Mismatches 91; Indels 9; Gaps 2;

QY 88 AAGTGTGTGACATGAGAGTGTGTCTATACCATTTCTGAGCAAGAGCAGCAAGAC 147
DB 7 AAGTTTGGCGGATGAGAGTGTGTGAGCAGCCTTATCTCCATGCTGTGGCCCTTCAGAG 66
QY 148 TACATGCCCCGAGCTGTAGTTCATCATGTGCAAGAAAGGAGCAGATCTATGTTAT 207
DB 67 TACATGCCCCGAGCTGTAGTTCATCATGTGCAAGAAAGGAGCAGATCTATGTTAT 126
QY 208 TCCAGCTGTGTAAAGAAATGAGCTGGGCGATTTCTGGCTGTGCACTGTTATGTGAC 267
DB 127 TCCAGCTG-----AAGGCCGTGGCGGCTCTTCTGGGAGAGCAGCTTCAGGGAGAT 180
QY 268 CACAGAGATGAGTGAAT---GTGGCTATTTTCCCGAGCAACTGTGTAGAGCA 324
DB 181 TACTATGAGATGTGTGCTGCGCTGCGCTGCTATTTTCCCGAGTATGTCGAGAGAC 240
QY 325 C 325
DB 241 C 241

RESULT 5
US-08-578-649-24
Sequence 24, Application US/08578649
Patent No. 5770366

GENERAL INFORMATION:
APPLICANT: Ulrich Bogdan
APPLICANT: Reinhard Butner
APPLICANT: Brigitte Kaluza
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 MB storage diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-July-1993


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COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
CLASSIFICATION: 435
Prior APPLICATION DATA:
APPLICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-July-1993
ATTORNEY/AGENT INFORMATION:
NAME: Andrew L. TiaoloJoff
REGISTRATION NUMBER: 31,575
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 688-3884
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3565 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 1378..1449
FEATURE:
NAME/KEY: exon
LOCATION: 1378..1504
FEATURE:
NAME/KEY: exon
LOCATION: 1586..1719
FEATURE:
NAME/KEY: exon
LOCATION: 2804..2914
FEATURE:
NAME/KEY: exon
LOCATION: 3232..3252
FEATURE:
NAME/KEY: -
LOCATION: one-of(2216)
OTHER INFORMATION: /note="N in position 2216
OTHER INFORMATION: denotes an indefinite number ans sequence of
OTHER INFORMATION: nucleotides"
US-08-578-649-3

Query Match 9.3%; Score 35.6; DB 1; Length 3565;
Best Local Similarity 60.2%; Pred. No. 0.07;
Matches 59; Conservative 0; Mismatches 39; Indels 0; Gaps 0

Qy 119 CCATTTCCTCGCAAGACAGACAGAGAACTACATGCGCCCGGACTGTAGTTCATCATG 178
Db 1589 CATATCCATGCTGTGTGGCCCTTCAGACTACATGAGCCCGGACTGCGATTCCTGACCA 1644

Qy 179 TCAAGAAAGGACAGACATCTATGTTTATTTCCAACTG 216
Db 1649 TTCACCGGGGCCAAGTGGTGTATGTCTTCTCCAACTG 1686

RESULT 7
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
;

```

CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)856-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: PTZpdt-F15
US-08-232-463-14

Query Match 8.5%; Score 32.8; DB 1; Length 7218;
Best Local Similarity 3.5%; Pred. No. 0.83;
Matches 10; Conservative 157; Mismatches 119; Indels 0; Gaps 0;

QY 67 ATGATAACTTCTTCTAGAAAGTGTGTGAGATGAGAGATGTGTCTATCCATTCT 126
DB 1451 ATAGAAGATTGTCACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1392
QY 127 CTGGCAGAGCAGAGAACTCAATGCCCCGACTGAGTTCATCATGTCAAGAA 186
DB 1391 RRR 1332
QY 187 GGGCAGACATCTATGTTTATTCAGCTGTAAACAGAAATGAGCTGGGCAATTCGG 246
DB 1331 RRR 1272
QY 247 GCTGAGAGTGTATGCTGACCAACGATGAGATGGCAATGTGGTATTTCCCGAC 306
DB 1271 RRR 1212
QY 307 AACTGTGTAAGAGACAGAGTGTCCAGGAGGCCACACAGAGAG 352
DB 1211 RRR 1166

RESULT 8
US-08-433-522A-1
Sequence 1, Application US/08433522A
Patent No. 6013514
GENERAL INFORMATION:
APPLICANT: CHONG, Pele
APPLICANT: THOMAS, Wayne
APPLICANT: YANG, Yan Ping
APPLICANT: LOOSMORE, Sheena
APPLICANT: SIA, Dwo Yuan Charles
APPLICANT: KLEIN, Michel
TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN

NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6TH Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,522A
FILING DATE: 12-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-434 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2949 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 75..2465
US-08-433-522A-1

Query Match 8.5%; Score 32.6; DB 3; Length 2949;
Best Local Similarity 5.9%; Pred. No. 0.65;
Matches 62; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 31 GGCCTTGCTGCTCTGTCGCGGCGCATGCATGTTTATGATAACTTCTTAAAGAG 90
DB 2055 GGACCTAACGCAATTATGCGCAATATGTAATGTAATGTGTACTGTACTTTAAGAG 2114
QY 91 TTGTGTCAGATGAGAGTGTCTATACCATTTCTCTGCAAGACAG 141
DB 2115 ATAAGTCTGATGATGATGTTGTGTATGCAATGCTACAGCTAGCGCAGAG 2165

RESULT 9
US-09-135-166-1
Sequence 1, Application US/09135166
Patent No. 6083743
GENERAL INFORMATION:
APPLICANT: CHONG, Pele
APPLICANT: THOMAS, Wayne
APPLICANT: YANG, Yan Ping
APPLICANT: LOOSMORE, Sheena
APPLICANT: SIA, Dwo Yuan Charles
APPLICANT: KLEIN, Michel
TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6TH Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/135,166
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA: 08/433,522
APPLICATION NUMBER: 12-SEP-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-829 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2949 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 75..2465
US-09-135-166-1

Query Match 8.5%; Score 32.6; DB 3; Length 2949;
Best Local Similarity 55.9%; Pred. No. 0.65; Indels 0; Gaps 0;
Matches 62; Conservative 0; Mismatches 49;

QY 31 GGCCTTGCGCTCTGTCGCCGCGCATGCTTTATGATAAATTCTCTTAAGAG 90
DB 2055 GGACCTAACGCAATTTATGCCGATATGTAATGTAAGTACTGTTAAGAG 2114

QY 91 TTGTGTGCGATGAGAGAGTGTCTATACCATTTCTCTGCGAAGACAG 141
DB 2115 ATAAGTTGTGATGTGATGTGTGTAATGCAATCGCTACAGCTAGCGCAGAG 2165

RESULT 10
US-08-942-046-1
Sequence 1, Application US/08942046
Patent No. 6264954
GENERAL INFORMATION:
APPLICANT: CHONG, Pele
APPLICANT: THOMAS, Wayne
APPLICANT: YANG, Yan Ping
APPLICANT: LOOSMORE, Sheena
APPLICANT: SIA, Dwo Yuan Charles
APPLICANT: KLEIN, Michel
TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6TH Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/942,046
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/433,522
FILING DATE: 12-SEP-1995

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-732 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2949 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 75..2465
US-08-942-046-1

Query Match 8.5%; Score 32.6; DB 3; Length 2949;
Best Local Similarity 55.9%; Pred. No. 0.65; Indels 0; Gaps 0;
Matches 62; Conservative 0; Mismatches 49;

QY 31 GGCCTTGCGCTCTGTCGCCGCGCATGCTTTATGATAAATTCTCTTAAGAG 90
DB 2055 GGACCTAACGCAATTTATGCCGATATGTAATGTAAGTACTGTTAAGAG 2114

QY 91 TTGTGTGCGATGAGAGAGTGTCTATACCATTTCTCTGCGAAGACAG 141
DB 2115 ATAAGTTGTGATGTGATGTGTGTAATGCAATCGCTACAGCTAGCGCAGAG 2165

RESULT 11
US-08-433-522A-5
Sequence 5, Application US/08433522A
Patent No. 6013514
GENERAL INFORMATION:
APPLICANT: CHONG, Pele
APPLICANT: THOMAS, Wayne
APPLICANT: YANG, Yan Ping
APPLICANT: LOOSMORE, Sheena
APPLICANT: SIA, Dwo Yuan Charles
APPLICANT: KLEIN, Michel
TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6TH Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,522A
FILING DATE: 12-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-434 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2950 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 334..2724
US-08-433-522A-5

Query Match 8.5%; Score 32.6; DB 3; Length 2950;
Best Local Similarity 55.9%; Pred. No. 0.65;
Matches 62; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 31 GGCTTGTGGCTCTCTGTCGGCGCATGGCATGTTATGATAAATTCTTCTTAAGAG 90
DB 2314 GGACCTAACGCAATTATGCCGAAATGCTAATGTAAGTGTAGTCTGTACTTTTAAGAG 2373
QY 91 TTGTGTGAGATGAGAGTGTCTATACCATTTCTCTGCAAGACAG 141
DB 2374 ATAACTTCTGATGTGATGTGTATGCAATCGCTACAGCTAGCGCAGAG 2424

RESULT 12

US-09-135-166-5
Sequence 5, Application US/09135166
Patent No. 6083743
GENERAL INFORMATION:
APPLICANT: CHONG, Pele
APPLICANT: THOMAS, Wayne
APPLICANT: YANG, Yan Ping
APPLICANT: LOOSMORE, Sheena
APPLICANT: SIA, Dwo Yuan Charles
APPLICANT: KLEIN, Michel
TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Slim & McBurney
STREET: 6TH Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/135,166
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/433,522
FILING DATE: 12-SEP-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-823 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2950 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 334..2724
US-09-135-166-5

Query Match 8.5%; Score 32.6; DB 3; Length 2950;
Best Local Similarity 55.9%; Pred. No. 0.65;
Matches 62; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 31 GGCTTGTGGCTCTCTGTCGGCGCATGGCATGTTATGATAAATTCTTCTTAAGAG 90
DB 2314 GGACCTAACGCAATTATGCCGAAATGCTAATGTAAGTGTAGTCTGTACTTTTAAGAG 2373
QY 91 TTGTGTGAGATGAGAGTGTCTATACCATTTCTCTGCAAGACAG 141
DB 2374 ATAACTTCTGATGTGATGTGTATGCAATCGCTACAGCTAGCGCAGAG 2424

RESULT 13

US-08-942-046-5
Sequence 5, Application US/08942046
Patent No. 6264954
GENERAL INFORMATION:
APPLICANT: CHONG, Pele
APPLICANT: THOMAS, Wayne
APPLICANT: YANG, Yan Ping
APPLICANT: LOOSMORE, Sheena
APPLICANT: SIA, Dwo Yuan Charles
APPLICANT: KLEIN, Michel
TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Slim & McBurney
STREET: 6TH Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/942,046
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/433,522
FILING DATE: 12-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-732 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2950 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 334..2724
US-08-942-046-5
Query Match 8.5%; Score 32.6; DB 3; Length 2950;
Best Local Similarity 55.9%; Pred. No. 0.65;
Matches 62; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 31 GGCTTGTGGCTCTCTGTCGGCGCATGGCATGTTATGATAAATTCTTCTTAAGAG 90
DB 2314 GGACCTAACGCAATTATGCCGAAATGCTAATGTAAGTGTAGTCTGTACTTTTAAGAG 2373

QY 91 TTGTGTGCAGATGAGAGTGTCTATACATTCTCTGGCAGACAG 141
DB 2374 ATAAAGTTCTGATGTGATGTGTATGCAATGCAATGCTAGCGCAGAG 2424

RESULT 14
US-08-433-522A-3

Sequence 3, Application US/08433522A
Patent No. 6013514
GENERAL INFORMATION:
APPLICANT: CHONG, Pele
APPLICANT: THOMAS, Wayne
APPLICANT: YANG, Yan Ping
APPLICANT: LOOSMORE, Sheena
APPLICANT: SIA, Dwo Yuan Charles
APPLICANT: KLEIN, Michel
TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6TH Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,522A
FILING DATE: 12-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-434 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2984 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 374..2764
US-08-433-522A-3

Query Match 8.5%; Score 32.6; DB 3; Length 2984;
Best Local Similarity 55.9%; Pred. No. 0.65;
Matches 62; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 31 GGCCTTGCTGCTCTGTGCGCGGCATGCGATGTTATGCAATTTCTTCTTAAGAG 90
DB 2354 GGACCTAACGCAATTATGCGCAATATGTAATGTAGTACTGTAATTTAAGAG 2413
QY 91 TTGTGTGCAGATGAGAGTGTCTATACATTCTCTGGCAGACAG 141
DB 2414 ATAAAGTTCTGATGTGATGTGTATGCAATGCAATGCTAGCGCAGAG 2464

RESULT 15
US-09-135-166-3
Sequence 3, Application US/09135166
Patent No. 6083743
GENERAL INFORMATION:
APPLICANT: CHONG, Pele
APPLICANT: THOMAS, Wayne

APPLICANT: YANG, Yan Ping
APPLICANT: LOOSMORE, Sheena
APPLICANT: SIA, Dwo Yuan Charles
APPLICANT: KLEIN, Michel
TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6TH Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/135,166
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/433,522
FILING DATE: 12-SEP-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-829 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2984 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 374..2764
US-09-135-166-3

Query Match 8.5%; Score 32.6; DB 3; Length 2984;
Best Local Similarity 55.9%; Pred. No. 0.65;
Matches 62; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 31 GGCCTTGCTGCTCTGTGCGCGGCATGCGATGTTATGCAATTTCTTCTTAAGAG 90
DB 2354 GGACCTAACGCAATTATGCGCAATATGTAATGTAGTACTGTAATTTAAGAG 2413
QY 91 TTGTGTGCAGATGAGAGTGTCTATACATTCTCTGGCAGACAG 141
DB 2414 ATAAAGTTCTGATGTGATGTGTATGCAATGCAATGCTAGCGCAGAG 2464

Search completed: December 30, 2003, 06:10:54
Job time: 33.014 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 29, 2003, 16:03:18 ; Search time 13.2661 Seconds
(without alignments)
927.898 Million cell updates/sec

Title: US-10-019-455A-47
Perfect score: 676
Sequence: 1 MARILLILGLGVALCAGHG.....RVYGEATKEIPTTDIDPCE 128

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length DB | ID | Description |
|------------|-------|-------------|-----------|----------|--------------------|
| 1 | 275.5 | 40.8 | 131 | 138019 | melanoma-derived g |
| 2 | 93.5 | 13.8 | 844 | 1 TVMSV | transforming prote |
| 3 | 91.5 | 13.5 | 839 | 1 TVHVV | transforming prote |
| 4 | 84.5 | 12.5 | 878 | 1 IS1940 | gene VAV2 protein |
| 5 | 82.5 | 12.2 | 1589 | 1 RGYC5 | cell division cont |
| 6 | 77 | 11.4 | 413 | 2 T31051 | transposase homolo |
| 7 | 77 | 11.4 | 722 | 2 G86746 | hypothetical prote |
| 8 | 75.5 | 11.2 | 1215 | 2 T32734 | myosin-1A - Acanth |
| 9 | 75 | 11.1 | 332 | 2 T04200 | hypothetical prote |
| 10 | 74 | 10.9 | 695 | 2 S6662 | protein-glutamine |
| 11 | 74 | 10.9 | 994 | 2 T21356 | hypothetical prote |
| 12 | 73.5 | 10.9 | 847 | 1 A53800 | mixed-lineage prot |
| 13 | 73 | 10.8 | 520 | 1 RDLNTZ | dihydrofolate redu |
| 14 | 73 | 10.8 | 670 | 1 S67383 | probable signal tr |
| 15 | 72 | 10.7 | 259 | 2 C64427 | hypothetical prote |
| 16 | 72 | 10.7 | 344 | 2 C81920 | epidermal growth f |
| 17 | 71.5 | 10.6 | 1717 | 1 A4558 | copper ABC transpo |
| 18 | 71 | 10.5 | 344 | 2 E81183 | connexin 45 - mous |
| 19 | 71 | 10.5 | 396 | 2 S23589 | ATP-dependent RNA |
| 20 | 71 | 10.5 | 585 | 2 G96995 | mixed-lineage prot |
| 21 | 71 | 10.5 | 954 | 1 S68178 | arginine kinase (E |
| 22 | 70.5 | 10.4 | 358 | 1 S46407 | hypothetical prote |
| 23 | 70 | 10.4 | 308 | 2 T48525 | hypothetical prote |
| 24 | 70 | 10.4 | 406 | 2 S07164 | transposase ISG133 |
| 25 | 70 | 10.4 | 414 | 2 C90364 | transposase ISG133 |
| 26 | 70 | 10.4 | 782 | 2 B83966 | formate dehydrogen |
| 27 | 69.5 | 10.3 | 223 | 2 F70469 | enolase-phosphatas |
| 28 | 69.5 | 10.3 | 461 | 2 AF2340 | sugar ABC transpor |
| 29 | 69.5 | 10.3 | 636 | 2 T06793 | receptor kinase ho |

| | | | | | |
|----|------|------|------|----------|--------------------|
| 30 | 69.5 | 10.3 | 1097 | 2 T31504 | hypothetical prote |
| 31 | 68.5 | 10.1 | 176 | 2 T18921 | hypothetical prote |
| 32 | 68.5 | 10.1 | 727 | 2 A55628 | translation initia |
| 33 | 68.5 | 10.1 | 839 | 2 G96719 | probable chromomet |
| 34 | 68.5 | 10.1 | 868 | 2 G71691 | hypothetical prote |
| 35 | 68 | 10.1 | 373 | 2 T39655 | VHS domain contain |
| 36 | 68 | 10.1 | 702 | 2 A75630 | ribonucleoside-dip |
| 37 | 68 | 10.1 | 722 | 2 AF1421 | hypothetical membr |
| 38 | 68 | 10.1 | 1084 | 2 T12925 | ribonucleotide red |
| 39 | 67.5 | 10.0 | 93 | 2 F84138 | hypothetical prote |
| 40 | 67.5 | 10.0 | 319 | 2 H70420 | conserved hypotet |
| 41 | 67.5 | 10.0 | 333 | 2 A84055 | transcription regu |
| 42 | 67.5 | 10.0 | 343 | 2 H86986 | probable heat-indu |
| 43 | 67.5 | 10.0 | 413 | 2 T02693 | S-receptor kinase |
| 44 | 67.5 | 10.0 | 505 | 1 S24550 | protein-tyrosine k |
| 45 | 67.5 | 10.0 | 506 | 1 S24553 | protein-tyrosine k |

ALIGNMENTS

RESULT 1

138019

melanoma-derived growth regulatory protein M1A - human

C.Species: Homo sapiens (man)

C.Date: 17-May-1996 #sequence #revision 17-May-1996 #text_change 04-Mar-2000

C.Accession: 138019, S40238

R.Blesch, A.; Bosserhoff, A.K.; Apfel, R.; Behl, C.; Hesseboerfer, B.; Schmitt, A.; Jact

Cancer Res. 54, 5695-5701, 1994

A>Title: Cloning of a novel malignant melanoma-derived growth-regulatory protein, M1A.

A.Reference number: 138019; MUID:95007612; PMID:7923218

A.Accession: 138019

A.Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: mRNA

A.Residues: 1-131 <RES>

A.Cross-references: EMBL:X75450; NID:G438057; PIDN:CA53203.1; PID:G438058

C.Genetics:

A.Gene: mla

C.Superfamily: human melanoma-derived growth regulatory protein M1A

Query Match 40.8% ; Score 275.5; DB 2; Length 131;
Best Local Similarity 44.4% ; Pred. No. 3.4e-21;
Matches 60; Conservative 27; Mismatches 37; Indels 11; Gaps 6;

| | | | |
|----|-----|---|-----|
| QY | 1 | MARILLILGLGVALCA--GHGMF---MDKLSKKLCADCECVYTISLARQEDYNAPDC | 55 |
| DB | 1 | MARSLV-CLGVILLISAFSGPVRGPMPLADRLCADQCSHPISMAVALQDMAPDC | 59 |
| QY | 56 | REINVKKQCOIYVSKVTENGAG-AFMAGSYGDHODEMGI--VGFPSNIVREGRYQE | 113 |
| DB | 60 | RELTTHRCQVYVFESK---KGRGLTFWGSVQGYDGLARLGYFPSSIVREDQTLKP | 116 |
| QY | 114 | ATKEIPTTDIDPCE | 128 |
| DB | 117 | GKVDVTKRMPYCO | 131 |

RESULT 2

TVMSV

transforming protein vav - mouse

C.Species: Mus musculus (house mouse)

C.Date: 03-May-1994 #sequence #revision 16-Feb-1996 #text_change 18-Jun-1999

C.Accession: A61187; A39576; S36941; S23669

R.Coppola, J.; Bryant, S.; Koda, T.; Conway, D.; Barbacid, M.

Cell Growth Differ. 2, 95-105, 1991

A>Title: Mechanism of activation of the vav protooncogene.

A.Reference number: A61187; MUID:9129578; PMID:2069873

A.Accession: A61187

A.Status: not compared with conceptual translation

A.Molecule type: mRNA

A.Residues: 1-844 <COP>

A.Ratav, S.; Cleveland, J.L.; Heslop, H.E.; Pulido, D.

Mol. Cell. Biol. 11, 1912-1920, 1991

A:Title: Loss of the amino-terminal helix-loop-helix domain of the vav proto-oncogene ad
A:Reference number: A39576; PMID:91172176; PMID:2005887
A:Accession: A39576
A:Molecule type: mRNA
A:Residues: 1-28, 'E', 'F', '30-93' <KAT>
A:Cross-references: GB:M59833; NID:g202343; PIDN:AAA63402.1; PID:g202344
R:Adams, J.M.
Submitted to the EMBL Data Library, January 1992
A:Reference number: S36941
A:Accession: S36941
A:Molecule type: mRNA
A:Residues: 1-323, 'DLMTPMQRVUKYHLLLOELVK', 346-347, 'ODAT', 352, 'K', 354, 'N', 355-453, 'R', 45
A:Cross-references: EMBL:X64361; NID:g955220; PIDN:CAA5713.1; PID:g955221
R:Adams, J.M.; Houston, H.; Allen, J.; Lints, T.; Harvey, R.
Oncogene 7, 611-618, 1992
A:Title: The hematopoietically expressed vav proto-oncogene shares homology with the dbl
A:Reference number: S23659; PMID:92228489; PMID:1565482
A:Contents: annotation; the authors note the frameshift difference with sequence in A611
A>Note: the complete sequence was submitted to Genbank; see S36941
C:Genetics:
A:Gene: vav
C:Superfamily: vav transforming protein; CDC24 homology; protein kinase C zinc-binding
C:Keywords: phosphoprotein; transforming protein; zinc finger
F:32-102/Region: leucine-rich
F:132-116/Region: acidic
F:194-458/Domain: CDC24 homology <CD24>
F:336-340/Region: proline-rich
F:486-493/Region: nuclear location signal
F:531-563/Domain: protein kinase C zinc-binding repeat homology <K21>
F:528-548/Region: zinc finger CCCC motif
F:553-566/Region: zinc finger HCH motif
F:575-582/Region: nuclear location signal
F:604-654/Domain: SH3 homology <SH3A>
F:606-609/Region: proline-rich
F:670-761/Domain: SH2 homology <SH2>
F:788-833/Domain: SH3 homology <SH3B>
F:439/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

Query Match 13.8%; Score 93.5; DB 1; Length 844;
Best Local Similarity 32.9%; Pred. No. 0.17;
Matches 23; Conservative 14; Mismatches 20; Indels 13; Gaps 3;

QY 44 ARAQEDYNAPDCRFITNVKKGQIIVYSKLVTEENGAGAFMAGSYGDHDEMGITGYRPPN 103
DB 786 AKARYDPCARDESELSLEKEDI-----KILNKKGGQGWRRGEIYGR-----IGWPPSN 834

QY 104 LVREQRVYQE 113
DB 835 YVEED--YSE 842

RESULT 3
TVHVV
transforming protein vav - human (fragments)
N:Alternate names: finger protein vav
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1991 #sequence_revision 03-May-1996 #text_change 18-Jun-1999
C:Accession: B39576; S05382
R:Katzav, S.; Cleveland, J.L.; Heslop, H.E.; Pulido, D.
Mol. Cell. Biol. 11, 1912-1920, 1991
A:Title: Loss of the amino-terminal helix-loop-helix domain of the vav proto-oncogene ac
A:Reference number: A39576; PMID:91172176; PMID:2005887
A:Accession: B39576
A:Molecule type: mRNA
A:Residues: 1-61 <KAT>
A:Cross-references: GB:M59834; NID:g340189; PIDN:AA63267.1; PID:g340190
A>Note: the authors translated the codon CAA for residue 6 as Glu, CAG for residue 13 as
R:Katzav, S.; Martin-Zanca, D.; Barbacid, M.
EMBO J. 8, 2283-2290, 1989
A:Title: vav, a novel human oncogene derived from a locus ubiquitously expressed in hema
A:Reference number: S05382; PMID:90005432; PMID:2477241
A:Accession: S05382
A:Molecule type: mRNA

A:Residues: 62-839 <KAT>
R:Adams, J.M.; Houston, H.; Allen, J.; Lints, T.; Harvey, R.
Oncogene 7, 611-618, 1992
A:Title: The hematopoietically expressed vav proto-oncogene shares homology with the d
A:Reference number: S23669; MUID:92228488; PMID:1565462
A:Contents: annotation
A>Note: in the sequence from mouse the authors find three additional nucleotides that I
C:Comment: In comparing these sequences with the mouse (see PIR:TVMSV), there appear
C:Genetics:
A:Gene: GDB:VAV1; VAV
A:Cross-references: GDB:127112; OMIM:164875
A:Map position: 19p13.3-19p13.3
C:Superfamily: vav transforming protein; CDC24 homology; protein kinase C zinc-binding
C:Keywords: phosphoprotein; transforming protein; zinc finger
F:126-170/Region: acidic
F:188-452/Domain: CDC24 homology <CD24>
F:509-557/Domain: protein kinase C zinc-binding repeat homology <K2>
F:522-542/Region: zinc finger CCCC motif
F:547-560/Region: zinc finger HCCCH motif
F:598-648/Domain: SH3 homology <SH3A>
F:664-756/Domain: SH2 homology <SH2>
F:783-831/Domain: SH3 homology <SH3B>
F:433/Binding site: phosphate (ser) (covalent) (by protein kinase A) #status predicted

Query Match 13.5%; Score 91.5; DB 1; Length 839;
Best Local Similarity 32.9%; Pred. No. 0.27; Mismatches 13; Gaps 3;
Matches 23; Conservative 14;

OY 44 ABAQSDVNAAPDGRFINVKKGGQIIVYSKLVTEGAGAFWAGSVYGDHODEMGIVGFPSN 103
DB 761 AKARYDFCARDRSELSLKEGDI-----KLUNKKGGQGMWRGELYGR-----VGMFPAN 829
OY 104 LVREQRYOE 113
DB 830 YVED--YSE 637

RESULT 4
151940
gene VAV2 protein - human
C:Species: Homo sapiens (man)
C:Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #ext_change 16-Jul-1999
C:Accession: I51940
R:Henske, E.P.; Short, M.P.; Jozwiak, S.; Bovey, C.M.; Ramlikhan, S.; Haines, J.L.; Kw
Ann. Hum. Genet. 59, 25-37, 1995
A:Title: Identification of VAV2 on 9q34 and its exclusion as the tubercous sclerosis ge
A:Reference number: I51940; MUID:9528325; PMID:7762882
A:Accession: I51940
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-878 <RES>
A:Cross-references: GB:S76992; NID:g913345; PIDN:AAB34377.1; PID:g913346
C:Genetics:
A:Gene: GDB:VAV2
A:Cross-references: GDB:370880; OMIM:600428
A:Map position: 9q34-9q34
C:Superfamily: vav transforming protein; CDC24 homology; protein kinase C zinc-binding
F:198-462/Domain: CDC24 homology <CD24>
F:524-572/Domain: protein kinase C zinc-binding repeat homology <K2>
F:673-764/Domain: SH2 homology <SH2>
F:823-872/Domain: SH3 homology <SH3>

Query Match 12.5%; Score 84.5; DB 2; Length 878;
Best Local Similarity 27.6%; Pred. No. 1.5;
Matches 21; Conservative 20; Mismatches 22; Indels 13; Gaps 3;

OY 38 VYT--ISLAPQEDYNAPDGRFINVKKGGQIIVYSKLVTEGAGAFWAGSVYGDHODEM 94
DB 812 VFPRVITGAIVAVRYNPAADMRSLREGDVVIRISIGDQG---WMKG-----ETN 861
OY 95 GIVGFPSNLYREQRY 110

A:Molecule type: DNA
 A:Residues: 1-1215 <LEES>
 A:Cross-references: EMBL:AR058185; NID:G3599477; PID:G3599478; PIDN:AAC3537.1
 A:Experimental source: Strain Neff
 C:Genetics:
 A:Gene: MIA
 A:Introns: 1/3; 41/3; 72/2; 103/2; 162/3; 184/1; 217/1; 296/1; 340/3; 390/3; 447/3; 500/3; Superfamily: protozoan myosin heavy chain IB; myosin motor domain homology; SH3 homolo
 F:14-674/Domain: myosin motor domain homology <MMO>

Query Match 11.2%; Score 75.5; DB 2; Length 1215;
 Best Local Similarity 28.6%; Pred. No. 18;
 Matches 20; Conservative 12; Mismatches 25; Indels 13; Gaps 2;

QY 38 VYTIISLRAQEDYVAPDCRFINVKKGQIYYSKLVTEHGAGFMAAGVYGDHDEMGIV 97
 DB 1158 VPIVGRCRALYDYGAGQADELTLEGGVIDYIQK-----SGEMWEGTLNGK-----T 1204

QY 98 GYFPSNLVRE 107
 DB 1205 GVFPANVYED 1214

RESULT 9
 T04200
 hypothetical protein T4F9.110 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999
 C:Accession: T04200
 R:Bayan, M.; Medler, H.; Medler, E.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.
 submitted to the Protein Sequence Database, March 1999
 A:Reference number: Z15260
 A:Accession: T04200
 A:Molecule type: DNA
 A:Residues: 1-332 <BEV>
 A:Cross-references: EMBL:AL049523
 A:Experimental source: cultivar Columbia; BAC clone T4F9
 C:Genetics:
 A:Map position: 4
 A:Introns: 57/3; 119/3; 137/3; 203/1; 266/3; 316/1
 A>Note: T4F9.110

Query Match 11.1%; Score 75; DB 2; Length 332;
 Best Local Similarity 21.5%; Pred. No. 5;
 Matches 28; Conservative 21; Mismatches 59; Indels 22; Gaps 4;

QY 3 RTILLLGLVALCAGH-----GMFMKLSKKLCADEECVYITSLAPQEDYNAP 53
 DB 125 QILFIISSELVQIGSHPRVYVLDTPGIFPPNLYDAE:CAKALATGLISTGHKONDYIPV 184

QY 54 DCRFINVKKGQIYYSKLVTEHGAGFMAAGVYGDHDEMGIVYFPSNLVREGRVQE 113
 DB 185 KYLF-----LYSHSRIAQR---AYWGAIPDDIVGELKLARLF-LTILNSHEYKK 231

QY 114 ATKELPTTDI 123
 DB 232 WAKLCKSQDL 241

RESULT 10
 S66662
 protein-glutamine gamma-glutamyltransferase (EC 2.3.2.13) - red sea bream
 N:Alternate names: transglutaminase
 C:Species: Chrysophrys major (red sea bream)
 C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 18-Jun-1999
 C:Accession: S66662
 R:Yasuda, H.; Nakanishi, K.; Kunazawa, Y.; Nagase, K.; Motoki, M.; Matsui, H.
 Eur. J. Biochem. 232, 411-419, 1995
 A:Title: Tissue-type transglutaminase from red sea bream (Pagrus major). Sequence analys
 A:Reference number: S66662; MUID:96035874; PMID:7556189
 A:Accession: S66662
 A:Molecule type: mRNA
 A:Residues: 1-695 <YAS>

A:Cross-references: GB:S79761; NID:G1176434; PIDN:AAB35370.1; PID:G1176435
 C:Superfamily: protein-glutamine gamma-glutamyltransferase
 C:Keywords: aminoacyltransferase
 F:272/Active site: Cys #status predicted

Query Match 10.9%; Score 74; DB 2; Length 695;
 Best Local Similarity 26.2%; Pred. No. 14;
 Matches 21; Conservative 21; Mismatches 28; Indels 10; Gaps 3;

QY 49 DYNAPDCRFINVKKGQIYYSKLVTEHGAGF---FMAAGVYGDHDEMGIVYFPSNLV 105
 DB 393 EVNADTIYIVQKQGR-----RKTEEDHAGVGNKISTKSYGNHREDVTLHYKPPGQ 447

QY 106 REGRVYQATKEI--PTTDI 123
 DB 448 KEREVYKAGRRVTEPSNEI 467

RESULT 11
 T21356
 hypothetical protein F25H2.13 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T21356; T21540
 R:Wilkinson, J.
 submitted to the EMBL Data Library, September 1996
 A:Reference number: Z19411
 A:Accession: T21356
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-994 <WIL>
 A:Cross-references: EMBL:T29754; PIDN:CAB02102.1; GSPDB:GN00019; CESP:F25H2.13
 A:Experimental source: clone F25H2
 R:Wilkinson, J.
 submitted to the EMBL Data Library, December 1996
 A:Reference number: Z19437
 A:Accession: T21540
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-994 <WIL>
 A:Cross-references: EMBL:T29754; PIDN:CAB02102.1; GSPDB:GN00019; CESP:F25H2.13
 A:Experimental source: clone F29C6
 C:Genetics:
 A:Gene: CESP:F25H2.13
 A:Map position: 1
 A:Introns: 129/2; 177/1; 206/2; 349/3; 436/3; 506/2; 626/3; 689/3; 772/3; 845/3; 903/3

Query Match 10.9%; Score 74; DB 2; Length 994;
 Best Local Similarity 27.8%; Pred. No. 21;
 Matches 37; Conservative 20; Mismatches 46; Indels 30; Gaps 8;

QY 23 MDKLSSKKL-----CADEECVYITSLAPQEDYNAPDCRFINVKKGQIYYSK- 71
 DB 339 MDKLFSSQSLKSPPLSGKASDGE-ILLETLAAGDANSVE-RVLDVLRDA:SYLSKXN 396

QY 72 ---LVTEHGAG---AFWAGVYGDH-QDEMGIYV-----YFPSNLVREGRVQE 114
 DB 397 BEVALTEKDGMEKRVADFLISTYSTHAQDVAAVAGETVLYVDRVDPKTVARCKLYIQK 456

QY 115 TKELPTTDIDFFC 127
 DB 457 DKONEKLTIRYFC 469

RESULT 12
 A53800
 mixed-lineage protein kinase (EC 2.7.1.1-) 3 - human
 N:Alternate names: protein kinase PRK1; protein kinase SPRK
 C:Species: Homo sapiens (man)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A53800; I58395
 R:Gallo, K.A.; Mark, M.R.; Scadden, D.T.; Wang, Z.; Gu, Q.; Godowski, P.J.
 J. Biol. Chem. 269, 15092-15100, 1994

A:Title: Identification and characterization of SPRK, a novel src-homology 3 domain-cont
A:Reference number: A53800; MUID:94253068; PMID:8195146
A:Accession: A53800
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-847 <GAL>
A:Cross-references: GB:U07747; NID:9464027; PIDN:AAA19647.1; PID:9464028
R:ing, Y.L.; Leung, I.W.; Heng, H.H.; Tsui, L.C.; Laessle, N.J.
Oncogene 9, 1745-1750, 1994
A:Title: MLK-3: Identification of a widely-expressed protein kinase bearing an SH3 domai
A:Reference number: 158395; MUID:94239754; PMID:8183572
A:Accession: 158395
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-847 <RES>
A:Cross-references: GB:U32976; NID:9488295; PIDN:AAA59859.1; PID:9488296
C:Genetics:
A:Gene: GDB:MLK3; PTK1; SPRK
A:Cross-references: GDB:134755; OMIM:600050
A:Map position: 11q13.1-11q13.3
C:Superfamily: mixed-lineage protein kinase 3; protein kinase homology; SH3 homology
C:Keywords: ATP; leucine zipper; phosphotransferase; serine/threonine-specific protein k
F:48-100/Domain: SH3 homology <SH32>
F:115-383/Domain: protein kinase homology <KIN>
F:133-131/Region: protein kinase ATP-binding motif
F:403-424/Region: leucine zipper motif
F:438-459/Region: leucine zipper motif
F:468-482/Region: basic

Query Match 10.9%; Score 73.5; DB 1; Length 847;
Best Local Similarity 33.3%; Pred. No. 20;
Matches 19; Conservative 8; Mismatches 23; Indels 7; Gaps 1;

Qy 49 DYNAPDCRFINVKKGQGIYVSKLVTEGAGAFWAGSVYGDHDEMGIVGFPNSLY 105
Db 51 DYEPGQDELALRKGRVETLSRDAISGDEGMWAGVGQ-----VGIFPSNYV 100

RESULT 13
RDLENTZ
dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Leishmania m
N:Contains: dihydrofolate reductase (EC 1.5.1.3); thymidylate synthase (EC 2.1.1.45)
C:Species: Leishmania mexicana amazonensis
C:Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 11-Jun-1999
C:Accession: S15756; G: Alonso, G.; Langer, P.J.; Beverley, S.M.
R:Nelson, K.; Alonso, G.; Langer, P.J.; Beverley, S.M.
Nucleic Acids Res. 18, 2819, 1990
A:Title: Sequence of the dihydrofolate reductase-thymidylate synthase (DHFR-TS) gene of
A:Reference number: S15756; MUID:90251468; PMID:2339068
A:Accession: S15756
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-520 <NLE>
A:Cross-references: EMBL:X51735; NID:99470; PIDN:CAA36020.1; PID:99471
C:Superfamily: bifunctional dihydrofolate reductase-thymidylate synthase; thymidylate sy
C:Keywords: deoxyribonucleotide biosynthesis; methyltransferase; multifunctional enzyme;
F:26-166/Domain: type I dihydrofolate reductase homology <DFR>
F:234-520/Domain: thymidylate synthase homology <TDS>
F:400/Active site: Cys #status predicted

Query Match 10.8%; Score 73; DB 1; Length 520;
Best Local Similarity 24.5%; Pred. No. 13;
Matches 34; Conservative 18; Mismatches 57; Indels 30; Gaps 5;

Qy 2 ARILLILGGIVAIACAGHGMFMDKLSKLCADBEVCYTISLARAQEDYNAPDCRFINVK 61
Db 124 AQQIVVANGGLAA-----VRLARPPYCSSETETVCYCGACVYADALSLSC---VE 172

Qy 62 KGQGIYV-----YSKLVTEGAGAFWAGSVYGDHDEMGIVGFPNSLY 104
Db 173 KLGQVYVLRITHTAPACGRFPFPENNAATWDLASQGRKRSKAVDLEFELICKYPRN- 231

Qy 105 VREGRVYQEAATKEIPTTDI 123

Db 232 -HEEROYDELDRIMKTGI 249

RESULT 14
667383
probable signal transduction protein - fission yeast (Schizosaccharomyces pombe)
N:Alternate names: FCH domain and SH3 domain containing protein
C:Species: Schizosaccharomyces pombe
C:Date: 19-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000
A:Accession: T39317; S67383
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Beck, A.; Reinhardt, R.
submitted to the EMBL Data Library, September 1998
A:Reference number: 221844
A:Accession: T39317
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-670 <WOO>
A:Cross-references: EMBL:AL031528; PIDN:CAA20684.1; GSPDB:GN00067; SPDB:SPBC11C11.02
A:Experimental source: strain 972h-; cosmid c11C11
C:Genetics:
A:Gene: SPBC11C11.02
A:Map position: 2
A:Introns: 23/3; 54/2; 612/1
C:Superfamily: SH3 homology
F:614-665/Domain: SH3 homology <SH3>

Query Match 10.8%; Score 73; DB 2; Length 670;
Best Local Similarity 39.1%; Pred. No. 17;
Matches 25; Conservative 6; Mismatches 21; Indels 12; Gaps 4;

Qy 49 DYNAPDCRFINVKKGQGIYVSKLVTEGAGAFWAGSVYGDHDEMGIVGFPNSLY 106
Db 617 DDAALPEIISFRKGDITAVLK--LYEDG--WMEGFVYGDHNR-----GQFPNSYVR 666

Qy 107 EQRV 110
Db 667 ELEV 670

RESULT 15
C64427
hypothetical protein MJ1020 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: C64427
R:Bull, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodex, A.
; son, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Weese,
A:Title: Complete genome sequence of the methanococcus jannaschii
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: C64427
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-259 <BUU>
A:Cross-references: GB:U67544; GB:L77117; NID:91591671; PIDN:AAB99024.1; PID:91591678;
C:Genetics:
A:Map position: FOR950420-951199

Query Match 10.7%; Score 72; DB 2; Length 259;
Best Local Similarity 22.9%; Pred. No. 7.8;
Matches 25; Conservative 21; Mismatches 47; Indels 16; Gaps 3;

Qy 11 GIVACAGHGMF--MDKLSKLCADBEVCYTISLARAQEDYNAPDCRFINVKKGQGIYV 68
Db 162 GVIAVADGDMTKGSRPIPCCKCYDHSVSAASER-----VEIKSDEKPI 209

Qy 69 YSKLVTEGAGAFWAGSVYGDHDEMGIVGFP--SNLVREGRVYQEAAT 115
Db 210 QIEVLISNEAGIFQIOEVLGKIKSGIKNYSVYARVKKKPYEEIT 258

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Db      181 AAGAAAGGCGCAGATCTATGTTATTCACAGCTGGTAACAGAAATGAGCTGGGCA 240
Qy      81 PheTpaIaGlySeVaIlyrGlyAspHisGlnAspGluMeCGlyLeValGlyTyrPhe 100
Db      241 TTCTGGCTGGCAGAGTTTATGTTGACCAACGAGATGAGGAAATGCTGTTATTC 300
Qy      101 ProSerAsnLeuValaArgGlnGlnaArgValTyrGlnGlnaIaThrLyseGluIleProThr 120
Db      301 CCCAGCACTTGTTAGAGACCAAGAGTACCGAGAGCCACCAAGAGATTCACACC 360
Qy      121 ThrAspIleAspPhePheCysGlu 128
Db      361 ACGGATATTGACTCTTCTGTGAA 384

RESULT 3
LOCUS      BD010805          384 bp      DNA          linear      PAT 31-JAN-2002
DEFINITION Novel polypeptide and DNA thereof.
ACCESSION  BD010805
VERSION     BD010805.1 GI:16639178
KEYWORDS   JP 2001069994-A/6.
SOURCE      Mus sp.
ORGANISM    Mus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 384)
AUTHORS     Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
            Yoshimura, K. and Tanaka, H.
TITLE       Novel polypeptide and DNA thereof
JOURNAL     Patent: JP 2001069994-A 6 21-MAR-2001;
            TAKEDA CHEMICAL INDUSTRIES LTD
COMMENT     OS Mus sp. (mouse)
            PN JP 2001069994-A/6
            PD 21-MAR-2001
            PR 29-JUN-2000 JP 2000195911
            PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI
            SHINICHI MOGI, KOJI YOSHIMURA, HIDEYUKI TANAKA
            PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC
            A61P19/08,
            PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC
            G01N33/53//
            PC C12P21/08, C12N15/00, A61K37/02, C12N5/00
            CC FH
            FH Key Location/Qualifiers
            FT source 1. 384
            FT /organism="Mus sp. (mouse)".
            FT Location/Qualifiers
FEATURES
    source          1..384
                    /organism="Mus sp."
                    /mol_type="genomic DNA"
                    /db_xref="taxon:10095"
BASE COUNT      98 a 68 c 111 g 107 t
ORIGIN
Alignment Scores:
Pred. No.:      1.8e-69      Length:      384
Score:          655.00      Matches:      123
Percent Similarity: 98.44%      Conservative: 3
Best Local Similarity: 96.09%      Mismatches: 2
Query Match:    96.89%      Indels:      0
DB:             6          Gaps:      0
US-10-019-455a-47 (1-128) x BD010805 (1-384)
Qy      1 MetAlaArgIleuLeuLeuLeuGlyGlyValaAlaLeuCysAlaGlyHisGly 20
Db      1 ATGGCAAGATATGATCTTTGCTGGGGGCTTGGTCTTATATGCGGGCATGCT 60
Qy      21 MetPheMetAlaPlyLeuSerSerLyseLyseCysAlaAspGluGluCysValTyrThr 40

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Db      61 GTATTATGATTAACCTTCTCTTAAGAACTGTGTGCCGATGAGAGTGTCTACT 120
Qy      41 IleSerLeuAlaArgIaGlnGlnaAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
Db      121 ATTTCTCTGCAAGAGACAGCAAGATTACATATGCCCAAGCTGTGATTCATCATGTC 180
Qy      61 LysLeuGlyGlnGlnIleTyrValTyrSerLyseLeuValThrGluAsnGlyAlaGlyAla 80
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Db      301 CCCAGCACTTGTTAGAGACCAAGAGTACCGAGAGCCACCAAGAGATTCACACC 360
Qy      121 ThrAspIleAspPhePheCysGlu 128
Db      361 ACGGATATTGACTCTTCTGTGAA 384

RESULT 4
LOCUS      BD093106          384 bp      DNA          linear      PAT 27-AUG-2002
DEFINITION Novel polypeptide and its DNA.
ACCESSION  BD093106
VERSION     BD093106.1 GI:22638694
KEYWORDS   WO 0102564-A/6.
SOURCE      Mus sp.
ORGANISM    Mus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 384)
AUTHORS     Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
            Yoshimura, K. and Tanaka, H.
TITLE       Novel polypeptide and its DNA
JOURNAL     Patent: WO 0102564-A 6 11-JAN-2001;
            TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO
            OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,
            HIDEYUKI TANAKA
COMMENT     OS Mus sp. (mouse)
            PN WO 0102564-A/6
            PD 11-JAN-2001
            PR 29-JUN-2000 WO 2000JP004278
            PR 30-JUN-1999 JP 99P 186718
            PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI
            MOGI,
            PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
            PC C12N15/12, C12N5/10, C12P21/02, C07K14/47, C07K16/18, A61K45/00, PC
            A61K38/17,
            PC A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/7088//C12P21/
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Best Local Similarity: 96.09%      Mismatches: 2
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 DEFINITION Novel polypeptide and DNA thereof.
 ACCESSION BD010835
 VERSION BD010835.1 GI:18639208
 KEYWORDS JP 2001069994-A/36.
 SOURCE Rattus sp.
 ORGANISM Rattus sp.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 384)
 Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
 Yoshimura, K. and Tanaka, H.
 Novel polypeptide and DNA thereof
 Patent: JP 2001069994-A 36 21-MAR-2001;
 TAKEDA CHEMICAL INDUSTRIES LTD
 OS Rattus sp. (rat)
 PN JP 2001069994-A/36
 PD 21-MAR-2001
 PF 29-JUN-2000 JP 2000195911
 PR YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI
 SHINICHI MOGI,
 PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
 PC C12N15/09, A61K39/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC
 A61P19/08, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC
 G01N33/53//
 CC C12P21/08, C12N15/00, A61K37/02, C12N5/00
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 QY 21 MetPheMetAspLysLeuSerSerLysLysLeuCySAAspGluGluCyValTyrThr 40
 DB 61 ATGTTTATGATTAACCTTTCTTAAGAAGTTGTGCAGATGAGAGAGTGTCTATACC 120
 QY 41 IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCySApPheIleAsnVal 60
 DB 121 ATTTCTCTGGCAAGACACAGAACTACATGCCCCGAGCTGTAGTTCATCAATGTC 180
 QY 61 LysLysGlnGlnGlnIleTyrValTyrSerLysLeuValThrGluGlnGlyAlaGlyAla 80
 DB 181 AAGAAAGGCGACGAGATCTATGTTATTCACACTGTGTAACAGAAATGAGCTGGGCGCA 240
 QY 81 PheTTPAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
 DB 241 TTCTGGGCTGGCAGTGTATGATGACACACAGAGATGAGATGGAATTTGGGTTATTTTC 300
 QY 101 ProSerAsnLeuValAlaGlnGluGlnArgValTyrGlnGlnAlaThrLysGlnIleProThr 120

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 QY 121 ThrAspIleAspPhePheCyGlu 128
 DB 361 ACGGATATGACTTCTCTGTGAA 384
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 LOCUS BD093136 384 bp DNA linear PAT 27-AUG-2002
 DEFINITION Novel polypeptide and its DNA.
 ACCESSION BD093136
 VERSION BD093136.1 GI:22688724
 KEYWORDS WO 0102564-A/36.
 SOURCE Rattus sp.
 ORGANISM Rattus sp.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 384)
 Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
 Yoshimura, K. and Tanaka, H.
 Novel polypeptide and its DNA
 Patent: WO 0102564-A 36 11-JAN-2001;
 TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO
 OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,
 HIDEYUKI TANAKA
 OS Rattus sp. (rat)
 PN WO 0102564-A/36
 PD 11-JAN-2001
 PF 29-JUN-2000 WO 2000P004278
 PR 30-JUN-1999 JP 99P 186718
 PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI
 MOGI,
 PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
 PC C12N15/12, C12N5/10, C12P21/02, C07K16/18, A61K45/00, PC
 A61K38/17,
 PC A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/0086//C12P21/02, C12R1.19)
 CC 02, C12R1.19)
 FH Key Location/Qualifiers
 FT source 1..384
 FT /organism="Rattus sp."
 /mol_type="genomic DNA"
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 Location/Qualifiers
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 /mol_type="genomic DNA"
 /db_xref="taxon:10118"
 Alignment Scores:
 Pred. No.: 5 45e-72 Length: 384
 Score: 676.00 Matches: 128
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
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 US-10-019-455A-47 (1-128) x BD093136 (1-384)
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 DB 1 ATGGCAAGAAATATGATCTTTCTTGGGGCCCTTGTGGCTCTCTGCGGGCATGGC 60
 QY 21 MetPheMetAspLysLeuSerSerLysLysLeuCySAAspGluGluCyValTyrThr 40
 DB 61 ATGTTTATGATTAACCTTTCTTAAGAAGTTGTGCAGATGAGAGAGTGTCTATACC 120
 QY 41 IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCySApPheIleAsnVal 60
 DB 121 ATTTCTCTGGCAAGACACAGAACTACATGCCCCGAGCTGTAGTTCATCAATGTC 180
 QY 61 LysLysGlnGlnGlnIleTyrValTyrSerLysLeuValThrGluGlnGlyAlaGlyAla 80

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: December 29, 2003, 16:11:59 ; Search time 2106.98 Seconds
(without alignments)
2485.278 Million cell updates/sec

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Fgapop 6.0 , Fgapext 7.0
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Searched: 2888711 seqs, 20454813386 residues
Total number of hits satisfying chosen parameters: 5777422

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-OUTFMT=pro -NOR=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000
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15: em_ba.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 5 | 655 | 96.9 | 929 | AF243504 | AF243504 Mus muscu |
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| 12 | 600 | 88.8 | 521 | AX358818 | AX358818 Sequence |
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| 16 | 600 | 88.8 | 846 | AF233261 | AF233261 Homo sapi |
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| 27 | 525 | 77.7 | 307 | BD010830 | BD010830 Novel pol |
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| 29 | 464 | 68.6 | 484 | AF233518 | AF233518 Gallus ga |
| 30 | 458 | 67.8 | 261 | BD010829 | BD010829 Novel pol |
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| 36 | 275.5 | 40.8 | 396 | BT007044 | BT007044 Homo sapi |
| 37 | 275.5 | 40.8 | 396 | BT007775 | BT007775 Synthetic |
| 38 | 275.5 | 40.8 | 459 | A42942 | A42942 Sequence 1 |
| 39 | 275.5 | 40.8 | 459 | AX016785 | AX016785 Sequence |
| 40 | 275.5 | 40.8 | 459 | AX525508 | AX525508 Sequence |
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| 43 | 275.5 | 40.8 | 518 | BC005910 | BC005910 Homo sapi |
| 44 | 273.5 | 40.5 | 433 | AX253435 | AX253435 Sequence |
| 45 | 270 | 39.9 | 548 | BTU51437 | US1437 Bos taurus |

ALIGNMENTS

RESULT 1

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REFERENCE/DOCCKET NUMBER:  INI-0266CP(IPC-048CP)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO.: 89:
SEQUENCE CHARACTERISTICS:
    LENGTH: 182 amino acids
    TYPE: amino acid
    TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
IS-08-466-793-89

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| Best Local Similarity | 24.7% | Pred. No. 0.29; | | |
| Matches | 37; | Conservative | 11; | Mismatches 39; |
| | | | | Indels 63; |
| | | | | Gaps 6; |

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2      US-08-491-661A-89
3      : Sequence 89: Application US/06491861A
4      : Patent No. 5939283
5      :
6      : GENERAL INFORMATION:
7      : APPLICANT: Morgenstern, Jay P.
8      : APPLICANT: Kanieczny, Andrey
9      : APPLICANT: Bizindakus, Christine B.
10     : APPLICANT: Brauer, Andrew W.
11     :
12     : TITLE OF INVENTION: Allergenic Proteins and Peptides from Dog
13     : TITLE OF INVENTION: Dander and Uses Therefor
14     : NUMBER OF SEQUENCES: 104
15     :
16     : CORRESPONDENCE ADDRESS:
17     : ADDRESSEE: LAHIVE & COCKFIELD, LLP
18     : STREET: 28 State Street
19     : CITY: Boston
20     :
21     : STATE: MA
22     :
23     : COUNTRY: USA
24     :
25     : ZIP: 02109
26     :
27     : COMPUTER READABLE FORM:
28     : MEDIUM TYPE: Floppy disk
29     : COMPUTER: IBM PC compatible
30     : OPERATING SYSTEM: PC-DOS/MS-DOS
31     : SOFTWARE: ASCII-text
32     :
33     : CURRENT APPLICATION DATA:
34     : APPLICATION NUMBER: US/08/491,861A
35     : FILING DATE: 27-OCT-1995
36     : CLASSIFICATION: 435
37     :
38     : PRIOR APPLICATION DATA:
39     : APPLICATION NUMBER: 07/999,712
40     : FILING DATE: 31-Dec-92
41     :
42     : ATTORNEY/AGENT INFORMATION:
43     : NAME: Mandiagouras, Amy E.
44     : REGISTRATION NUMBER: 36,207
45     : REFERENCE/DOCKET NUMBER: 1M1-026CP(IPC-048CP)
46     : TELECOMMUNICATION INFORMATION:
47     : TELEPHONE: (617) 227-7400
48     : TELEFAX: (617) 742-4214
49     :
50     : INFORMATION FOR SEQ ID NO: 89:
51     : SEQUENCE CHARACTERISTICS:
52     : LENGTH: 182 amino acids
53     : TYPE: amino acid
54     : TOPOLOGY: linear

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; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-491-861A-89

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| Best Local Similarity | 24.7%; | Pred. No. 0.29; | | |
| Matches | 37; | Conservative | 11; | Mismatches 39; |
| | | | | Indels 63; |
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; Sequence 89, Application US/09374671A
; Patent No. 6489118
; GENERAL INFORMATION:
; APPLICANT: Morgenstern, Jay P.
;               Konieczny, Andrzej
;               Bizindaukas, Christine B.
;               Brauer, Andrew W.
; TITLE OF INVENTION: Allergenic Protein and Peptides from Dog
;                   Dander and Uses Therefor
; NUMBER OF SEQUENCES: 109
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amy E. Mandragouras
; STREET: 28 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/374.671A
; FILING DATE: 16-Aug-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/156,549
; FILING DATE: 1993-NOV-22
; APPLICATION NUMBER: US 07/999,712
; FILING DATE: 1992-DEC-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Digioorgio, Jeanne M.
; REGISTRATION NUMBER: 41,710
; REFERENCE/DOCKET NUMBER: IM1-026C2CNCPA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 89:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 182 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: Internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 89:
US-09-374-671A-89

Query Match          10.9%; Score 73.5; DB 4; Length 182;
Best Local Similarity 24.7%; Pred. No. 0.29; 39; Indels 63; Gaps 6
Matches 37; Conservative 11; Mismatches 39; Indels 63; Gaps 6

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DB 116 DYERYVMEHLVNVNNGBAFQLMELYGRTKD 145

RESULT 15
US-08-630-915A-194
Sequence 194, Application US/08630915A
Patent No. 6309820

GENERAL INFORMATION:

APPLICANT: SPARKS, Andrew B.
APPLICANT: HOFEMAN, No. 6309820h
APPLICANT: HAY, Brian K.
APPLICANT: FOMLIES, Dana M.
APPLICANT: MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915A
FILING DATE: 03-APR-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 194:
SEQUENCE CHARACTERISTICS:
LENGTH: 509 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-630-915A-194

Query Match 10.5%; Score 71; DB 4; Length 509;
Best Local Similarity 21.2%; Pred. No. 2.7;
Matches 36; Conservative 24; Mismatches 38; Indels 72; Gaps 10;

QY 11 GIVALCAGHGMFMDLUSKULCA-----DEECVYI-----ISLARAOEDY----- 50
DB 203 GSVSDIHGQGVVNLKQALCSWTAKKDNHNLFSKHDITVLDQENWMPGEVHGGRGW 262
QY 51 -----NAPDCRFINVK-----GQO-----IVYSK----- 71
DB 263 PPKSYVKIIPGSEVVRKEPEALYAANKKPTSAAYSVEEYIALYPPSYSVEPGDLTFTEG 322

QY 72 ---LVTENGAGAFWAGSVYGDHODENGIVGFPNNIV--REQRYQEAATK 116
DB 323 EEILVTQKD-GEMWTGSI-GDRS-----GIFPSNVYKXKQDESFGSASK 364

Search completed: December 29, 2003, 16:11:51
Job time: 9.32213 secs

Tue Dec 30 10:20:50 2003

us-10-019-455a-47.rpt

Page 6

Search completed: December 29, 2003, 16:10:41
Job time : 14.2661 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 29, 2003, 16:03:18 ; Search time 5.01961 Seconds
(without alignments)
1199.181 Million cell updates/sec

Title: US-10-019-455A-47

Sequence: 1 MARILLILGLVALCAGHG.....RVQGEATKEIPTDIDFCE 128

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 655 | 96.9 | 128 | 1 | OTOR_MOUSE |
| 2 | 600 | 86.8 | 128 | 1 | OTOR_HUMAN |
| 3 | 464 | 68.6 | 132 | 1 | OTOR_CHICK |
| 4 | 404 | 59.8 | 133 | 1 | OTOR_RANCA |
| 5 | 275.5 | 40.8 | 131 | 1 | MIA_HUMAN |
| 6 | 270 | 39.9 | 130 | 1 | MIA_BOVIN |
| 7 | 268 | 39.6 | 130 | 1 | MIA_RAT |
| 8 | 251 | 37.1 | 130 | 1 | MIA_MOUSE |
| 9 | 93.5 | 13.8 | 843 | 1 | VAV_RAT |
| 10 | 93.5 | 13.8 | 845 | 1 | VAV_MOUSE |
| 11 | 93.5 | 13.8 | 847 | 1 | VAV3_MOUSE |
| 12 | 91.5 | 13.5 | 845 | 1 | VAV_HUMAN |
| 13 | 91.5 | 13.5 | 847 | 1 | VAV3_HUMAN |
| 14 | 85.5 | 12.6 | 868 | 1 | VAV2_MOUSE |
| 15 | 84.5 | 12.5 | 878 | 1 | VAV2_HUMAN |
| 16 | 82.5 | 12.2 | 1589 | 1 | CC25_YEAST |
| 17 | 79 | 11.7 | 2161 | 1 | SHK1_HUMAN |
| 18 | 77 | 11.4 | 2167 | 1 | SHK1_RAT |
| 19 | 74 | 10.9 | 695 | 1 | TCM2_PAGNA |
| 20 | 73 | 10.8 | 620 | 1 | DRTS_LEIAM |
| 21 | 73 | 10.8 | 670 | 1 | VAV2_SCHRO |
| 22 | 72 | 10.7 | 259 | 1 | VAV2_METJA |
| 23 | 72 | 10.7 | 1815 | 1 | SHK3_RAT |
| 24 | 71 | 10.5 | 396 | 1 | CKA7_MOUSE |
| 25 | 71 | 10.5 | 745 | 1 | BFGM_DROME |
| 26 | 71 | 10.5 | 776 | 1 | ARM6_HUMAN |
| 27 | 71 | 10.5 | 933 | 1 | ZO3_HUMAN |
| 28 | 71 | 10.5 | 954 | 1 | MARK_HUMAN |
| 29 | 71 | 10.5 | 1696 | 1 | ITN2_HUMAN |
| 30 | 70.5 | 10.4 | 358 | 1 | KARG_NORWA |
| 31 | 70 | 10.4 | 406 | 1 | YCX9_EUGER |
| 32 | 70 | 10.4 | 1217 | 1 | ITN1_RAT |
| 33 | 69 | 10.2 | 380 | 1 | NCK2_HUMAN |

| | | | | | | |
|----|------|------|------|---|------------|--------------------|
| 34 | 69 | 10.2 | 451 | 1 | TBG_ENTHI | P54401 entamoeba h |
| 35 | 69 | 10.2 | 1721 | 1 | ITN1_HUMAN | Q15811 homo sapien |
| 36 | 68.5 | 10.1 | 727 | 1 | IF2M_HUMAN | P46199 homo sapien |
| 37 | 68 | 10.1 | 427 | 1 | AROA_STRP8 | O8P0H1 streptococc |
| 38 | 68 | 10.1 | 430 | 1 | AROA_STRPY | Q99783 streptococc |
| 39 | 68 | 10.1 | 646 | 1 | PIXE_HUMAN | Q14155 homo sapien |
| 40 | 68 | 10.1 | 733 | 1 | VINE_MOUSE | Q91288 mus musculu |
| 41 | 67.5 | 10.0 | 343 | 1 | HRCA_MYCLE | Q9C8N2 mycobacteri |
| 42 | 67.5 | 10.0 | 505 | 1 | SRK1_SPOLA | P42686 spongilla 1 |
| 43 | 67.5 | 10.0 | 506 | 1 | SRK4_SPOLA | P42690 spongilla 1 |
| 44 | 67.5 | 10.0 | 713 | 1 | RIR3_ECOLI | P39452 escherichia |
| 45 | 67.5 | 10.0 | 751 | 1 | EFG1_HUMAN | Q961P9 homo sapien |

ALIGNMENTS

```

RESULT 1
OTOR_MOUSE
AC Q91EJ3;
ID 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Otoraplin precursor (Melanoma inhibitory activity-like protein).
GN OTOR OR MIAL.
OS Mus musculus (Mouse).
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP MEDLINE=20334619; PubMed=10973378;
RA Robertson N.G., Heller S., Lin J.S., Resendes B.L., Weremowicz S.,
RA Denis C.S., Bell A.M., Hudspeth A.J., Morton C.C.;
RT "A novel conserved cochlear gene, OTOR: identification, expression
RT analysis, and chromosomal mapping.";
RL Genomics 66:242-248(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Petal;
RX MEDLINE=21100875; PubMed=1161796;
RA Rendtorff N.D., Frodin W., Attie-Bltach T., Vekemans M., Tomerup N.;
RT "Identification and characterization of an inner ear-expressed human
RT melanoma inhibitory activity (MIA)-like gene (MIAL) with a frequent
RT polymorphism that abolishes translation.";
RL Genomics 71:40-52(2001).
CC -1- SUBCELLULAR LOCATION: secreted (Potential).
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN COCHLEA.
CC -1- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
CC -1- SIMILARITY: Contains 1 SH3 domain.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; AF233333; AAF82079.1; -
DR EMBL; AF243339; CAC27444.1; -
DR HSSP; Q16674; 1110.
DR MGD; MGI:1888678; Otor.
DR GO; GO:0001502; P:cartilage condensation; IMP.
DR InterPro; IPR001452; SH3.
DR Pfam; PF00018; SH3; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS50002; SH3; 1.
DR SIGNAL; SH3 domain.
FT CHAIN 1..18 POTENTIAL.
FT DOMAIN 19..128 OTORAPLIN.
FT 33 110 SH3.

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FT DISUFID 32 37 BY SIMILARITY.
FT DISUFID 55 127 BY SIMILARITY.
SQ SEQUENCE 128 AA; 14328 MW; 3DD47D4C77CAAFD CRC64;

Query Match
Best Local Similarity 96.7%; Score 655; DB 1; Length 128;
Matches 123; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MARILLILGVALCAGHGMFMDKSSKLCADDECVYITISLARAQEDYNAPDCRFINV 60
DB 1 MARILLILGVALCAGHGMFMDKSSKLCADDECVYITISLARAQEDYNAPDCRFIV 60
QY 61 KKGQOIYYSKLVYENGAGAFMAGSVYGDHDEMGIVGFPPSNLVREORVYQATKEIPT 120
DB 61 KKGQOIYYSKLVYENGAGAFMAGSVYGDHDEMGIVGFPPSNLVREORVYQATKEIPT 120
QY 121 TDIDFCE 128
DB 121 TDIDFCE 128

RESULT 2
OTOR HUMAN STANDARD; PRT; 128 AA.
ID OTOR HUMAN STANDARD; PRT; 128 AA.
AC QSNRC9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Otoraplin precursor (fibrocyte-derived protein) (Melanoma inhibitory
DE activity like protein).
GN OTOR OR FDP OR MIAL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cochlea;
RX MEDLINE=20334619; PubMed=10873378;
RA Robertson N.G., Heller S., Lin J.S., Resendes B.L., Weremowicz S.,
RA Denis C.S., Bell A.M., Hudspeth A.J., Morton C.C.;
RT "A novel conserved cochlear gene, OTOR: identification, expression
RT analysis, and chromosomal mapping.";
RL Genomics 66:242-248(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20568254; PubMed=10998416;
RA Cohen-Salmon M., Frenz D., Liu W., Verpy E., Voegelings S., Petit C.;
RT "Fdp, a new fibrocyte-derived protein related to MIA/CD-RAP, has an
RT in vitro effect on the early differentiation of the inner ear
RT mesenchyme.";
RL J. Biol. Chem. 275:40036-40041(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, and Cochlea;
RX MEDLINE=21100875; PubMed=11161796;
RA Rendtorff N.D., Frodin M., Attie-Bitach T., Vekemans M., Tommerup N.;
RT "Identification and characterization of an inner ear-expressed human
RT melanoma inhibitory activity (MIA)-like gene (MIAL) with a frequent
RT polymorphism that abolishes translation.";
RL Genomics 71:40-52(2001).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley C.P., Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J.,
RA Buck D., Buttrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp W., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,

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RA Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Lehteväaho M.H., Levesha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McJay K., Murray A.A.,
RA Milne S.A., Misty D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilting L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN COCHLEA.
CC -1- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
CC -1- SIMILARITY: Contains 1 SH3 domain.
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CC -----
DR EMBL, AF233261; AAF82078.1; -
DR EMBL, AF243505; AAG42356.1; -
DR EMBL, AJ242552; CAC27443.1; -
DR EMBL, AJ252324; CAC28085.1; -
DR EMBL, AJ252325; CAC28085.1; JOINED.
DR EMBL, AJ252326; CAC28085.1; JOINED.
DR EMBL, AJ252327; CAC28085.1; JOINED.
DR EMBL, AL034428; CAC16848.1; -
DR HSSP; Q16674; 111J.
DR Gensu; HGNC:8517; OTOR.
DR MIM; 606067; -.
DR GO; GO:0007605; P-hearing; TAs.
DR InterPro; IPR001452; SH3.
DR Pfam; PF00018; SH3; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS50002; SH3; FALSE_NEG.
DR SIGNAL; SH3 domain.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 128 OTORAPLIN.
FT DOMAIN 32 37 SH3.
FT DISUFID 55 127 BY SIMILARITY.
FT DISUFID 128 127 BY SIMILARITY.
SQ SEQUENCE 128 AA; 14332 MW; 9BB52C7F5D4B700 CRC64;

Query Match
Best Local Similarity 88.8%; Score 600; DB 1; Length 128;
Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 1 MARILLILGVALCAGHGMFMDKSSKLCADDECVYITISLARAQEDYNAPDCRFINV 60
DB 1 MARILLILGVALCAGHGMFMDKSSKLCADDECVYITISLARAQEDYNAPDCRFIV 60
QY 61 KKGQOIYYSKLVYENGAGAFMAGSVYGDHDEMGIVGFPPSNLVREORVYQATKEIPT 120
DB 61 KKGQOIYYSKLVYENGAGAFMAGSVYGDHDEMGIVGFPPSNLVREORVYQATKEIPT 120
QY 121 TDIDFCE 128
DB 121 TDIDFCE 128

RESULT 3

```

OTOR CHICK STANDARD; PRT: 132 AA.

ID OTOR CHICK STANDARD; PRT: 132 AA.

AC Q918P6:

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Otoraplin precursor.

GN OTOR.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

NCBI_TaxID=9031;

RM [1]

RP MEDLINE=20334619; PubMed=10873378;

RA Robertson N.G., Heller S., Lin J.S., Resendes B.L., Weremowicz S., Denis C.S., Bell A.M., Hudspeth A.J., Morton C.C.;

RT "A novel conserved cochlear gene, OTOR: identification, expression analysis, and chromosomal mapping.";

RL Genomics 66:242-248(2000).

CC -1- SUBCELLULAR LOCATION: Secreted (Potential).

CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN COCHLEA.

CC -1- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.

CC -1- SIMILARITY: Contains 1 SH3 domain.

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CC -----

CC EMBL: AF233519; AAF82727.1; -

DR HSSP: Q16674; 111J

DR InterPro: IPR001452; SH3.

DR SMART: SM00326; SH3; 1.

DR PROSITE: PS50002; SH3; 1.

KW SIGNAL; SH3 domain.

FT SIGNAL 1 23 POTENTIAL.

FT CHAIN 24 132 OTORAPLIN.

FT DOMAIN 42 114 SH3.

FT DISULFID 35 40 BY SIMILARITY.

FT DISULFID 58 131 BY SIMILARITY.

SEQUENCE 132 AA; 15177 MW; 9D1CB07FD353CE1C CRC64;

Query Match 68.6%; Score 464; DB 1; Length 132;

Best Local Similarity 71.4%; Pred. No. 3.5e-40;

Matches 90; Conservative 14; Mismatches 20; Indels 2; Gaps 2;

QY 4 ILILLGLVALCAQHGMFKDKLSSKKLCADEECVYITISLARAQEDYNAPDCRFINVKKG 63

DB 8 IVLFGLGELMWPFA-TGIFMDKLASKKLCADDCVITISLVRABEDYNAPDCRFINVKKG 66

QY 64 QQIVYVSKLVTEAGAGAFWAGSYTG-DHODEMGIVGFPSNLVREQRYVQEAITEPTTD 122

DB 67 QLIIVYVSKLVTEKESGEFVAGSYGEEYEDHMGIVGFPSNLVSECHVYQEAINTIPTTD 126

QY 123 IDFECE 128

DB 127 IDFECE 132

RESULT 4

OTOR_RANCA STANDARD; PRT: 133 AA.

AC Q918P5;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Otoraplin precursor.

GN OTOR.

OS Rana catesbeiana (Bull frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.

NCBI_TaxID=400;

RM [1]

RP MEDLINE=20334619; PubMed=10873378;

RA Robertson N.G., Heller S., Lin J.S., Resendes B.L., Weremowicz S., Denis C.S., Bell A.M., Hudspeth A.J., Morton C.C.;

RT "A novel conserved cochlear gene, OTOR: identification, expression analysis, and chromosomal mapping.";

RL Genomics 66:242-248(2000).

CC -1- SUBCELLULAR LOCATION: Secreted (Potential).

CC -1- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.

CC -1- SIMILARITY: Contains 1 SH3 domain.

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CC -----

CC EMBL: AF233519; AAF82728.1; -

DR HSSP: Q16674; 111J

DR InterPro: IPR001452; SH3.

DR SMART: SM00326; SH3; 1.

DR PROSITE: PS50002; SH3; 1.

KW SIGNAL; SH3 domain.

FT SIGNAL 1 23 POTENTIAL.

FT CHAIN 24 133 OTORAPLIN.

FT DOMAIN 48 115 SH3.

FT DISULFID 35 40 BY SIMILARITY.

FT DISULFID 58 132 BY SIMILARITY.

SEQUENCE 133 AA; 15243 MW; 25440C1A3CF911AE CRC64;

Query Match 59.8%; Score 404; DB 1; Length 133;

Best Local Similarity 56.0%; Pred. No. 4.3e-34;

Matches 70; Conservative 28; Mismatches 19; Indels 8; Gaps 3;

QY 12 LVALCG-----HGFMFKLSSKKLCADEECVYITISLARAQEDYNAPDCRFINVKKG 65

DB 9 VIVLCTGFTHORAYGYMOKLSDKLCADDECIVYISFGRADYVAPDCRFVNLKKGEL 68

QY 66 IYVYVSKLVTEAGAGAFWAGSYTG-DHODEMGIVGFPSNLVREQRYVQEAITEPTTD 123

DB 69 VIIVYVSKLVTEKESGEFVAGSYGEEYEDHMGIVGFPSNLVTELVYKDELQELPTTV 128

QY 124 DEFECE 128

DB 129 DEFECE 133

RESULT 5

MIA_HUMAN STANDARD; PRT: 131 AA.

AC Q16674;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Melanoma derived growth regulatory protein precursor (Melanoma inhibitory activity).

DB MIA.

GN Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

NCBI_TaxID=9606;

RM [1]

RP MEDLINE=95007612; PubMed=7923218;

RA Blesch A., Boeserhoff A.-K., Apfel R., Behl C., Hesseboerfer B.,

RA Schmitt A., Jachimczak P., Lotzsch F., Buettner R., Bogdahn U.;
RT "Cloning of a novel malignant melanoma-derived growth-regulatory
RL protein, MIA.";
RN Cancer Res. 54:5695-5701 (1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=66132947, PubMed=8550608;
RA Bossenhardt A.-K., Hein R., Bogdahn U., Buettner R.;
RT "Structure and promoter analysis of the gene encoding the human
RL melanoma-inhibiting protein MIA.";
RJ J. Biol. Chem. 271:490-495 (1996).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22386257, PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heisler F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
RA Stickleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussid T.B., Tosh yukl S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwen P.J., McKenran K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Wuzny D.M., Sodergergen E.J., Lu X., Gibbs R.A.,
RA Faley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.T., Skalska U., Smailus D.E.,
RA Schermer A., Schein J.E., Jones S.J.W., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RL human and mouse cDNA sequences.";
RJ Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (1.39 ANGSTROMS) OF 25-111.
RX MEDLINE=21244635, PubMed=11331761;
RA Longhead J.C., Holton J.M., Alber T., Bazan J.F., Handel T.M.;
RT "Structure of melanoma inhibitory activity protein, a member of a
RL recently identified family of secreted proteins.";
RJ Proc. Natl. Acad. Sci. U.S.A. 98:5515-5520 (2001).
RN [5]
RP FUNCTION: ELICITS GROWTH INHIBITION ON MELANOMA CELLS IN VITRO
CC AS WELL AS SOME OTHER NEUROECTODERMAL TUMORS, INCLUDING GLIOMAS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: ALL MALIGNANT MELANOMA CELL LINES TESTED AND
CC INREQUENTLY IN GLIOMA CELL LINES.
CC -1- PTM: MAY POSSESS TWO INTRAMOLECULAR DISULFIDE BONDS.
CC -1- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
CC -1- SIMILARITY: Contains 1 SH3 domain.
CC -----
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CC or send an email to license@isb-stb.ch).
CC -----
DR EMBL, X75450, CAAS3203.1, -;
DR EMBL, X84707, CAAS9195.1, -;
DR EMBL, BC005910, AAH05910.1, -;
DR PIR, I38019, I38019.
DR PIR, I38019, I38019.
DR PDB, 1HJL, 16-MAY-01.
DR PDB, 1HJL, 29-JAN-02.
DR PDB, 1K0X, 24-JUL-02.
DR Genew, HGNC:7076, MIA.
DR MIM, 601340, -;
DR GO, GO:0005615, C:extracellular space; TAS.
DR GO, GO:0008283, F:cell proliferation; TAS.
DR InterPro, IPR001452, SH3.
DR Pfam, PF00018, SH3, 1.

| | |
|-------------|---|
| DR | SMART; SW00326; SH3; 1. |
| DR | POSITIVE; PS50002; SH3; 1. |
| KM | Growth factor; Signal; SH3 domain; 3D-structure. |
| FT | SIGNAL CHAIN |
| FT | DOMAIN |
| FT | DISEUFIID |
| FT | DISEUFIID |
| FT | TURND |
| FT | STRAND |
| FT | STRAND |
| FT | TURND |
| FT | STRAND |
| FT | STRAND |
| FT | TURND |
| FT | STRAND |
| FT | TURND |
| FT | STRAND |
| FT | STRAND |
| FT | TURND |
| FT | HELIIX |
| SO | SEQUENCE |
| Query Match | Best Local Similarity 40.8%; Score 275.5; DB 1; Length 131; |
| Matches | 60; Conservative 27; Mismatches 37; Indels 11; Gaps 6 |
| QY | 1 MARILLGGVALCA--GHGMF---MDXSKKLGADBCVYTISLARGEDYNAPDC 55 |
| DB | 1 MASLV-CGVITILSAPSGPCVRGPMPLAKDKLCADQCSPISAVALQDYMAPDC 59 |
| QY | 56 RFINVKGOOIVYSKYLTENGAG-AFWAGSVYGDPHDEMGI-VGYFPNVLVEQRYYOE 113 |
| DB | 60 RLFLTHRGVVVFSLK--KGGRLPFGGSVGDDYODLARUGYFPSSIVREDQTLPK 116 |
| QY | 114 ATKEIPTTDFECE 128 |
| DB | 117 GKVDVKTDXWDFYCQ 131 |
| <hr/> | |
| RESULT 6 | |
| MIA_BOVIN | STANDARD; PRT; 130 AA. |
| ID | OZ8038; |
| AC | 028038; |
| DT | 01-NOV-1997 (Rel. 35, Last sequence update) |
| DT | 28-FEB-2003 (Rel. 41, Last annotation update) |
| DE | Melanoma derived growth regulatory protein precursor (Melanoma inhibitory activity) (Cartilage-derived retinoic acid-sensitive protein) (CD-RAP). |
| DE | MIA OR CDRAP. |
| GN | Bos taurus (Bovine). |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| OC | Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea; |
| OC | Bovidae; Bovine; Bos. |
| OX | NCBI_TaxId=9913; |
| RN | [1] |
| RP | SEQUENCE FROM N.A. |
| RX | MEDLINE=96216414; PubMed=8621736; |
| RA | Dietz U.H., Sandell L.J.: |
| RT | "Cloning of a retinoic acid-sensitive mRNA expressed in cartilage and during chondrogenesis." |
| RU | J. Biol. Chem. 271:3511-3516(1996). |
| CC | - FUNCTION: MAY FUNCTION DURING CARTILAGE DEVELOPMENT AND MAINTENANCE. |
| CC | - SUBCELLULAR LOCATION: Secreted |
| CC | |

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CC -1- TISSUE SPECIFICITY: CARTILAGE PRIMORDIA AND CARTILAGE.
CC -1- INDUCTION: Repressed by retinoic acid.
CC -1- PFM: MAY POSSESS TWO INTRAMOLECULAR DISULFIDE BONDS.
CC -1- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
CC -1- SIMILARITY: Contains 1 SH3 domain.
-----
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-----
CC EMBL; U51437; AAC48523.1; -
CC DR HSSP; Q16674; 111U.
CC DR InterPro; IPR001452; SH3.
CC DR Pfam; PF00018; SH3; 1.
CC DR SMART; SM00326; SH3; 1.
CC DR PROSITE; PS50002; SH3; 1.
CC DR Growth factor; Signal; SH3 domain.
CC FT SIGNAL 1 22 BY SIMILARITY.
CC FT CHAIN 23 130 MELANOMA DERIVED GROWTH REGULATORY
CC FT DOMAIN 42 112 PROTEIN.
CC FT DISULFID 35 40 BY SIMILARITY.
CC FT DISULFID 58 129 BY SIMILARITY.
CC SQ SEQUENCE 130 AA; 14353 MW; 95D153161C78E02A CRC64;

Query Match 39.9%; Score 270; DB 1; Length 130;
Best Local Similarity 44.4%; Pred. No. 1.7e-20;
Matches 60; Conservative 24; Mismatches 39; Indels 12; Gaps 5;

QY 1 MARILLILGLVNLCA-----GHGEMDKLSKKLCADCECYTTISLAPGQYNAPDC 55
DB 1 MAMSLVFL--GVLLSAPPPGSGRPMKLDKRCDECHSPISAVLQGVAPDC 58
QY 56 RFINKKGOQIVYVSKLVTENGAG-AFWAGSYVGDH-QDEMGIYGFPSNLVREQRYOE 113
DB 59 RFLTHGQVYVYSKLT---KGRGRLFMGSGVGGDYGDGAARLGYPSSIVREDQLKP 115
QY 114 ATKEIPTTIDIFPCE 128
DB 116 AKTDVKTDIMDFYCQ 130

RESULT 7
MIA_MOUSE
ID MIA_MOUSE STANDARD; PRT; 130 AA.
AC Q62946; P97591;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Melanoma derived growth regulatory protein precursor (Melanoma
DE inhibitory activity) (Cartilage-derived retinoic acid-sensitive
DE protein) (CD-RAP).
DE MIA OR CDRAIP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
OX [1]
RN SEQUENCE FROM N.A.
RP STRAIN-Sprague-Dawley; TISSUE-Mammary gland;
RA Lu J.X.;
RT "Gene expression changes associated with chemically-induced rat
RT mammary carcinogenesis."
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 34-124 FROM N.A.
RC TISSUE=Cartilage;
RX MEDLINE=96216414; PubMed=8621736;
RA Dietz U.H.; Sandell L.J.;

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RT "Cloning of a retinoic acid-sensitive mRNA expressed in cartilage and
RT during ontogeny."
RL J. Biol. Chem. 271:3311-3316(1996).
CC -1- FUNCTION: MAY FUNCTION DURING CARTILAGE DEVELOPMENT AND
CC MAINTENANCE.
CC -1- SUBCELLULAR LOCATION: secreted.
CC -1- TISSUE SPECIFICITY: CARTILAGE PRIMORDIA AND CARTILAGE.
CC -1- INDUCTION: Repressed by retinoic acid.
CC -1- PFM: MAY POSSESS TWO INTRAMOLECULAR DISULFIDE BONDS.
CC -1- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
CC -1- SIMILARITY: Contains 1 SH3 domain.
-----
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-----
CC EMBL; U51438; AAC52481.1; -
CC DR EMBL; U67884; AAB40659.1; -
CC DR HSSP; Q16674; 111U.
CC DR InterPro; IPR001452; SH3.
CC DR Pfam; PF00018; SH3; 1.
CC DR SMART; SM00326; SH3; 1.
CC DR PROSITE; PS50002; SH3; FALSE NEG.
CC DR Growth factor; Signal; SH3 domain.
CC FT SIGNAL 1 22 POTENTIAL.
CC FT CHAIN 23 130 MELANOMA DERIVED GROWTH REGULATORY
CC FT DOMAIN 42 112 PROTEIN.
CC FT DISULFID 35 40 SH3.
CC FT DISULFID 58 129 BY SIMILARITY.
CC FT CONFLICT 46 47 MA -> VT (IN REF. 2).
CC SQ SEQUENCE 130 AA; 14536 MW; 5F99149AECF74501 CRC64;

Query Match 39.6%; Score 268; DB 1; Length 130;
Best Local Similarity 43.8%; Pred. No. 2.7e-20;
Matches 56; Conservative 25; Mismatches 37; Indels 10; Gaps 4;

QY 8 LLGLVNLCAHGQM-----FMDKLSKKLCADCECYTTISLAPGQYNAPDCRFINKVK 62
DB 6 VLLGIYILSVFSLGRADAMKPLADKLCADCECHSPISMAVLDYAPDCRFITVR 65
QY 63 GQGIYVYVSKLVTENGAG-AFWAGSYVGDH-QDEMGI-VGYFPSNLVREQRYOEATKEIPT 120
DB 66 GQVYVYVSKLT---KGRGRLFMGSGVGGDYGDLAHLGYPSSIVREDQLKPKVDKMT 122
QY 121 TDIDFCE 128
DB 123 DEWDYFCQ 130

RESULT 8
MIA_MOUSE
ID MIA_MOUSE STANDARD; PRT; 130 AA.
AC Q61865; O09086; P97495;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Melanoma derived growth regulatory protein precursor (Melanoma
DE inhibitory activity) (Cartilage-derived retinoic acid-sensitive
DE protein) (CD-RAP).
DE MIA OR CDRAIP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
OX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=BA1B/C;
RX MEDLINE=95007612; PubMed=7923218;

```

RA Blesch A., Bosserhoff A.-K., Apfel R., Behl C., Hessedeferer B.,
 RA Schmitt A., Jachimczak P., Lottspeich F., Buetner R., Bogdahn U.,
 RT "Cloning of a novel malignant melanoma-derived growth-regulatory
 RT protein, MA.", Cancer Res. 54:5695-5701(1994).
 RL (2)
 RN SEQUENCE FROM N.A.
 RP STRAIN=129/SV;
 RC MEDLINE=97251341; PubMed=9097023;
 RX Bosserhoff A.K., Kondo S., Moser M., Dietz U., Copeland N.G.,
 RA Gilbert D.J., Jenkins N.A., Buetner R., Sandell L.J.,
 RT "Mouse CD-RAP/MA gene: structure, chromosomal localization, and
 RT expression in cartilage and chondrosarcoma.",
 RL Dev. Dyn. 208:516-525(1997).
 CC -1- FUNCTION: ELICITS GROWTH INHIBITION ON MELANOMA CELLS IN VITRO AS
 CC WELL AS SOME OTHER NEUROECTODERMAL TUMORS, INCLUDING GLIOMAS (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: ALL MALIGNANT MELANOMA CELL LINES TESTED AND
 CC INDEPENDENTLY IN GLIOMA CELL LINES.
 CC -1- PTM: MAY POSSESS TWO INTRAMOLECULAR DISULFIDE BONDS.
 CC -1- SIMILARITY: BELONGS TO THE MA / OTOR FAMILY.
 CC -1- SIMILARITY: Contains 1 SH3 domain.
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 CC
 DR EMBL, X94322; CAA63983.1; -
 DR EMBL, U85612; AAB42082.1; -
 DR EMBL, X97965; CAA66608.1; -
 DR HSSP, Q16674; 111J.
 DR MGD; MGI:109615; Ma.
 DR GO; GO:0007160; P:cell-matrix adhesion; IMP.
 DR GO; GO:0030198; P:extracellular matrix organization and bioge. .; IMP.
 DR InterPro: IPR001452; SH3.
 DR Pfam; PF00018; SH3; 1.
 DR SMART; SM00326; SH3; 1.
 DR PROSITE; PS50002; SH3; FALSE NEG.
 DR Growth factor; Signal; SH3 domain.
 FT STGNAL 1 22 POTENTIAL.
 FT CHAIN 23 130 MELANOMA DERIVED GROWTH REGULATORY
 FT DOMAIN 42 112 PROTEIN.
 FT DISULFID 35 40 SH3.
 FT DISULFID 58 129 BY SIMILARITY.
 FT CONFLICT 112 113 TL -> NS (IN REF. 1).
 FT SEQUENCE 130 AA; 14593 MW; 16C957459C5B85F9 CRC64;
 Query Match 37.1%; Score 251; DB 1; Length 130;
 Best Local Similarity 43.0%; Pred. No. 1,4e-18;
 Matches 55; Conservative 22; Mismatches 41; Indels 10; Gaps 4;
 QY 8 LGGIYALCAGHG-----WFMDSLSSKKLCADBECCYTTISLAPADEYNAPCRFINVKK 62
 DB 6 VLLGIIVLVSFGSPBDRAMPKLAADWKLCADEBEGSHPSMAVALQDYVAPDCRELTIVR 65
 QY 63 GQGIIVYYSKLVTEANGG-AFMAGSYVGDHODEMGT-VGFPSNIVRECVYVEAKKEIPT 120
 DB 66 GQVYVYVFSKL--KGRGLFWGSGVGGYGGDLARLGFPSIVREDITLTKPKIDMKT 122
 QY 121 TDIDPFCE 128
 DB 123 DQWDFYCO 130

AC P54100; 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Vav proto-oncogene (p95).
 GN VAV1 OR VAV.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CX NCBI_Taxid=10116;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99321974; PubMed=10395673;
 RA Song J.S., Haleem-Smith H., Arudchandran R., Gomez J., Scott P.M.,
 RA Mill J.F., Tan T.-H., Rivera J.,
 RT "Tyrosine phosphorylation of Vav stimulates IL-6 production in mast
 RT cells by a Rac/C-Jun N-terminal kinase-dependent pathway".
 RL J. Immunol. 163:802-810(1999).
 CC -1- FUNCTION: Couples tyrosine kinase signals with the activation of
 CC the Rac/Rac GTPases, thus leading to cell differentiation and/or
 CC proliferation.
 CC -1- SUBUNIT: Interacts with SLA (By similarity).
 CC -1- PTM: Phosphorylated on tyrosine residues.
 CC -1- SIMILARITY: Contains 1 calponin-homology (CH) domain.
 CC -1- SIMILARITY: Contains 1 DBL-homology (DH) domain.
 CC -1- SIMILARITY: Contains 1 PH domain.
 CC -1- SIMILARITY: Contains 1 zinc-dependent phospho-ester and DAG
 CC binding domain.
 CC -1- SIMILARITY: Contains 1 SH2 domain.
 CC -1- SIMILARITY: Contains 2 SH3 domains.
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 CC
 DR EMBL, U39476; AAA98606.1; -
 DR HSSP, P29354; 1GR1.
 DR InterPro: IPR001715; Calponin-1like.
 DR InterPro: IPR003247; CH type.
 DR InterPro: IPR002219; DAG PE-bind.
 DR InterPro: IPR001331; GDS_CDC24.
 DR InterPro: IPR001849; PH.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR003096; SM22_calponin.
 DR Pfam; PF00307; CH; 1.
 DR Pfam; PF00130; DAG_PE-bind; 1.
 DR Pfam; PF00169; PH; 1.
 DR Pfam; PF00621; RhogEF; 1.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 2.
 DR PRINTS; PRO0401; SH2DOMAIN.
 DR PRINTS; PRO0452; SH3DOMAIN.
 DR PRINTS; PRO0888; SM22CALPONIN.
 DR PRODOM; PD001527; CH type; 1.
 DR PRODOM; PD000093; SH2; 1.
 DR PRODOM; PD000066; SH3; 1.
 DR SMART; SM00109; CL; 1.
 DR SMART; SM00033; CH; 1.
 DR SMART; SM00233; PH; 1.
 DR SMART; SM00325; RhogEF; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 2.
 DR PROSITE; PS50021; CH; 1.
 DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
 DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
 DR PROSITE; PS50010; DH_2; 1.
 DR PROSITE; PS00741; DH_1; 1.

| | | | |
|---|---|---|-----------------------------------|
| DR | PROSITE: | PS50003; | PH DOMAIN; 1. |
| DR | PROSITE: | PS50001; | SH2; 1. |
| DR | PROSITE: | PS50002; | SH3; 2. |
| KM | Proto-oncogene, | Phorbol-ester binding; | Zinc, SH2 domain, SH3 domain, |
| KM | Guanine-nucleotide | releasing factor; | Repeat, Phosphorylation. |
| FT | DOMAIN | 1 | 119 CH. |
| FT | DOMAIN | 194 | 379 DH. |
| FT | DOMAIN | 402 | 504 PH. |
| FT | DOMAIN | 516 | 564 PH. |
| FT | DOMAIN | 615 | 658 SH3.1. |
| FT | DOMAIN | 669 | 763 SH2. |
| FT | DOMAIN | 780 | 840 SH3.2. |
| SQ | SEQUENCE | 843 AA; | 97953 MM; CA45CAQD45FCB80E CRC64; |
| | | | |
| Query Match | | | |
| Best local Similarity 32.9%; Score 93.5; DB 1; Length 843; | | | |
| Matches 23; Conservative 14; Mismatches 20; Indels 13; Gaps 3 | | | |
| Qy | 44 | AARQEDYNNPDCRFIVKKGGQIIYYXSKLVNENGAGFMAQSVYGDPHDEMGIYGVPPSN | 103 |
| Db | 785 | AKRYPFCARDNSESLKEGDIIL---KILNKKGQGMMREIYGR-----IGWPPSN | 833 |
| Qy | 104 | IYVECRVYOE | 113 |
| Dd | 834 | YVED--YSE | 841 |
| | | | |
| RESULT 10 | | | |
| VAV_MOUSE | ID | VAV_MOUSE | STANDARD; PRT; 845 AA. |
| AC | P27870; | | |
| DT | 01-AUG-1992 (Rel. 23, Created) | | |
| DT | 01-AUG-1992 (Rel. 23, Last sequence update) | | |
| DT | 15-SEP-2003 (Rel. 42, Last annotation update) | | |
| DE | Vav proto-oncogene. | | |
| GN | VAV1 OR VAV. | | |
| OS | Mus musculus (Mouse). | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | |
| OX | NCBI_Taxid=10090; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RP | MEDLINE=92228488; PubMed=1555462; | | |
| RA | Adams J.A., Houston H., Allen U., Lints T., Harvey R.; | | |
| RT | "The hematopoietically expressed vav proto-oncogene shares homology | | |
| RT | with the dbl GTP-GDP exchange factor, the bcr gene and a yeast gene | | |
| RT | (CDC24) involved in cytoskeletal organization."; | | |
| RL | Oncogene 7:611-618(1992). | | |
| RN | [2] | | |
| RP | SEQUENCE OF 1-93 FROM N.A. | | |
| RP | MEDLINE=91172176; PubMed=2005887; | | |
| RA | Katzav S., Cleveland J.L., Heslop H.E., Pulido D.; | | |
| RT | "Loss of the amino-terminal helix-loop-helix domain of the vav proto- | | |
| RT | oncogene activates its transforming potential."; | | |
| RL | Mol. Cell. Biol. 11:1912-1920(1991). | | |
| RN | [3] | | |
| RP | INTERACTION WITH SLA. | | |
| RP | MEDLINE=20130290; PubMed=10662792; | | |
| RA | Sosinowski T., Pandey A., Dixit V.M., Weiss A.; | | |
| RT | "Src-like adaptor protein (SLAP) is a negative regulator of T cell | | |
| RT | receptor signaling."; | | |
| RL | J. Exp. Med. 191:463-474(2000). | | |
| CC | - FUNCTION: Couples tyrosine kinase signals with the activation of | | |
| CC | the Rho/Rac Gases, thus leading to cell differentiation and/or | | |
| CC | proliferation. | | |
| CC | - SUBUNIT: Interacts with SLA. | | |
| CC | - TISSUE SPECIFICITY: Widely expressed in hematopoietic cells but | | |
| CC | not in other cell types. | | |
| CC | - PTM: Phosphorylated on tyrosine residues (By similarity). | | |
| CC | - SIMILARITY: Contains 1 calponin-homology (CH) domain. | | |
| CC | - SIMILARITY: Contains 1 DBL-homology (DH) domain. | | |
| CC | - SIMILARITY: Contains 1 PH domain. | | |
| CC | - SIMILARITY: Contains 1 zinc-dependent phorbol-ester and DAG | | |

```

CC      binding domain.
CC      -1- SIMILARITY: Contains 1 SH2 domain.
CC      -1- SIMILARITY: Contains 2 SH3 domains.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL; X64361; CAA5713.1; -.
CC      DR EMBL; M59833; AAA63402.1; -.
CC      DR PIR; A61187; TVMSV.
CC      DR PDB; 1FSX; 15-SEP-00.
CC      DR PDB; 1GCP; 28-JAN-03.
CC      DR PDB; 1GCO; 28-JAN-03.
CC      DR PDB; 1K12; 18-DEC-02.
CC      TRNSFAC; T01230; -.
CC      DR MGD; MGI:98923; Vav1.
CC      DR InterPro; IPR001715; Calponin-like.
CC      DR InterPro; IPR003247; CH type.
CC      DR InterPro; IPR002219; DAG_PE-bind.
CC      DR InterPro; IPR001331; GDS_CDC24.
CC      DR InterPro; IPR001849; PH.
CC      DR InterPro; IPR000219; RHOGEF.
CC      DR InterPro; IPR000980; SH2.
CC      DR InterPro; IPR001452; SH3.
CC      DR InterPro; IPR003096; SM22_calponin.
CC      DR Pfam; PF00307; CH; 1.
CC      DR Pfam; PF00130; DAG_PE-bind; 1.
CC      DR Pfam; PF00169; PH; 1.
CC      DR Pfam; PF00621; RHOGEF; 1.
CC      DR Pfam; PF00017; SH2; 1.
CC      DR Pfam; PF00018; SH3; 2.
CC      DR PRINTS; PR00401; SH2DOMAIN.
CC      DR PRINTS; PR00452; SH3DOMAIN.
CC      DR PRINTS; PR00888; SM22CALPONIN.
CC      DR ProDom; PD001527; CH type; 1.
CC      DR ProDom; PD000093; SH2; 1.
CC      DR ProDom; PD000066; SH3; 1.
CC      DR SMART; SM00109; CL; 1.
CC      DR SMART; SM00033; CH; 1.
CC      DR SMART; SM00233; PH; 1.
CC      DR SMART; SM00325; RHOGEF; 1.
CC      DR SMART; SM00252; SH2; 1.
CC      DR SMART; SM00326; SH3; 2.
CC      DR PROSITE; PS50021; CH; 1.
CC      DR PROSITE; PS50047; DAG_PE_BIND_DOM_1; 1.
CC      DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
CC      DR PROSITE; PS50010; DH_2; 1.
CC      DR PROSITE; PS00741; DH_1; 1.
CC      DR PROSITE; PS50003; PH_DOMAIN; 1.
CC      DR PROSITE; PS50001; SH2; 1.
CC      DR PROSITE; PS50002; SH3; 2.
CC      KW Proto-oncogene; Phorbol-ester binding; Zinc; SH2 domain; SH3 domain;
CC      Guanine-nucleotide releasing factor; Repeat; Phosphorylation;
CC      3D-structure.
CC      KM
CC      FT DOMAIN 1 119 CH.
CC      FT DOMAIN 194 373 DH.
CC      FT DOMAIN 402 504 PH.
CC      FT DOMAIN 516 564 PHORBOL-ESTER AND DAG BINDING.
CC      FT DOMAIN 617 660 SH3 1.
CC      FT DOMAIN 671 765 SH2.
CC      FT DOMAIN 782 842 SH3 2.
CC      FT CONFLICT 29 Q -> E (IN REF. 2).
CC      SQ SEQUENCE 845 AA; 98136 MW; 366DCCD1C5229DA CRC64;

```

QY 44 AAPQEDYNAPDGRFINKKGGQIIVYSKLVNTENGAGAFWAGSYGDHODENGIVGYPFSPN 103
 DB 787 AARAYDFCARDBSELSTKEGDI-----KILKKKGCGGGMWRGEIYR-----ICMFPSN 835
 QY 104 LVREGRVYOE 113
 DB 836 YVEED--YSE 843

RESULT 11
 VAV3_MOUSE
 ID VAV3_MOUSE STANDARD; PRT; 847 AA.
 AC Q9R0C8;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Vav-3 protein.
 GN VAV3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 NC NCB1_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20179693; PubMed=10713454;
 RA Trenkle T., McClelland M., Adlkofer K., Welsh J.;
 RT "Major transcript variants of VAV3, a new member of the VAV family of
 RT guanine nucleotide exchange factors";
 RL Gene 245:113-119(2000).
 CC -1- FUNCTION: EXCHANGE FACTOR FOR GTP-BINDING PROTEINS RHOA, RHOG AND,
 CC TO A LESSER EXTENT, RAC-1. BINDS PHYSICALLY TO THE NUCLEOTIDE-FREE
 CC STATES OF THOSE GTPASES (BY SIMILARITY).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Alpha;
 CC IsoId=Q9R0C8-1; Sequence=Displayed;
 CC Name=Beta;
 CC IsoId=Q9R0C8-2; Sequence=Not described;
 CC -1- SIMILARITY: Contains 1 calponin-homology (CH) domain.
 CC -1- SIMILARITY: Contains 1 DBL-homology (DH) domain.
 CC -1- SIMILARITY: Contains 1 PH domain.
 CC -1- SIMILARITY: Contains 1 zinc-dependent phorbol-ester and DAG
 CC binding domain.
 CC -1- SIMILARITY: Contains 1 SH2 domain.
 CC -1- SIMILARITY: Contains 2 SH3 domains.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF067816; AAF09171.1; -
 CC HSSP: P29355; 1SEM.
 DR MGD; MG1:1888518; Vav3.
 DR InterPro: IPR001715; Calponin-like.
 DR InterPro: IPR003247; CH type.
 DR InterPro: IPR002219; DAG_PE_bind.
 DR InterPro: IPR001331; GDS_CDC24.
 DR InterPro: IPR001849; PH.
 DR InterPro: IPR000219; RhogEF.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR003096; SM22_calponin.
 DR Pfam: PF00307; CH; 1.
 DR Pfam: PF00130; DAG_PE_bind; 1.
 DR Pfam: PF00169; PH; 1.
 DR Pfam: PF00621; RhogEF; 1.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1.
 DR PRINTS; PR00401; SH2DOMAIN.

DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00888; SM22CALPONIN.
 DR ProDom; PD001527; CH type; 1.
 DR ProDom; PD000093; SH2; 1.
 DR ProDom; PD000066; SH3; 1.
 DR SMART; SM00109; C1; 1.
 DR SMART; SM00033; CH; 1.
 DR SMART; SM00233; PH; 1.
 DR SMART; SM00325; RhogEF; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 2.
 DR PROSITE; PS50021; CH; 1.
 DR PROSITE; PS500479; DAG_PE_BIND_DOM_1; 1.
 DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
 DR PROSITE; PS50010; DH 2; 1.
 DR PROSITE; PS00741; DH 1; 1.
 DR PROSITE; PS50003; PH_DOMAIN; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 2.
 DR Phorbol-ester binding; Zinc; SH2 domain; SH3 domain; Repeat;
 KM Guanine-nucleotide releasing factor; Alternative splicing.
 FT DOMAIN 1 119 CH.
 FT DOMAIN 192 371 PH.
 FT DOMAIN 400 502 PHORBO-ESTER AND DAG BINDING.
 FT DOMAIN 514 562 SH3 1.
 FT DOMAIN 592 660 SH2.
 FT DOMAIN 672 766 SH3 2.
 FT DOMAIN 788 847
 SQ SEQUENCE 847 AA; 97946 MW; 9A6B63F0D9E0F8F CRC64;

Query Match 13.8%; Score 93.5; DB 1; Length 847;
 Best Local Similarity 32.8%; Pred. No. 0.1;
 Matches 22; Conservative 13; Mismatches 21; Indels 11; Gaps 2;

QY 41 ISLRAGEYNAPDGRFINKKGGQIIVYSKLVNTENGAGAFWAGSYGDHODENGIVGYP 100
 DB 790 LGIARDFCARDBSELSTKEGDI-----SANGMWRGEVNGR-----VGWF 838

QY 101 PSNLVRE 107
 DB 839 PSTYVEE 845

RESULT 12
 VAV_HUMAN
 ID VAV_HUMAN STANDARD; PRT; 845 AA.
 AC P15498; Q15860;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Vav proto-oncogene.
 GN VAV1 OR VAV.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCB1_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Denninger D.J., Borges C.R., Shaw C.L., Cushman A.M., Kawahara R.S.;
 RT "Transcriptional regulation of the vav proto-oncogene."
 RT Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 62-845 FROM N.A.
 RX MEDLINE=90005432; PubMed=2477241;
 RA Katzav S., Martin-Zanca D., Barbacid M.;
 RT "vav, a novel human oncogene derived from a locus ubiquitously
 RT expressed in hematopoietic cells."
 RL EMBO J. 8:2283-2290(1989).
 RN [3]
 RP SEQUENCE OF 1-61 FROM N.A.
 RX MEDLINE=91172176; PubMed=2005887;
 RA Katzav S., Cleveland J.L., Heslop H.E., Pulido D.;
 RT "Loss of the amino-terminal helix-loop-helix domain of the vav proto-

RT oncogene activates its transforming potential.";
 RL Mol. Cell. Biol. 11:1912-1920(1991).
 RN (4)
 RP SEQUENCE OF 299-837 FROM N.A.
 RA Romero F.;
 RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
 RN (5)
 RP SEQUENCE OF 299-334 FROM N.A.
 RA MEDLINE=96038695; PubMed=7478592;
 RA Ramos-Morales F., Romero F., Schweighoffer F., Bismuth G., Camonis J.,
 RA Torcero M., Fischer S.;
 RL "The proline-rich region of Vav binds to Grb2 and Grb3-3.";
 RL Oncogene 11:1665-1668(1995).
 RN (6)
 RP SIMILARITY TO CDC24 FAMILY.
 RA MEDLINE=92228488; PubMed=1565462;
 RA Adams J.M., Houston H., Allen J., Lints T., Harvey R.;
 RL "The hematopoietically expressed vav proto-oncogene shares homology
 RT with the Dbl GTP-GTP exchange factor, the bcr gene and a yeast gene
 RT (CDC24) involved in cytoskeletal organization.";
 RL Oncogene 7:611-618(1992).
 CC -1- FUNCTION: Couples tyrosine kinase signals with the activation of
 CC the Rho/Rac GTPases, thus leading to cell differentiation and/or
 CC proliferation.
 CC -1- SUBUNIT: Interacts with SLA (By similarity). Interacts with Grb2
 CC and Grb3.
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED IN HEMATOPOIETIC CELLS BUT
 CC NOT IN OTHER CELL TYPES.
 CC -1- PTM: Phosphorylated on tyrosine residues.
 CC -1- MISCELLANEOUS: Vav' stands for the sixth letter of the Hebrew
 CC alphabet.
 CC -1- SIMILARITY: Contains 1 calponin-homology (CH) domain.
 CC -1- SIMILARITY: Contains 1 Dbl-homology (DH) domain.
 CC -1- SIMILARITY: Contains 1 PH domain.
 CC -1- SIMILARITY: Contains 1 zinc-dependent phospho-ester and DAG
 CC binding domain.
 CC -1- SIMILARITY: Contains 1 SH2 domain.
 CC -1- SIMILARITY: Contains 2 SH3 domains.
 CC -1- CAUTION: Ref.2 sequence differs from that shown due to frameshifts
 CC in position 322 and 355.
 CC
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 CC
 CC EMBL: AF030227; AAC25011.1;
 DR EMBL: AF030201; AAC25011.1; JOINED.
 DR EMBL: AF030202; AAC25011.1; JOINED.
 DR EMBL: AF030203; AAC25011.1; JOINED.
 DR EMBL: AF030204; AAC25011.1; JOINED.
 DR EMBL: AF030205; AAC25011.1; JOINED.
 DR EMBL: AF030206; AAC25011.1; JOINED.
 DR EMBL: AF030207; AAC25011.1; JOINED.
 DR EMBL: AF030208; AAC25011.1; JOINED.
 DR EMBL: AF030209; AAC25011.1; JOINED.
 DR EMBL: AF030210; AAC25011.1; JOINED.
 DR EMBL: AF030211; AAC25011.1; JOINED.
 DR EMBL: AF030212; AAC25011.1; JOINED.
 DR EMBL: AF030213; AAC25011.1; JOINED.
 DR EMBL: AF030214; AAC25011.1; JOINED.
 DR EMBL: AF030215; AAC25011.1; JOINED.
 DR EMBL: AF030216; AAC25011.1; JOINED.
 DR EMBL: AF030217; AAC25011.1; JOINED.
 DR EMBL: AF030218; AAC25011.1; JOINED.
 DR EMBL: AF030219; AAC25011.1; JOINED.
 DR EMBL: AF030220; AAC25011.1; JOINED.
 DR EMBL: AF030221; AAC25011.1; JOINED.
 DR EMBL: AF030222; AAC25011.1; JOINED.
 DR EMBL: AF030223; AAC25011.1; JOINED.

DR EMBL: AF030224; AAC25011.1; JOINED.
 DR EMBL: AF030225; AAC25011.1; JOINED.
 DR EMBL: AF030226; AAC25011.1; JOINED.
 DR EMBL: X16316; CA34383.1; ALT_FRAME.
 DR EMBL: M59834; AAA63267.1;
 DR EMBL: X83931; CA58783.1;
 DR PIR: B39576; TVHUV.
 DR HSSP: P2354; 1GRI.
 DR TRASPAC: T00880;
 DR Genew: HGNC:12657; VAV1.
 DR MIM: 164875;
 DR GO: GO:0003700; F:transcription factor activity; TAS.
 DR GO: GO:0007048; P:oncogenesis; TAS.
 DR InterPro: IPR001715; Calponin-like.
 DR InterPro: IPR003247; CH type.
 DR InterPro: IPR002219; DAG_PE-bind.
 DR InterPro: IPR003331; GDS_CDC24.
 DR InterPro: IPR001849; PH.
 DR InterPro: IPR000219; RhogEF.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR003096; SM22-calponin.
 DR Pfam: PF00307; CH; 1.
 DR Pfam: PF00130; DAG_PE-bind; 1.
 DR Pfam: PF00169; PH; 1.
 DR Pfam: PF00621; RhogEF; 1.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 2.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR PRINTS: PR00888; SM22CALPONIN.
 DR ProDom: PD001527; CH type; 1.
 DR ProDom: PD000993; SH2; 1.
 DR ProDom: PD000066; SH3; 1.
 DR SMART: SM00109; C1; 1.
 DR SMART: SM00033; CH; 1.
 DR SMART: SM00233; PH; 1.
 DR SMART: SM00325; RhogEF; 1.
 DR SMART: SM00252; SH2; 1.
 DR SMART: SM00326; SH3; 2.
 DR PROSITE: PS50021; CH; 1.
 DR PROSITE: PS00479; DAG_PE_BIND_DOM_1; 1.
 DR PROSITE: PS50081; DAG_PE_BIND_DOM_2; 1.
 DR PROSITE: PS50010; DH_2; 1.
 DR PROSITE: PS00741; DH_1; 1.
 DR PROSITE: PS50003; PH_DOMAIN; 1.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 2.
 KM Guanine-nucleotide phospho-ester binding; Zinc; SH2 domain; SH3 domain;
 KM Guanine-nucleotide releasing factor; Repeat; Phosphorylation.
 FT DOMAIN 1 119 CH.
 FT DOMAIN 194 373 DH.
 FT DOMAIN 402 504 PH.
 FT DOMAIN 516 564 PHORBOL-ESTER AND DAG BINDING.
 FT DOMAIN 617 660 SH3 1.
 FT DOMAIN 671 765 SH2.
 FT DOMAIN 782 842 SH3 2. (IN REF. 2).
 FT CONFLICT 264 264 A -> P (IN REF. 2).
 FT CONFLICT 718 718 I -> TV (IN REF. 2).
 SQ SEQUENCE 845 AA; 98313 MW; AC3BC9736FD2138 CRC64;

Query Match 13.5%; Score 91.5; DB 1; Length 845;
 Best Local Similarity 32.9%; Pred. No. 0.16;
 Matches 23; Conservative 14; Mismatches 20; Indels 13; Gaps 3;

QY 44 AAAGDYNAPDPCRFNNKKGGQIYYSLVYENGAGATWAGSVYGDHDDMGIVGYPFSN 103
 DB AAGARDPCARDSESLKGGDI-----KLNKKGGQGWRRGIVGR-----VGMPPAN 835
 QY 104 LVREQRYOE 113
 DB 836 YVEED--YSE 843

```

DR Pfam: PF00169; PH; 1.
DR Pfam: PF00621; Rhogef; 1.
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF00018; SH3; 1.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR PRINTS; PR00868; SM22CALPONIN.
DR PRODOM; PD001527; CH type: 1.
DR Prodom; PDD00093; SH2; 1.
DR Prodom; PDD00063; SH3; 1.
DR SMART; SMO0109; C1; 1.
DR SMART; SMO0033; CH; 1.
DR SMART; SMO0233; PH; 1.
DR SMART; SMO0325; Rhogef; 1.
DR SMART; SMO0252; SH2; 1.
DR SMART; SMO0326; SH3; 2.
DR PROSITE; PS50021; CH; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS50010; DH_2; 1.
DR PROSITE; PS500741; DH_1; 1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 2.
KM Phorbol-ester binding; Zinc; SH2 domain; SH3 domain; Repeat; factor; Alternative splicing.
KM Guanine-nucleotide releasing CH.
FT DOMAIN 1 119
FT DOMAIN 192 371
FT DOMAIN 400 502
FT DOMAIN 514 562
FT DOMAIN 592 660
FT DOMAIN 672 766
FT DOMAIN 768 847
FT DOMAIN 1 107
FT VARSPPLIC
FT FT
FT FT
FT CONFLICT 107 107 K->E (IN REF. 2). /FtId=VSP_001820.
FT CONFLICT 217 217 Y->H (IN REF. 1; AAD20348) .
FT CONFLICT 298 298 T->S (IN REF. 2) .
FT CONFLICT 429 429 V->A (IN REF. 1; AAD20348) .
SQ SEQUENCE 847 AA; 97775 MM; CLE2PEFB0B94CB721 CRC64;
Query Match Best Local Similarity 13.5%; Score 91.5; DB 1; Length 847; Matches 22; Conservative 13; Mismatches 21; Indels 11; Gaps 2

QY 41 ISLARPGEYNMPPDFRFINWKKGOIYYSKLVENAGAFMWGSYGVDHQDEMGIAYVE 100
DB LGAIARYPDRCARDRELSLKGDVKYLITRM-----SANGWMRGVENGR-----VGWF 838
      790          |::|::|::|||
OY 101 PSTLYAE 107
DB                ||||
      839 PSTTYEE 845

RESULT 14
VA_VAV2_MOUSE ID VA_VAV2_MOUSE STANDARD; PRT; 868 AA.
AC Q60992; DT 01-NOV-1997 (Rel. 35, Created) OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. OX NCBI_TaxID=10090; RN [1] RP SEQUENCE FROM N.A. KC STRAIN=C57BL/6;
```

RX MEDLINE=96313271; PubMed=8710375;
 RA Schubeil K.E., Bustelo X.R., Nielsen D.A., Song B.J., Barbacid M.,
 RA Goldman D., Lee I.J.;
 RT "isolation and characterization of murine vav2, a member of the vav
 RT family of proto-oncogenes";
 RL Oncogene 13:363-371(1996).
 CC -1- FUNCTION: Guanine nucleotide exchange factor for the Rho family
 CC of Ras-related GTPases (By similarity).
 CC -1- SIMILARITY: Contains 1 calponin-homology (CH) domain.
 CC -1- SIMILARITY: Contains 1 DBI-homology (DH) domain.
 CC -1- SIMILARITY: Contains 1 zinc-dependent phospho-ester and DAG
 CC binding domain.
 CC -1- SIMILARITY: Contains 1 SH2 domain.
 CC -1- SIMILARITY: Contains 2 SH3 domains.
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 CC -----
 DR EMBL; U37017; AAC52761.1; -.
 DR HSSP; G60631; 1GB0.
 DR MGD; MGI:102718; Vav2.
 DR InterPro; IPR001715; Calponin-like.
 DR InterPro; IPR003247; CH type.
 DR InterPro; IPR002219; DAG_PE-bind.
 DR InterPro; IPR001331; GDS_CDC24.
 DR InterPro; IPR001849; RHGEF.
 DR InterPro; IPR000219; RHGEF.
 DR InterPro; IPR000950; SH2.
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF00307; CH; 1.
 DR Pfam; PF00130; DAG_PE-bind; 1.
 DR Pfam; PF00169; PH; 1.
 DR Pfam; PF00621; RHGEF; 1.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 2.
 DR PRINTS; PRO0401; SH2DOMAIN.
 DR PRINTS; PRO0452; SH3DOMAIN.
 DR PRODOM; PD001527; CH_type; 1.
 DR PRODOM; PD000093; SH2; 1.
 DR PRODOM; PD000066; SH3; 2.
 DR SMART; SM00109; CH; 1.
 DR SMART; SM00003; CH; 1.
 DR SMART; SM00233; PH; 1.
 DR SMART; SM00325; RHGEF; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 2.
 DR PROSITE; PS50021; CH; 1.
 DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
 DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
 DR PROSITE; PS50010; DH_2; 1.
 DR PROSITE; PS00741; DH_1; 1.
 DR PROSITE; PS50003; PH_DOMAIN; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 2.
 KW Phospho-ester binding; Zinc; SH2 domain; SH3 domain;
 KW Guanine-nucleotide releasing factor; Repeat; Phosphorylation.
 FT DOMAIN 1 119 CH.
 FT DOMAIN 193 371 DH.
 FT DOMAIN 400 502 PH.
 FT DOMAIN 514 562 PHORBOL-ESTER AND DAG BINDING.
 FT DOMAIN 576 642 SH3 1.
 FT DOMAIN 663 757 SH2.
 FT DOMAIN 806 867 SH3 2.
 FT MOD_RES 142 142 PHOSPHORYLATION (BY EGFR) (BY
 FT SIMILARITY).
 FT MOD_RES 159 159 PHOSPHORYLATION (BY EGFR) (BY
 FT SIMILARITY).

FT MOD_RES 172 172 PHOSPHORYLATION (BY EGFR) (BY
 FT SIMILARITY).
 SQ SEQUENCE 868 AA; 99915 MW; D18581E7EEB2BC2 CRC64;
 Query Match 12.6%; Score 85.5; DB 1; Length 868;
 Best Local Similarity 28.9%; Pred. No. 0.67; Indels 13; Gaps 3;
 Matches 22; Conservative 19; Mismatches 22;
 QY 38 VY---ISLAARDYNAPDCRFNVKKGQOIVYYSKLTENGAGAFWAGSVGDHODEM 94
 DB 802 VFTFRVIGTAVARINFPAPDKRELRLRGDVVKYISIGDQG---WKKG-----ETN 851
 QY 95 GIVGYFSPNLYREQRV 110
 DB 852 GRIGMFPSTVEEGV 867
 RESULT 15
 ID VAV2 HUMAN STANDARD; PRT; 878 AA.
 AC P52735.
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Vav-2 protein.
 GN VAV2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 ON NCBI_TaxId=9606;
 OX [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=95283235; PubMed=7762982;
 RA Henske E.P., Short M.P., Jozwiak S., Bovey C.M., Ramlakhan S.,
 RA Haines J.L., Kwiatkowski D.J.;
 RT "Identification of VAV2 on 9q34 and its exclusion as the tuberous
 RT sclerosis gene TSC1";
 RL Ann. Hum. Genet. 59:25-37(1995).
 RN [2]
 RP PHOSPHORYLATION OF TYR-142; TYR-159 AND TYR-172.
 RX MEDLINE=22464432; PubMed=12454019;
 RA Tanas P., Soliti Z., Bauer P., Illes A., Sipkei S., Bauer A.,
 RA Parago A., Downward J., Buday L.;
 RT "Mechanism of epidermal growth factor regulation of Vav2, a guanine
 RT nucleotide exchange factor for Rac";
 RL J. Biol. Chem. 278:5163-5171(2003).
 CC -1- FUNCTION: Guanine nucleotide exchange factor for the Rho family
 CC of Ras-related GTPases.
 CC -1- TISSUE SPECIFICITY: Widely expressed.
 CC -1- SIMILARITY: Contains 1 calponin-homology (CH) domain.
 CC -1- SIMILARITY: Contains 1 DBI-homology (DH) domain.
 CC -1- SIMILARITY: Contains 1 PH domain.
 CC -1- SIMILARITY: Contains 1 zinc-dependent phospho-ester and DAG
 CC binding domain.
 CC -1- SIMILARITY: Contains 1 SH2 domain.
 CC -1- SIMILARITY: Contains 2 SH3 domains.
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 CC -----
 DR EMBL; S76992; AAB34377.1; -.
 DR PIR; I51940; I51940.
 DR HSSP; P08631; 1BU1.
 DR Genew; HGNC:12658; VAV2.
 DR MIM; 600428; -.
 DR InterPro; IPR001715; Calponin-like.
 DR InterPro; IPR003247; CH_type.

DR InterPro: IPR002219; DAG_PE-bind.
 DR InterPro: IPR001331; GDS_CDC24.
 DR InterPro: IPR001849; PH.
 DR InterPro: IPR000219; RhogEF.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR Pfam: PF00307; CH; 1.
 DR Pfam: PF00130; DAG_PE-bind; 1.
 DR Pfam: PF00169; PH; 1.
 DR Pfam: PF00621; RhogEF; 1.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 2.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR ProDom; PD001527; CH_type; 1.
 DR ProDom; PD000093; SH2; 1.
 DR ProDom; PD000066; SH3; 2.
 DR SMART; SM00109; C1; 1.
 DR SMART; SM00033; CH; 1.
 DR SMART; SM00233; PH; 1.
 DR SMART; SM00325; RhogEF; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 2.
 DR PROSITE; PS50021; CH; 1.
 DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
 DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
 DR PROSITE; PS50010; DH_2; 1.
 DR PROSITE; PS00741; DH_1; 1.
 DR PROSITE; PS50003; PH_DOMAIN; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 2.
 DR Phorbol-ester binding; Zinc; SH2 domain; SH3 domain;
 KW Phorbol-ester binding; Zinc; SH2 domain; SH3 domain;
 K1 Guanine-nucleotide releasing factor; Repeat; Phosphorylation.
 FT DOMAIN 1 119 CH.
 FT DOMAIN 198 376 DH.
 FT DOMAIN 405 512 PH.
 FT DOMAIN 524 572 PHORBOL-ESTER AND DAG BINDING.
 FT DOMAIN 586 652 SH3 1.
 FT DOMAIN 673 767 SH2.
 FT DOMAIN 816 877 SH3 2.
 FT MOD_RES 142 142 PHOSPHORYLATION (BY EGFR).
 FT MOD_RES 159 159 PHOSPHORYLATION (BY EGFR).
 FT MOD_RES 172 172 PHOSPHORYLATION (BY EGFR).
 SQ SEQUENCE 878 AA; 101256 MW; C8FF7681032146B4 CRC64;

Query Match 12.5%; Score 84.5; DB 1; Length 878;
 Best local similarity 27.6%; Pred. No. 0.85;
 Matches 21; Conservative 20; Mismatches 22; Indels 13; Gaps 3;

QY 38 VY--ISLARAEEDYNAPDCRFNVKKGOIYVYSKLVTEENGAGAFWAGSVYGDHODEM 94
 DB 812 VETPRVITAVARVNFARADRELSTREGDVVRISRIIGDQG--WWKG-----ETN 861
 QY 95 GIVGYFPSNLYVEQRV 110
 DB 862 GRIGWFPSYVEEERI 877

Search completed: December 29, 2003, 16:04:14
 Job time : 5.01961 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 29, 2003, 16:03:18 ; Search time 19.7199 Seconds
(without alignments)
1674.996 Million cell updates/sec

Title: US-10-019-455A-47
Perfect score: 676
Sequence: 1 MARITILLGLVALCAGHG.....RVQENTKEIPTIDPFCE 128

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 segs, 258052504 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeop:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-----------|---------------------|
| 1 | 234.5 | 34.7 | 96 | 11 Q9J109 | Q9J109 mesocricetu |
| 2 | 215 | 31.8 | 268 | 11 Q8BUE9 | Q8BUE9 mus musculu |
| 3 | 215 | 31.8 | 1239 | 11 Q8B184 | Q8B184 mus musculu |
| 4 | 189 | 28.0 | 68 | 11 Q8C899 | Q8C899 mus musculu |
| 5 | 184.5 | 27.3 | 137 | 11 Q921X3 | Q921X3 mus musculu |
| 6 | 176.5 | 26.1 | 88 | 13 Q90XF1 | Q90XF1 tetradon n |
| 7 | 166 | 24.6 | 119 | 4 Q96PCS | Q96PCS homo sapien |
| 8 | 160 | 23.7 | 119 | 11 Q91ZV0 | Q91ZV0 mus musculu |
| 9 | 160 | 23.7 | 166 | 11 Q08526 | Q08526 mus musculu |
| 10 | 93.5 | 13.8 | 287 | 11 Q8R076 | Q8R076 mus musculu |
| 11 | 93.5 | 13.8 | 806 | 11 Q8VDU4 | Q8VDU4 mus musculu |
| 12 | 93.5 | 13.8 | 845 | 11 Q8RTV7 | Q8RTV7 mus musculu |
| 13 | 93.5 | 13.8 | 846 | 13 Q8UTX6 | Q8UTX6 gallus galli |
| 14 | 91.5 | 13.5 | 719 | 4 Q96D17 | Q96D17 homo sapien |
| 15 | 86.5 | 12.8 | 839 | 13 Q8UUX5 | Q8UUX5 gallus galli |
| 16 | 83 | 12.3 | 1257 | 5 Q9VMA8 | Q9VMA8 drosophila |

| | | | | | |
|----|------|------|------|-----------|--------------------|
| 17 | 83 | 12.3 | 1430 | 5 Q9VMA7 | Q9VMA7 drosophila |
| 18 | 82 | 12.1 | 827 | 13 Q8UWE6 | Q8UWE6 tetradon n |
| 19 | 79 | 11.7 | 569 | 6 Q28616 | Q28616 cyctolagus |
| 20 | 78.5 | 11.6 | 365 | 11 Q9CXH0 | Q9CXH0 mus musculu |
| 21 | 78.5 | 11.6 | 636 | 10 Q9FTZ8 | Q9FTZ8 oryza sativ |
| 22 | 78.5 | 11.6 | 1196 | 4 Q9H0H2 | Q9H0H2 homo sapien |
| 23 | 78.5 | 11.6 | 1196 | 4 Q8N157 | Q8N157 homo sapien |
| 24 | 77 | 11.4 | 413 | 1 Q93709 | Q93709 sulfolobus |
| 25 | 77 | 11.4 | 722 | 16 Q9CGW7 | Q9CGW7 lactococcus |
| 26 | 76 | 11.2 | 344 | 10 Q9FU07 | Q9FU07 oryza sativ |
| 27 | 76 | 11.2 | 615 | 10 Q94E30 | Q94E30 oryza sativ |
| 28 | 76 | 11.2 | 638 | 10 Q9AT05 | Q9AT05 triticum ae |
| 29 | 76 | 11.2 | 643 | 10 Q9FU04 | Q9FU04 oryza sativ |
| 30 | 75.5 | 11.2 | 259 | 10 Q8RZ28 | Q8RZ28 oryza sativ |
| 31 | 75.5 | 11.2 | 509 | 16 Q9S5E5 | Q9S5E5 streptomyce |
| 32 | 75.5 | 11.2 | 635 | 10 Q9FU01 | Q9FU01 oryza sativ |
| 33 | 75.5 | 11.2 | 1215 | 5 Q77202 | Q77202 acanthamoeb |
| 34 | 75 | 11.1 | 432 | 10 Q9T0C2 | Q9T0C2 arabidopsis |
| 35 | 74 | 10.9 | 608 | 17 Q8T146 | Q8T146 methanobarc |
| 36 | 74 | 10.9 | 850 | 11 Q9CU15 | Q9CU15 mus musculu |
| 37 | 74 | 10.9 | 994 | 5 Q93575 | Q93575 caenorhabdi |
| 38 | 73.5 | 10.9 | 533 | 4 Q8WY10 | Q8WY10 dictyosteli |
| 39 | 73.5 | 10.9 | 847 | 4 Q16584 | Q16584 homo sapien |
| 40 | 73.5 | 10.9 | 901 | 5 Q81774 | Q81774 trypanosoma |
| 41 | 73 | 10.8 | 352 | 10 Q94EK2 | Q94EK2 allium asca |
| 42 | 73 | 10.8 | 352 | 10 Q94EK5 | Q94EK5 allium wake |
| 43 | 73 | 10.8 | 479 | 10 Q43366 | Q43366 allium cepa |
| 44 | 73 | 10.8 | 479 | 10 Q9SYV1 | Q9SYV1 allium cepa |
| 45 | 73 | 10.8 | 641 | 10 Q9AT06 | Q9AT06 triticum ae |

ALIGNMENTS

RESULT 1

ID Q9J109 PRELIMINARY: PRT: 96 AA.

AC Q9J109; 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Melanoma inhibitory activity protein (Fragment).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetidae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]

RP SEQUENCE FROM N.A.
RA Guba M., Bosserhoff A.K., Steinbauer M., Antuber M., Buettner R.,
RT Jauch K.W.;
RT "Overexpression of MIA enhances extravasation and metastasis of A-mel3
RT melanoma cells";
RT Submitted (May-2000) to the EMBL/GenBank/DBJ databases.
CC 1. SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DR EMBL: AF271694; AAF76220.1; ..
DR HSSP: Q16674; 111J.
DR InterPro: IPR001452; SH3.
DR Pfam: PF00018; SH3; 1.
DR SMART: SM00326; SH3; 1.
DR PROSITE: PS50002; SH3; 1.
KW SH3 domain.
FT NON TER 1
FT NON TER 96
SQ SEQUENCE 96 AA; 10756 MW; E7B46C3B5505BFB CRC64;

Query Match 34.7%; Score 234.5; DB 11; Length 96;
Best Local Similarity 46.4%; Pred. No. 5.7e-18;
Matches 45; Conservative 21; Mismatches 26; Indels 5; Gaps 3;

QY 26 LSKSLCADEECVYITSLAQEDYNAPDCRPINVKGQGIYVSKLTENGAG-AFWAG 84
DB 1 LADRLCADQECSPHISMAVALQDMAPDCRFITTHRGQVYVFSKL--KGRGLFWGG 57

QY 85 SVYGDHODEMGI-VGYFSPNLYREORVQEATKEIPT 120
DB 58 SVQGDYGDALRLGTFPSSIVREDOTLKPGKVDVKT 94

RESULT 2

Q8BJE9 PRELIMINARY; PRT; 268 AA.
AC Q8BJE9;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Weakly similar to NPIP-like protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Eye;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AK04344; BAC39164.1; -
FT NON TER 268
SQ SEQUENCE 268 AA; 29722 MW; 67339C562F684402 CRC64;
Query Match 31.8%; Score 215; DB 11; Length 268;
Best Local Similarity 41.3%; Pred. No. 2.8e-15;
Matches 45; Conservative 13; Mismatches 39; Indels 12; Gaps 4;
QY 19 HGMEMDKSLKKLCADEECVYITISLARAQEDYNAPDCRFINVKKGQIYYVSKLVTENGA 78
DB 28 HGR---RFSDLKVCGBDECSMLMRGKALDEFTGPDRCFVFKKGGDVVYVYKLA--GGS 82
QY 79 GAFNAGSVYGDHODEMGI-VGYFSPNLYREORVQEATKEIPTTIDDFPC 127
DB 83 LEIMAGSV--EHS-----FGYFPKDLIKVLAHKYTEELHIPADETDFVC 124

RESULT 3

Q8BI84 PRELIMINARY; PRT; 1239 AA.
AC Q8BI84;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Weakly similar to NPIP-like protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Retina;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AK044743; BAC32064.1; -
SQ SEQUENCE 1239 AA; 136350 MW; 6E16P9D42ECEEFF05 CRC64;
Query Match 31.8%; Score 215; DB 11; Length 1239;
Best Local Similarity 41.3%; Pred. No. 1.8e-14;
Matches 45; Conservative 13; Mismatches 39; Indels 12; Gaps 4;
QY 19 HGMEMDKSLKKLCADEECVYITISLARAQEDYNAPDCRFINVKKGQIYYVSKLVTENGA 78

DB 28 HGR---RFSDLKVCGBDECSMLMRGKALDEFTGPDRCFVFKKGGDVVYVYKLA--GGS 82
QY 79 GAFNAGSVYGDHODEMGI-VGYFSPNLYREORVQEATKEIPTTIDDFPC 127
DB 83 LEIMAGSV--EHS-----FGYFPKDLIKVLAHKYTEELHIPADETDFVC 124

RESULT 4

Q8C899 PRELIMINARY; PRT; 68 AA.
AC Q8C899;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Otoraplin.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AK047965; BAC33202.1; -
SQ SEQUENCE 68 AA; 7431 MW; 3CBET5527D3CB7F7 CRC64;
Query Match 28.0%; Score 189; DB 11; Length 68;
Best Local Similarity 61.5%; Pred. No. 3.6e-13;
Matches 40; Conservative 6; Mismatches 9; Indels 10; Gaps 2;

QY 1 MARILILIGIVLACAGHGMFMDKSLKKLCADEECV-----YTISLARAQEDYNA 52
DB 1 MARILILIGIVLACAGHGMFMDKSLKKLCADEECVCKALLTVFSLFHIGNLISG 60
QY 53 --PDC 55
DB 61 KQPDG 65

RESULT 5

Q92IX3 PRELIMINARY; PRT; 137 AA.
AC Q92IX3;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Similar to cartilage derived retinoic acid sensitive protein.
GN CDAP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strauberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC009815; AA009815.1; -
DR MGD; MGI:109615; Cdtrap.
DR InterPro; IPR001452; SH3.
DR Pfam; PF00018; SH3; 1.
DR SMART; SM00326; SH3; 1.
SQ SEQUENCE 137 AA; 15441 MW; 971415552E6FDS36 CRC64;
Query Match 27.3%; Score 184.5; DB 11; Length 137;
Best Local Similarity 49.4%; Pred. No. 2.7e-12;
Matches 42; Conservative 11; Mismatches 23; Indels 9; Gaps 3;

QY 8 ILGLGLVALCAGHG-----MFMKLSKKLCADEECVYTIISLRAQEDYNAPPCRFINVK 62
 Db 6 VILGIVLVSVFSGPSRADAMPPLADWKLCADECSHPIISAVLADYVAPDPCRLITFR 65
 QY 63 GQIIVYVSKLVTENGAG-AFWAGSV 86
 Db 66 GGVVVFESKL---KGRGLFWGGSV 87

RESULT 6

Q90XFL1 PRELIMINARY; PRT; 88 AA.
 ID Q90XFL1
 AC Q90XFL1
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Melanoma inhibitory activity protein (Fragment).
 OS Tetradonoma nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodon.
 OC NCBI_TaxID=99883;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bosserhoff A.K., Buettner R.;
 RT "Characterization of the MIA gene family";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF390176; AAL26991.1; -
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF00018; SH3; 1.
 DR SMART; SM00326; SH3; 1.
 FT NON TER 1
 FT SEQUENCE 88 AA; 10080 MM; C355CIFEQ4DA22EA CRC64;

Query Match 26.1%; Score 176.5; DB 13; Length 88;
 Best Local Similarity 42.4%; Pred. No. 1.2e-11;
 Matches 39; Conservative 16; Mismatches 26; Indels 11; Gaps 4;

QY 41 ISLRAQEDYNAPPCRFINVKKGQIIVYVSKLVTENGAGA-FWAGSV---YGDHDEMG 95
 Db 3 IIMARALQDYVPACXCTIPRQGLIYVAML---KGRSGFWAGSVQDSYQGEAR-- 57
 QY 96 IVGYFSPNLVREQRYQEQATKEIPTDIDFFC 127
 Db 58 -IGHFSSIVETHTPLMAAQTEVATSWMDYFC 88

RESULT 7

Q96PCS PRELIMINARY; PRT; 119 AA.
 ID Q96PCS
 AC Q96PCS
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Melanoma inhibitory activity protein 2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Bosserhoff A.K., Buettner R.;
 RT "Characterization of the MIA gene family";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF390175; AAL26990.1; -
 DR InterPro; IPR001452; SH3.
 DR SMART; SM00326; SH3; 1.
 SQ SEQUENCE 119 AA; 13535 MM; AEF529762D880ACS CRC64;

Query Match 24.6%; Score 166; DB 4; Length 119;
 Best Local Similarity 34.4%; Pred. No. 2.4e-10;

Matches 44; Conservative 14; Mismatches 46; Indels 24; Gaps 4;
 QY 6 ILGLGLVALCAGHGFMKLSKKL-----CADEECVYTIISLRAQEDYNAPPCRFIN 59
 Db 9 ILLALISLTK-----LESTKLADLKKGGDECEALINRVSMRQVGPDCRYLN 59
 QY 60 VKKQGIIVYVSKLVTENGAGAFWAGSVYGDHDEMGIVGYFSPNLVREQRYQEQATEIP 119
 Db 60 FTKEISVYVKLAGER--EDLMAGSKGE-----FGYFPRDAVQIEEVFISEIOM 110
 QY 120 TTDIDFFC 127
 Db 111 TXESDFLC 118

RESULT 8

Q91ZV0 PRELIMINARY; PRT; 119 AA.
 ID Q91ZV0
 AC Q91ZV0
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Melanoma inhibitory activity protein 2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bosserhoff A.K., Buettner R.;
 RT "Characterization of the MIA gene family";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF390177; AAL26992.1; -
 DR InterPro; IPR001452; SH3.
 DR SMART; SM00326; SH3; 1.
 SQ SEQUENCE 119 AA; 13397 MM; 589F390C0B49D1C7 CRC64;

Query Match 23.7%; Score 160; DB 11; Length 119;
 Best Local Similarity 35.2%; Pred. No. 1.1e-09;
 Matches 44; Conservative 18; Mismatches 49; Indels 14; Gaps 5;

QY 3 ILLILGLVALCAGHGFMKLSKKLCADEECVYTIISLRAQEDYNAPPCRFINVK 62
 Db 8 ILLILVVS--LAKCL-EGTKL--LHLKKCGLBCELTLSRYLALRDYGPCCRLINFTT 62
 QY 63 GQIIVYVSKLVTENGAGAFWAGSVYGDHDEMGIVGYFSPNLVREQRYQEQATEIPTD 122
 Db 63 GEISVYVKLGDR--EDLMAGSKGD-----FGYFPRDAVQIEEVFISEIOMSTKE 113

QY 123 IDFFC 127
 Db 114 SDFLC 118

RESULT 9

Q08526 PRELIMINARY; PRT; 166 AA.
 ID Q08526
 AC Q08526
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Vav-T.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=day; TISSUE=Testis;
 RX MEDLINE=97190224; PubMed=9038379;
 RA Okumura K., Kaneko Y., Nonoguchi K., Nishiyama H., Yokoi H.,

| QY | 101 | PSNLVRE | 107 |
|---------|--|--|---------------------------------------|
| Db | 279 | PSYVEE | 285 |
| RESULT | 11 | | |
| Q8VDU4 | PRELIMINARY; | PTI; | 806 AA. |
| AC | Q8VDU4 | | |
| DT | 01-MAR-2002 (TREMBlrel. 20, Created) | | |
| DT | 01-MAR-2002 (TREMBlrel. 20, Last sequence update) | | |
| DT | 01-MAR-2003 (TREMBlrel. 23, Last annotation update) | | |
| DT | Similar to vav oncogene. | | |
| GN | VAV. | | |
| OS | Mus musculus (Mouse). | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | |
| OX | NCBI_TaxId=10090; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RA | Strausberg R.; | | |
| RU | Submitted (Jan-2002) to the EMBL/GenBank/DBJ databases. | | |
| CC | !-SIMILARITY: CONTAINS 1 PH DOMAIN. | | |
| DR | EMBL; BC020487; AAR20487.1; -. | | |
| DR | MGD; MGI:98923; Vav. | | |
| DR | InterPro; IPR005613; AIP3. | | |
| DR | InterPro; IPR001715; Calponin-like. | | |
| DR | InterPro; IPR003219; CH type. | | |
| DR | InterPro; IPR001311; GDS_CDC24. | | |
| DR | InterPro; IPR001849; PH. | | |
| DR | InterPro; IPR000219; RHOGEF. | | |
| DR | InterPro; IPR000980; SH2. | | |
| DR | InterPro; IPR001452; SH3. | | |
| DR | InterPro; IPR003096; SM22_calponin. | | |
| DR | Pfam; PF003915; AIP3; 1. | | |
| DR | Pfam; PF001307; CH; 1. | | |
| DR | Pfam; PF001169; DAG_PE-bind; 1. | | |
| DR | Pfam; PF00621; RHOGEF; 1. | | |
| DR | Pfam; PF00017; SH2; 1. | | |
| DR | PRINTS; PR00452; SH3DOMAIN. | | |
| DR | PRINTS; PR00888; SM22CALPONIN. | | |
| DR | ProDom; PD001527; CH type; 1. | | |
| DR | ProDom; PD000093; SH2; 1. | | |
| DR | ProDom; PD000066; SH3; 1. | | |
| DR | SMART; SM00109; C1; 1. | | |
| DR | SMART; SM00033; PH; 1. | | |
| DR | SMART; SM00325; RHOGEF; 1. | | |
| DR | SMART; SM00352; SH2; 1. | | |
| DR | SMART; SM00326; SH3; 2. | | |
| DR | PROSITE; PS50021; CH; 1. | | |
| DR | PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1. | | |
| DR | PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1. | | |
| DR | PROSITE; PS00741; DH_1; 1. | | |
| DR | PROSITE; PS50010; DH_2; 1. | | |
| DR | PROSITE; PS50003; PH_DOMAIN; 1. | | |
| DR | PROSITE; PS50001; SH2; 1. | | |
| DR | PROSITE; PS50002; SH3; 2. | | |
| DR | SEQUENCE 806 AA; 93868 MW; F4368CD13A62D695 CRC64; | | |
| QY | Query Match | 13.8%; | Score 93.5; DB 11; Length 806; |
| Db | Best Local Similarity | 32.9%; | Pred. No. 0.22; 20; Indels 13; Gaps 3 |
| Matches | 23; Conservative | 14; Mismatches | |
| QY | 44 | ARAEVDNAPDCRFINVKKGGQQLYYVSKLVTEAGAGAFNAGSVYGDHDEMGIIGVYFSPN | 103 |
| Db | 748 | AKARIYDFPCADREBLTKGSDII-----KILNKKGGQGMWRGEIYGR-----IGWFPN | 796 |
| QY | 104 | LVREGRVYGE | 113 |

Db 797 YVEED-YSE 804

RESULT 12

PRELIMINARY; PRT; 845 AA.

Q8BTU7
AC Q8BTU7: PRELIMINARY; PRT; 845 AA.
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE VAV proto-oncogene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus; PubMed=12466851;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Genome Consortium
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL; AK089586; BAC40436.1;
DR EMBL; AK089586; BAC40436.1;
SQ SEQUENCE 845 AA; 98093 MW; 5D0DE0D9311DF88B CRC64;

Query Match 13.8%; Score 93.5; DB 11; Length 845;
Best Local Similarity 32.9%; Pred. No. 0.24;
Matches 23; Conservative 14; Mismatches 20; Indels 13; Gaps 3;

QY 44 ARAQEDYNAPDCRFINKKGGQIIVYSKLTENCGAFMAGSVYGDHDEMGIYGVFPN 103
Db 787 AKARYDFCARDRSELSKEGDI---KILKKGGCGGQWGEIYGR-----IGWFPN 835

QY 104 LVREGRVYQE 113
Db 836 YVEED-YSE 843

RESULT 13

PRELIMINARY; PRT; 846 AA.

Q8UTX6
AC Q8UTX6: PRELIMINARY; PRT; 846 AA.
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE GDP/GTP exchange factor VAV3.
GN VAV3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCB1_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=11805146;
RA Inaba K., Ishai M., Scharenberg A.M., Freshney N., Downward J.,
RA Kurosaki T.,
RA "Vav Modulates B Cell Receptor Responses by Regulating
RT Phosphoinositide 3-Kinase Activation."
RT J. Exp. Med. 195:189-200(2002).
CC -1- SIMILARITY: CONTAINS 2 SH3 DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
DR EMBL; AY046815; AA06249.1;
DR InterPro; IPR001715; Calponin-like.
DR InterPro; IPR003247; CH_type.
DR InterPro; IPR002219; DAG_PE_bind.
DR InterPro; IPR001331; GDS_CDC24.
DR InterPro; IPR001849; PH.
DR InterPro; IPR000219; RhogEF.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.

DR InterPro; IPR003096; SM22_calponin.

DR Pfam; PF00307; CH; 1.

DR Pfam; PF00330; DAG_PE_bind; 1.

DR Pfam; PF00169; PH; 1.

DR Pfam; PF00621; RhogEF; 1.

DR Pfam; PF00017; SH2; 1.

DR Pfam; PF00018; SH3; 1.

DR PRINTS; PRO0401; SH2DOMAIN.

DR PRINTS; PRO0452; SH3DOMAIN.

DR PRINTS; PRO0888; SM22CALPONIN.

DR ProDom; PD001527; CH_type; 1.

DR ProDom; PD000093; SH2; 1.

DR ProDom; PD000066; SH3; 1.

DR SMART; SM00109; C1; 1.

DR SMART; SM00033; CH; 1.

DR SMART; SM00233; PH; 1.

DR SMART; SM00325; RhogEF; 1.

DR SMART; SM00252; SH2; 1.

DR SMART; SM00326; SH3; 2.

DR PROSITE; PS00821; CH; 1.

DR PROSITE; PS00879; DAG_PE_BIND_DOM_1; 1.

DR PROSITE; PS00881; DAG_PE_BIND_DOM_2; 1.

DR PROSITE; PS00741; DH_1; 1.

DR PROSITE; PS00010; DH_2; 1.

DR PROSITE; PS00003; PH_DOMAIN; 1.

DR PROSITE; PS00001; SH2; 1.

DR PROSITE; PS00002; SH3; 2.

DR SH3 domain.

QY 41 ISLARQEDYNAPDCRFINKKGGQIIVYSKLTENCGAFMAGSVYGDHDEMGIYGVF 100
Db 789 IGAIARVDFCARDRSELSLKGDVVKIYTKM-----SANGWRGEVNGR-----VGWF 837

QY 101 PSNLYRE 107
Db 838 PSTYVEE 844

RESULT 14

PRELIMINARY; PRT; 719 AA.

Q96D37
AC Q96D37: PRELIMINARY; PRT; 719 AA.
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Placenta;
RA Strauberg R.,
RA Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 2 SH3 DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
DR EMBL; BC013361; AAH13361.1;
DR InterPro; IPR002219; DAG_PE_bind.
DR InterPro; IPR001331; GDS_CDC24.
DR InterPro; IPR001849; PH.
DR InterPro; IPR000219; RhogEF.
DR InterPro; IPR000219; RhogEF.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR Pfam; PF00130; DAG_PE_bind; 1.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00621; RhogEF; 1.
DR Pfam; PF00017; SH2; 1.

DR Pfam; PF00018; SH3; 2.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH2DOMAIN.
 DR Prodom; PD000093; SH2; 1.
 DR Prodom; PD000066; SH3; 1.
 DR SMART; SM00109; CL; 1.
 DR SMART; SM00233; PH; 1.
 DR SMART; SM00325; RHOGEF; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 2.
 DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
 DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
 DR PROSITE; PS00741; DH_1; 1.
 DR PROSITE; PS50010; DH_2; 1.
 DR PROSITE; PS50003; PH_DOMAIN; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 2.
 DR Hypothetical protein; SH3 domain.
 KW SEQUENCE 719 AA; 83727 MW; AS1B757DA543BAC CRC64;
 SQ

Query March 13.5%; Score 91.5; DB 4; Length 719;
 Best Local Similarity 32.9%; Pred. No. 0.32;
 Matches 23; Conservative 14; Mismatches 20; Indels 13; Gaps 3;

QY 44 ARAGEDYNAPDCRFINVKGGQIYVYSKLTENGAGAFWAGSVYGDHODEMGIVGPPSN 103
 DB 661 AKARYDFCARDRSELTKEDII-----KLNKKGQGGMMRGELVGR-----VGWFPAN 709

QY 104 LVREGRVYQE 113
 DB 710 YVEED--YSE 717

RESULT 15
 Q8UUX5 PRELIMINARY; PRT; 839 AA.
 ID Q8UUX5;
 AC 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 23, Last annotation update)
 DE GDP/GTP exchange factor VAV2.
 GN VAV2.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 OX [1]
 RN SEQUENCE FROM N.A.
 RP PubMed=11805146;
 RX Inabe K., Ishai M., Scharenberg A.M., Freshney N., Downward J.,
 RA Kurowski T.;
 RT "Vav3 Modulates B Cell Receptor Responses by Regulating
 RT Phosphoinositide 3-Kinase Activation.";
 RL J. Exp. Med. 195;189-200(2002).
 CC -1- SIMILARITY: CONTAINS 2 SH3 DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
 DR EMBL; AY046916; AAL06250.1; -;
 DR InterPro; IPR001715; Galponin-like.
 DR InterPro; IPR003247; CH_type.
 DR InterPro; IPR002219; DAG_PE-bind.
 DR InterPro; IPR001331; GDS_CDC24.
 DR InterPro; IPR001849; PH_1.
 DR InterPro; IPR000219; RHOGEF.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF00307; CH; 1.
 DR Pfam; PF00130; DAG_PE-bind; 1.
 DR Pfam; PF00169; PH_1.
 DR Pfam; PF00621; RHOGEF; 1.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 2.
 DR PRINTS; PR00401; SH2DOMAIN.

DR PRINTS; PR00452; SH3DOMAIN.
 DR Prodom; PD001527; CH_type; 1.
 DR Prodom; PD000093; SH2; 1.
 DR Prodom; PD000066; SH3; 2.
 DR SMART; SM00109; CL; 1.
 DR SMART; SM00033; CH; 1.
 DR SMART; SM00233; PH; 1.
 DR SMART; SM00325; RHOGEF; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 2.
 DR PROSITE; PS50021; CH; 1.
 DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
 DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
 DR PROSITE; PS00741; DH_1; 1.
 DR PROSITE; PS50010; DH_2; 1.
 DR PROSITE; PS50003; PH_DOMAIN; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 2.
 KW SH3 domain.
 SQ SEQUENCE 839 AA; 97500 MW; 6C1322ABAC23A530 CRC64;

Query Match 12.8%; Score 86.5; DB 13; Length 839;
 Best Local Similarity 30.3%; Pred. No. 1.4;
 Matches 23; Conservative 18; Mismatches 22; Indels 13; Gaps 3;

QY 38 VYT---ISLARRAGEDYNAPDCRFINVKGGQIYVYSKLTENGAGAFWAGSVYGDHODEM 94
 DB 773 VFTPRVITGAIVARVNFPAARDRELRLRSDVVKITSRIGDGG---WKKG-----ETN 822

QY 95 GIYGFPPSNLVREGRV 110
 DB 823 GRVGFPPSTVVEEGV 838

Search completed: December 29, 2003, 16:06:27
 Job time : 20.7199 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2003, 16:03:18 ; Search time 25.098 Seconds
(without alignments)
809.506 Million cell updates/sec

Title: US-10-019-455A-47

Perfect score: 676
Sequence: 1 MARITILLGLVNLCAHG.....RVGEATKEIPTIDFCE 128

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: A_Geneseq_19Jun03:*
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
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19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-------------|--------------------|
| 1 | 676 | 100.0 | 128 | 22 AAB69130 | Rat MLP protein se |
| 2 | 655 | 96.9 | 128 | 22 AAB69125 | Mouse MLP protein |
| 3 | 600 | 88.8 | 128 | 22 AAB69123 | Human growth regul |
| 4 | 600 | 88.8 | 128 | 22 AAB69123 | Human MLP protein |
| 5 | 600 | 88.8 | 128 | 23 AAB95602 | Human angiotensin |
| 6 | 600 | 88.8 | 128 | 23 AAB84966 | Human PRO9873 prot |
| 7 | 600 | 88.8 | 128 | 23 AAU83627 | Human PRO protein, |
| 8 | 600 | 88.8 | 128 | 23 AAU08871 | Novel human secret |
| 9 | 591 | 87.4 | 110 | 22 AAB69131 | Rat MLP protein se |

| | | | | | |
|----|-------|------|------|-------------|--------------------|
| 10 | 574 | 84.9 | 110 | 22 AAB69127 | Mouse MLP protein |
| 11 | 541 | 80.0 | 110 | 22 AAB69126 | Human MLP protein |
| 12 | 515 | 76.2 | 105 | 22 AAB82572 | Human growth regul |
| 13 | 462 | 68.3 | 87 | 22 AAB69129 | Rat MLP protein se |
| 14 | 275.5 | 40.8 | 131 | 16 AAB69811 | Melanoma inhibiti |
| 15 | 275.5 | 40.8 | 131 | 22 AAG65614 | Human MIA protein |
| 16 | 273.5 | 40.5 | 137 | 22 AAG65615 | Recombinant human |
| 17 | 247 | 36.5 | 130 | 16 AAB69812 | Melanoma inhibiti |
| 18 | 215 | 31.8 | 125 | 23 AAB62119 | Mouse TANGO 130 MI |
| 19 | 215 | 31.8 | 105 | 23 AAB62119 | Human PRO polypept |
| 20 | 215 | 31.8 | 303 | 22 AAB87608 | Human PRO polypept |
| 21 | 215 | 31.8 | 303 | 22 AAB87608 | Human PRO polypept |
| 22 | 215 | 31.8 | 303 | 23 AAB84994 | Human PRO polypept |
| 23 | 215 | 31.8 | 303 | 23 AAB84994 | Human PRO polypept |
| 24 | 215 | 31.8 | 303 | 24 AAB71382 | Human secreted/tra |
| 25 | 215 | 31.8 | 303 | 24 AAB71382 | Human secreted/tra |
| 26 | 215 | 31.8 | 303 | 24 AAB72034 | Human secreted/tra |
| 27 | 215 | 31.8 | 303 | 24 AAB72034 | Human secreted/tra |
| 28 | 215 | 31.8 | 303 | 24 AAB65849 | Human secreted/tra |
| 29 | 215 | 31.8 | 303 | 24 AAB65849 | Human secreted/tra |
| 30 | 215 | 31.8 | 303 | 24 AAB65849 | Human secreted/tra |
| 31 | 215 | 31.8 | 303 | 24 AAB65849 | Human secreted/tra |
| 32 | 215 | 31.8 | 303 | 24 AAB65849 | Human secreted/tra |
| 33 | 215 | 31.8 | 303 | 24 AAB65849 | Human secreted/tra |
| 34 | 215 | 31.8 | 303 | 24 AAB65849 | Human secreted/tra |
| 35 | 215 | 31.8 | 303 | 24 AAB65849 | Human secreted/tra |
| 36 | 215 | 31.8 | 303 | 24 AAB65849 | Human secreted/tra |
| 37 | 215 | 31.8 | 303 | 24 AAB65849 | Human secreted/tra |
| 38 | 208.5 | 30.8 | 125 | 23 AAB82120 | Human TANGO 130 po |
| 39 | 207.5 | 30.7 | 410 | 21 AAB70210 | Human TANGO 130 po |
| 40 | 207.5 | 30.7 | 410 | 21 AAB70210 | Human TANGO 130 po |
| 41 | 207.5 | 30.7 | 410 | 21 AAB70210 | Human TANGO 130 po |
| 42 | 207.5 | 30.7 | 1907 | 23 AAB82117 | Human TANGO 130 po |
| 43 | 199 | 29.4 | 499 | 22 AAB82117 | Human TANGO 130 po |
| 44 | 199 | 29.4 | 499 | 24 AAB82117 | Human TANGO 130 po |
| 45 | 199 | 29.4 | 499 | 24 AAB82117 | Human TANGO 130 po |

ALIGNMENTS

RESULT 1
ID AAB69130 standard; Protein; 128 AA.
XX AAB69130:
XX 23-APR-2001 (first entry)
XX Rat MLP protein sequence SEQ ID NO:47.
XX
XX
XX MLP, M1; melanoma inhibitory activity; cancer; bone disease;
XX joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
XX cardiant; gene therapy; secretory cell function regulator; promoter;
XX inhibitor.
XX
XX Rattus sp.
XX
XX WO200102564-A1.
XX
XX 11-JAN-2001.
XX
XX 29-JUN-2000; 2000MO-JP04278.
XX
XX 30-JUN-1999; 99JP-0186718.
XX
XX (TAKE) TAKEDA CHEM IND LTD.
XX
XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
XX Tanaka H;
XX WPI; 2001-159271/16.
XX
XX N-PSDB; AAF59098.

XX Safe, low-toxicity secretory cell function-regulatory protein and
PT encoded DNA, applicable as drugs, in diagnosis and development of
PT promoters and inhibitors for preventing or treating e.g. bone and joint
PT diseases -

PS Claim 6; Page 106; 11pp; Japanese.

XX The present invention describes novel MLP proteins and their encoding
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
CC activities, and can be used in gene therapy and as secretory cell
CC function regulators. The MLP proteins and DNAs can be used in drugs, in
CC the diagnosis and development of promoters and inhibitors for preventing
CC or treating bone and joint diseases as well as pathologic angiogenesis.
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
CC in the exemplification of the present invention.

XX Sequence 128 AA;

SO Query Match 100.0%; Score 676; DB 22; Length 128;

Best Local Similarity 100.0%; Pred. No. 1.2e-74; Indels 0; Gaps 0;

Matches 128; Conservative 0; Mismatches 0;

QY 1 MARILLLLGLVLCAGHGMFMKLSKKLCADEECYTTISLARAQEDYNAPDCRFINV 60

DB 1 MARILLLLGLVLCAGHGMFMKLSKKLCADEECYTTISLARAQEDYNAPDCRFINV 60

QY 61 KKGGQIYVYSKLVTEGAGAFWAGSVYGDHODEMGI VGFPSNLVREQRYOEAATKEIPT 120

DB 61 KKGGQIYVYSKLVTEGAGAFWAGSVYGDHODEMGI VGFPSNLVREQRYOEAATKEIPT 120

QY 121 TDIDPFCE 128

DB 121 TDIDPFCE 128

RESULT 2

AAB69125

ID AAB69125 standard; Protein; 128 AA.

XX AAB69125;

DT 23-APR-2001 (first entry)

DE Mouse MLP protein sequence SEQ ID NO:12.

XX MLP; MIA; melanoma, inhibitory activity; cancer; bone disease;

KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;

KM cardiant; gene therapy; secretory cell function regulator; promoter;

KW inhibitor.

XX Mus musculus.

OS WO200102564-A1.

PN 11-JAN-2001.

PD 29-JUN-2000; 2000WO-JP04278.

PF 30-JUN-1999; 99JP-0186718.

PR (TAKE) TAKEDA CHEM IND LTD.

XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;

PI Tanaka H;

DR WPI; 2001-159271/16.

DR N-PSDB; AAF59068.

XX Safe, low-toxicity secretory cell function-regulatory protein and

PT encoded DNA, applicable as drugs, in diagnosis and development of

PT promoters and inhibitors for preventing or treating e.g. bone and joint

PT diseases -

XX Claim 4; Page 93-94; 11pp; Japanese.

PS The present invention describes novel MLP proteins and their encoding
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
CC activities, and can be used in gene therapy and as secretory cell
CC function regulators. The MLP proteins and DNAs can be used in drugs, in
CC the diagnosis and development of promoters and inhibitors for preventing
CC or treating bone and joint diseases as well as pathologic angiogenesis.
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
CC in the exemplification of the present invention.

XX Sequence 128 AA;

SO Query Match 96.9%; Score 655; DB 22; Length 128;

Best Local Similarity 96.1%; Pred. No. 4.7e-72; Indels 0; Gaps 0;

Matches 123; Conservative 3; Mismatches 2;

QY 1 MARILLLLGLVLCAGHGMFMKLSKKLCADEECYTTISLARAQEDYNAPDCRFINV 60

DB 1 MARILLLLGLVLCAGHGMFMKLSKKLCADEECYTTISLARAQEDYNAPDCRFINV 60

QY 61 KKGGQIYVYSKLVTEGAGAFWAGSVYGDHODEMGI VGFPSNLVREQRYOEAATKEIPT 120

DB 61 KKGGQIYVYSKLVTEGAGAFWAGSVYGDHODEMGI VGFPSNLVREQRYOEAATKEIPT 120

QY 121 TDIDPFCE 128

DB 121 TDIDPFCE 128

RESULT 3

AAB82671

ID AAB82671 standard; Protein; 128 AA.

XX AAB82671;

DT 02-OCT-2001 (first entry)

DE Human growth regulatory-like polypeptide.

XX Growth regulatory-like polypeptide; human; cartilage; melanoma;

KW neuroectodermal tumour; glioma; cancer; therapy; diagnosis.

KM Homo sapiens.

OS Homo sapiens.

PN WO200155332-A2.

PD 02-AUG-2001.

PF 25-JAN-2001; 2001WO-US02455.

PR 25-JAN-2000; 2000US-0491404.

PR 02-MAY-2000; 2000US-0563786.

XX (HYSE-) HYSEQ INC.

XX Mize NK, Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C;

PI Drmanac RT;

DR WPI; 2001-483233/52.

DR N-PSDB; AAB26343.

XX Isolated human growth regulatory-like polypeptide useful for treating

PT e.g. Alzheimer's disease, cancer, autoimmune disorders,

PT hyperproliferative disorders, coagulation disorders, and nervous system

PT disorders -

XX Claim 10; Page 116-117; 119pp; English.

XX The present sequence is that of a novel human growth regulatory-like
 CC polypeptide (GRUP). The amino acid sequence is predicted from a
 CC novel assembled cDNA (see AAB26343) based on HySeq clone number
 CC 16372272. The protein has a mol.wt. of 14 kDa unglycosylated. GRUP
 CC belongs to the same protein family as growth regulatory proteins,
 CC growth factors, human melanoma derived growth regulatory proteins,
 CC precursor (64% similarity and 45% identity over 111 amino acids)
 CC or melanoma inhibitory activity, cattle cartilage-derived
 CC retinoic acid sensitive protein (CD-RAP, 44% identity and 64%
 CC similarity over 126 amino acids) and other retinoic acid-sensitive
 CC proteins. GRUP polypeptides and polynucleotides of the invention
 CC can be used in the prophylaxis, treatment (including gene therapy)
 CC and diagnosis of disorders and diseases caused by, or involving,
 CC cartilage development and maintenance, inhibition of melanoma cell
 CC growth and tumours, including neuroectodermal tumours such as
 CC gliomas. The polypeptides, which include the GRUP mature protein,
 CC may also have nutritional uses, cytokine and cell proliferation
 CC or differentiation activity, stem cell growth factor activity,
 CC haematopoiesis, regulating activity, tissue growth activity,
 CC immunosuppressive or immunostimulant activity, activating/inhibiting
 CC activity, chemotactic/chemokinetic activity, haemostatic and
 CC thrombolytic activity, use in cancer diagnosis and therapy,
 CC drug screening, receptor/ligand activity, anti-inflammatory,
 CC activity and treatment of leukaemia, nervous system disorders,
 CC arthritis and inflammation.

XX Sequence 128 AA;

XX Query Match: 88.8%; Score 600; DB 22; Length 128;

XX Best Local Similarity 86.7%; Pred. No. 2.6e-65;

XX Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

| | | | |
|----|-----|---|-----|
| QY | 1 | MARILLLLGLVALLCAGHGMFMDKLSKKLCADEECVYITSLAQEDYNAPDCRFINV | 60 |
| DB | 1 | MARILLFLPGLVAVCAVHGIFMDRLASKLCADEECVYITSLAQEDYNAPDCRFINV | 60 |
| QY | 61 | KKGQIYYYSKLVTEHGAGAFWAGSVYGDHDEMGIVGPPSNLVREQRYQEAATKEIPT | 120 |
| DB | 61 | KKGQIYYYSKLVTEHGAGAFWAGSVYGDHDEMGIVGPPSNLVREQRYQEAATKEIPT | 120 |
| QY | 121 | TDIDFCE 128 | |
| DB | 121 | TDIDFCE 128 | |

RESULT 4

ID AAB69123 standard; Protein; 128 AA.

XX AAB69123;

XX 23-APR-2001 (first entry)

XX Human MLP protein sequence SEQ ID NO:6.

XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
 KW joint disease; pathologic angiogenesis; diagnosis; anti-inflammatory;
 KW cardiant; gene therapy; secretory cell function regulator; promoter;
 KW inhibitor.

XX Homo sapiens.

XX WO200102564-A1.

XX 11-JAN-2001.

XX 29-JUN-2000; 2000WO-JP04278.

XX 30-JUN-1999; 99JP-0186718.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K,

XX Tanaka H;

XX WPI; 2001-159271/16.

XX N-PSDB; AAF59065.

XX Safe, low-toxicity secretory cell function-regulatory protein and

XX encoded DNA, applicable as drugs, in diagnosis and development of

XX promoters and inhibitors for preventing or treating e.g. bone and joint

XX diseases -

XX Claim 2; Page 91-92; 111pp; Japanese.

XX The present invention describes novel MLP proteins and their encoding

XX DNAs. The MLP proteins and DNAs have anti-inflammatory and cardiant

XX activities, and can be used in gene therapy and as secretory cell

XX function regulators. The MLP proteins and DNAs can be used in drugs, in

XX the diagnosis and development of promoters and inhibitors for preventing

XX or treating bone and joint diseases as well as pathologic angiogenesis.

XX AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used

XX in the exemplification of the present invention.

XX Sequence 128 AA;

XX Query Match: 88.8%; Score 600; DB 22; Length 128;

XX Best Local Similarity 86.7%; Pred. No. 2.6e-65;

XX Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

| | | | |
|----|-----|---|-----|
| QY | 1 | MARILLLLGLVALLCAGHGMFMDKLSKKLCADEECVYITSLAQEDYNAPDCRFINV | 60 |
| DB | 1 | MARILLFLPGLVAVCAVHGIFMDRLASKLCADEECVYITSLAQEDYNAPDCRFINV | 60 |
| QY | 61 | KKGQIYYYSKLVTEHGAGAFWAGSVYGDHDEMGIVGPPSNLVREQRYQEAATKEIPT | 120 |
| DB | 61 | KKGQIYYYSKLVTEHGAGAFWAGSVYGDHDEMGIVGPPSNLVREQRYQEAATKEIPT | 120 |
| QY | 121 | TDIDFCE 128 | |
| DB | 121 | TDIDFCE 128 | |

RESULT 5

ID AAB95602 standard; Protein; 128 AA.

XX AAB95602;

XX 19-JUL-2002 (first entry)

XX Human angiogenesis related protein PRO9873 SEQ ID NO: 360.

XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
 KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
 KW cardiant; cytosolic; antiangiogenic; hypotensive; vulnary;

XX Homo sapiens.

XX WO200208284-A2.

XX 31-JAN-2002.

XX 09-JUL-2001; 2001WO-US21735.

XX 20-JUL-2000; 2000US-219556P.

XX 25-JUL-2000; 2000US-220624P.

XX 28-JUL-2000; 2000WO-US20710.

XX 02-AUG-2000; 2000US-222695P.

XX 17-AUG-2000; 2000US-0643857.

PR 23-AUG-2000; 2000MO-US23522.
 PR 24-AUG-2000; 2000MO-US23328.
 PR 07-SEP-2000; 2000US-23078P.
 PR 15-SEP-2000; 2000US-00000P.
 PR 18-SEP-2000; 2000US-0664610.
 PR 18-SEP-2000; 2000US-0665350.
 PR 24-OCT-2000; 2000US-242922P.
 PR 08-NOV-2000; 2000US-0709228.
 PR 08-NOV-2000; 2000MO-US30952.
 PR 10-NOV-2000; 2000MO-US30873.
 PR 01-DEC-2000; 2000MO-US32678.
 PR 20-DEC-2000; 2000MO-US34956.
 PR 20-DEC-2000; 2000US-0747259.
 PR 22-JAN-2001; 2001US-0767609.
 PR 28-FEB-2001; 2001US-0796498.
 PR 28-FEB-2001; 2001MO-US06520.
 PR 01-MAR-2001; 2001MO-US06666.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0809689.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854280.
 PR 10-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 25-MAY-2001; 2001MO-US17092.
 PR 30-MAY-2001; 2001US-0870574.
 PR 30-MAY-2001; 2001MO-US17443.
 PR 01-JUN-2001; 2001MO-US17800.
 PR 20-JUN-2001; 2001MO-US19692.
 PR 28-JUN-2001; 2001MO-US00000.
 XX (GERTH) GENENTECH INC.
 PA (BAKER/) BAKER K P.
 PA (FERR/) FERRARA N.
 PA (GERB/) GERBER H.
 PA (GERR/) GERRITSEN M E.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GURN/) GURNEY A L.
 PA (HILL/) HILLAN K J.
 PA (MARS/) MARSTERS S A.
 PA (PANJ/) PANI J.
 PA (PAON/) PAONI N F.
 PA (STEP/) STEPHAN J F.
 PA (WATA/) WATANABE C K.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pani NF, Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W, WPI; 2002-171999/22.
 DR N-PSDB; ABL95740.
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal -
 PT
 XX Claim 11; Fig 360; 567P; English.
 XX The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a PRO protein of the invention.
 CC
 XX Sequence 128 AA;

Query Match 88.8%; Score 600; DB 23; Length 128;
 Best Local Similarity 86.7%; Pred. No. 2,66-65;
 Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;
 QY 1 MARILLILGGIIVACAGHGMFMDKLSKKICABECCYTTISLRAQEDYNAPDGRFINV 60
 DB 1 MARILLILFLPGIVAVCAVHGIFMDRLASKKLCADECYTTISLSAQEDYNAPDGRFINV 60
 QY 61 KKGQIYYTSKVLVTNGAGAPFAGSVGDHDEMGIYGVPPSNLYREQRYQEAATKEIPT 120
 DB 61 KKGQIYYTSKVLKXENGAPEFWAGSVGDGDEMGVGIFPRNLVKEQRYVQEAATKEIPT 120
 QY 121 TDIDPFCE 128
 DB 121 TDIDPFCE 128
 RESULT 6
 ABB84996 standard; Protein; 128 AA.
 ID ABB84996;
 XX ABB84996;
 AC 16-MAY-2002 (first entry)
 DT
 XX
 XX Human PRO9873 protein sequence SEQ ID NO:360.
 DE
 XX
 XX Human; angiogenesis; cardiatic; cytosatic; antiangiogenic; hypotensive;
 KW vulnary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
 KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
 KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
 KW age-related macular degeneration; arterial restenosis; angina;
 KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
 KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
 KW wound healing; chromosome mapping; gene mapping.
 KW
 XX Homo sapiens.
 OS
 XX MO200200690-A2.
 PN
 XX 03-JAN-2002.
 PD
 XX
 XX 20-JUN-2001; 2001MO-US19692.
 PF
 XX
 XX 23-JUN-2000; 2000US-213637P.
 PR 20-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 25-JUL-2000; 2000US-220664P.
 PR 28-JUL-2000; 2000MO-US20710.
 PR 02-AUG-2000; 2000US-222695P.
 PR 17-AUG-2000; 2000US-0643657.
 PR 23-AUG-2000; 2000MO-US23522.
 PR 24-AUG-2000; 2000MO-US23328.
 PR 07-SEP-2000; 2000US-23078P.
 PR 18-SEP-2000; 2000US-0664610.
 PR 18-SEP-2000; 2000US-0665350.
 PR 24-OCT-2000; 2000US-242922P.
 PR 08-NOV-2000; 2000MO-US30952.
 PR 10-NOV-2000; 2000MO-US30873.
 PR 01-DEC-2000; 2000MO-US32678.
 PR 20-DEC-2000; 2000US-0747259.
 PR 20-DEC-2000; 2000MO-US34956.
 PR 22-JAN-2001; 2001US-0767609.
 PR 28-FEB-2001; 2001US-0796498.
 PR 28-FEB-2001; 2001MO-US06520.
 PR 01-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0809689.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854280.
 PR 10-MAY-2001; 2001US-0866028.

PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 30-MAY-2001; 2001US-0870574.
 PR 30-MAY-2001; 2001WO-US17443.
 PR 01-JUN-2001; 2001WO-US17800.
 (GENTH) GENENTECH INC.
 Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF, Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 N-PSDB; ABL88251.
 WPI: 2002-090516/12.
 DR One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal -
 PT infarction), endothelial or angiogenic disorders in a mammal -
 PS Claim 11; Fig 360; 565pp; English.
 XX ABL88072 to ABL88258 encode the PRO proteins given in ABL84817 to
 CC ABL85003. The PRO proteins and polynucleotides have cardiant, cyostatic,
 CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
 CC activities, and can be used in gene therapy. The PRO polynucleotides,
 CC proteins, agonists and antagonists are useful for treating or diagnosing
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal,
 CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular
 CC degeneration, atherosclerosis, hypertension, arterial restenosis,
 CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
 CC lymphangitis, tumor angiogenesis (such as breast carcinoma and liver
 CC carcinoma) and wound healing. The PRO polynucleotides have applications
 CC in molecular biology, including use as hybridisation probes, and in
 CC chromosomes and gene mapping. ABL8259 to ABL8267 represent primers and
 CC probes used in the exemplification of the present invention.
 XX Sequence 128 AA;
 SQ
 Query Match 88.8%; Score 600; DB 23; Length 128;
 Best Local Similarity 86.7%; Pred. No. 2.6e-65;
 Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;
 QY 1 MARILLGLGVALCAGHGMFMDLSKSLCADEECYTTISLARAQEDYNAPPCRFINV 60
 DB 1 MARILLFLPGIVAVCAVHGIFMDRLASKSLCADEECYTTISLARAQEDYNAPPCRFINV 60
 QY 61 KKGQOIYYYSKLVTEGAGAFWAGSVYGDHDEMGIYGFPSNIVREQRYVQEAATKEIPT 120
 DB 61 KKGQOIYYYSKLVTEGAGAFWAGSVYGDHDEMGIYGFPSNIVREQRYVQEAATKEIPT 120
 QY 121 TDIIDFCE 128
 DB 121 TDIIDFCE 128
 RESULT 7
 AAU83627 standard; Protein; 128 AA.
 ID AAU83627;
 AC AAU83627;
 DT 08-MAY-2002 (first entry)
 DE Human PRO protein, Seg ID No 72.
 XX Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
 KM breast cancer; prostate tumour; rectal tumour; liver tumour;
 KM pericyte cell proliferation; chondrocyte cell proliferation;
 KM tumour necrosis factor-alpha.
 XX Homo sapiens.
 OS

PN HQ00208288-A2.
 XX 31-JAN-2002.
 XX 29-JUN-2001; 2001WO-US21066.
 XX 20-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220585P.
 PR 25-JUL-2000; 2000US-220605P.
 PR 25-JUL-2000; 2000US-220607P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 25-JUL-2000; 2000US-220639P.
 PR 25-JUL-2000; 2000US-220664P.
 PR 25-JUL-2000; 2000US-220666P.
 PR 26-JUL-2000; 2000US-220893P.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 23-AUG-2000; 2000WO-US23352.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 15-SEP-2000; 2000US-000000P.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 28-NOV-2000; 2000US-253646P.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000US-0747259.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001WO-US17092.
 (GENTH) GENENTECH INC.
 XX Baker KP, Deanoys L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 N-PSDB; ABK3571.
 WPI: 2002-172001/22.
 DR One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful for treating a PRO related disorder and for diagnosing tumours
 PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
 PT tumour or liver tumour -
 PS Claim 11; Figure 72; 359pp; English.
 XX The invention relates to one hundred and twenty two nucleic acids
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
 CC agonists and antagonists are useful for treating tumours, especially lung
 CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. The PRO polypeptides are useful for stimulating the
 CC proliferation of, or gene expression, in pericyte cells, for stimulating
 CC the proliferation or differentiation of chondrocyte cells, for
 CC stimulating the release of tumour necrosis factor-alpha from human blood,
 CC for stimulating or inhibiting the proliferation of normal human dermal
 CC fibroblast cells. The PRO polypeptide may also be used as molecular
 CC weight markers and for tissue typing. The PRO nucleic acids have
 CC applications in molecular biology, including use as hybridisation probes,
 CC and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
 CC protein sequences of the invention.
 XX Sequence 128 AA;
 SQ
 Query Match 88.8%; Score 600; DB 23; Length 128;
 Best Local Similarity 86.7%; Pred. No. 2.6e-65;
 Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;
 QY 1 MARILLGLGVALCAGHGMFMDLSKSLCADEECYTTISLARAQEDYNAPPCRFINV 60
 DB 1 MARILLFLPGIVAVCAVHGIFMDRLASKSLCADEECYTTISLARAQEDYNAPPCRFINV 60
 QY 61 KKGQOIYYYSKLVTEGAGAFWAGSVYGDHDEMGIYGFPSNIVREQRYVQEAATKEIPT 120
 DB 61 KKGQOIYYYSKLVTEGAGAFWAGSVYGDHDEMGIYGFPSNIVREQRYVQEAATKEIPT 120

QY 121 TDIDFCE 128
DB 121 TDIDFCE 128

RESULT 8

AAU09871 standard; Protein; 128 AA.

AAU09871;

26-FEB-2002 (first entry)

Novel human secreted protein #12.

Secreted protein; cytostatic; immunosuppressive; vulnery; vaccine;
antitumor; neuroprotective; nephrotropic; cardiovascular;
human; cancer; autoimmune disease; wound healing; infection;
haematopoietic disorder; inflammatory disorder; infertility;
neurological disease; psychiatric disease; cardiovascular disease;
respiratory disease; renal; gastrointestinal.

Homo sapiens.

WO200179454-A1.

25-OCT-2001.

11-APR-2001; 2001WO-US11797.

13-APR-2000; 2000US-196603P.

24-APR-2000; 2000US-199417P.

(SMIK) SMITHKLINE BEECHAM CORP.

(SMIK) SMITHKLINE BEECHAM PLC.

Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;

WPI; 2002-061975/08.

N-PSDB; AAS17583.

New secreted proteins or polypeptides, useful for treating e.g. cancer,

autoimmune diseases, wound healing disorder, infections, haematopoietic

disorders, inflammatory disorders, infertility, cancer -

disorders, inflammatory disorders, infertility, cancer -

disorders, inflammatory disorders, infertility, cancer -

disorders, inflammatory disorders, infertility, cancer -

disorders, inflammatory disorders, infertility, cancer -

disorders, inflammatory disorders, infertility, cancer -

disorders, inflammatory disorders, infertility, cancer -

disorders, inflammatory disorders, infertility, cancer -

disorders, inflammatory disorders, infertility, cancer -

disorders, inflammatory disorders, infertility, cancer -

disorders, inflammatory disorders, infertility, cancer -

disorders, inflammatory disorders, infertility, cancer -

DB 1 MARILLFLPGLVAVCAVHGIFMDRLASKKLCADEBCVYTISLASAEDYNAPDCRFINV 60

QY 61 KKGQOIVYVSKLTVENAGAFMAGSVYGDHODEMGIVGFPNSLVREORYOATKEIPT 120

DB 61 KKGQOIVYVSKLTVENAGAFMAGSVYGDHODEMGIVGFPNSLVREORYOATKEIPT 120

QY 121 TDIDFCE 128

DB 121 TDIDFCE 128

RESULT 9

AA669131 standard; Protein; 110 AA.

AA669131;

23-APR-2001 (first entry)

Rat MLP protein sequence SEQ ID NO:49.

M.P. MIA: melanoma inhibitory activity; cancer; bone disease;
joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
cardiac; gene therapy; secretory cell function regulator; promoter;
inhibitor.

Rattus sp.

WO200102564-A1.

11-JAN-2001.

29-JUN-2000; 2000WO-JP04278.

30-JUN-1999; 99JP-0186718.

(TAKE) TAKEEDA CHEM IND LTD.

Itch Y, Nishi K, Ogi K, Okubo S, Mogi S, Noguchi Y, Yoshimura K;

Tanaka H;

WPI; 2001-159271/16.

N-PSDB; AAF59099.

Safe, low-toxicity secretory cell function-regulatory protein and

encoded DNA, applicable as drugs, in diagnosis and development of

promoters and inhibitors for preventing or treating e.g. bone and joint

diseases -

diseases -

diseases -

diseases -

diseases -

diseases -

diseases -

diseases -

diseases -

diseases -

diseases -

Sequence 110 AA;

Query Match 87.4%; Score 591; DB 22; Length 110;

Best Local Similarity 100.0%; Pred. No. 2.7e-64;

Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 19 HGFMDLSSKSLCADEBCVYTISLASAEDYNAPDCRFINVKKGQOIVYVSKLTVENGA 78

QY 79 GAFMAGSVYGDHODEMGIVGFPNSLVREORYOATKEIPTTDIDFCE 128

DB 61 GAFMAGSVYGDHODEMGIVGFPNSLVREORYOATKEIPTTDIDFCE 110

RESULT 10
AAB69127
ID AAB69127 standard; Protein; 110 AA.

XX AAB69127;

DT 23-APR-2001 (first entry)

DE Mouse MLP protein sequence SEQ ID NO:26.

XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
XX joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
XX cardiact; gene therapy; secretory cell function regulator; promoter;
XX inhibitor.

XX Mus musculus.

XX WO200102564-A1.

XX 11-JAN-2001.

XX 29-JUN-2000; 2000WO-JP04278.

XX 30-JUN-1999; 99JP-0186718.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
XX Tanaka H;

XX WPI: 2001-159271/16.

XX N-PSDB; AAF59080.

XX Safe, low-toxicity secretory cell function-regulatory protein and

XX encoded DNA, applicable as drugs, in diagnosis and development of

XX promoters and inhibitors for preventing or treating e.g. bone and joint

XX diseases

XX Claim 3; Page 98-99; 11pp; Japanese.

XX The present invention describes novel MLP proteins and their encoding
XX DNAs. The MLP proteins and DNAs have antiinflammatory and cardiact
XX activities, and can be used in gene therapy and as secretory cell
XX function regulators. The MLP proteins and DNAs can be used in drugs, in
XX the diagnosis and development of promoters and inhibitors for preventing
XX or treating bone and joint diseases as well as pathologic angiogenesis.
XX AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
XX in the exemplification of the present invention.

XX Sequence 110 AA;

XX Query Match 84.9%; Score 574; DB 22; Length 110;

XX Best Local Similarity 96.4%; Pred. No. 3.3e-62;

XX Matches 106; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 19 HGFMMDKLSKKLCADEECYTTISLARAQEDYNAPDRCFINVKKGQOIYYSKLVTENGA 78

DB 1 HGVFMDKLSKKLCADEECYTTISLARAQEDYNAPDRCFINVKKGQOIYYSKLVTENGA 60

QY 79 GAFWAGSVYGDHODEMGIYGFPSNLVREORVYGEATKEIPTTDIDFCE 128

DB 61 GEFWAGSVYGDHODEMGIYGFPSNLVREORVYGEATKEIPTTDIDFCE 110

RESULT 11
AAB69126
ID AAB69126 standard; Protein; 110 AA.

XX AAB69126;

DT 23-APR-2001 (first entry)

XX Human MLP protein sequence SEQ ID NO:24.

XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
XX joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
XX cardiact; gene therapy; secretory cell function regulator; promoter;
XX inhibitor.

XX Homo sapiens.

XX WO200102564-A1.

XX 11-JAN-2001.

XX 29-JUN-2000; 2000WO-JP04278.

XX 30-JUN-1999; 99JP-0186718.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
XX Tanaka H;

XX WPI: 2001-159271/16.

XX N-PSDB; AAF59079.

XX Safe, low-toxicity secretory cell function-regulatory protein and

XX encoded DNA, applicable as drugs, in diagnosis and development of

XX promoters and inhibitors for preventing or treating e.g. bone and joint

XX diseases

XX Claim 1; Page 97-98; 11pp; Japanese.

XX The present invention describes novel MLP proteins and their encoding
XX DNAs. The MLP proteins and DNAs have antiinflammatory and cardiact
XX activities, and can be used in gene therapy and as secretory cell
XX function regulators. The MLP proteins and DNAs can be used in drugs, in
XX the diagnosis and development of promoters and inhibitors for preventing
XX or treating bone and joint diseases as well as pathologic angiogenesis.
XX AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
XX in the exemplification of the present invention.

XX Sequence 110 AA;

XX Query Match 80.0%; Score 541; DB 22; Length 110;

XX Best Local Similarity 89.1%; Pred. No. 3.6e-58;

XX Matches 98; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 19 HGFMMDKLSKKLCADEECYTTISLARAQEDYNAPDRCFINVKKGQOIYYSKLVTENGA 78

DB 1 HGVFMDKLSKKLCADEECYTTISLARAQEDYNAPDRCFINVKKGQOIYYSKLVTENGA 60

QY 79 GAFWAGSVYGDHODEMGIYGFPSNLVREORVYGEATKEIPTTDIDFCE 128

DB 61 GEFWAGSVYGDHODEMGIYGFPSNLVREORVYGEATKEIPTTDIDFCE 110

RESULT 12
AAB82672
ID AAB82672 standard; Protein; 105 AA.

XX AAB82672;

XX 02-OCT-2001 (first entry)

XX Human growth regulatory-like polypeptide (mature protein).

XX Growth regulatory-like polypeptide; human; cartilage; melanoma;

XX neuroectodermal tumour; glioma; cancer; therapy; diagnosis.

XX Homo sapiens.

XX WO200155332-A2.

XX 02-AUG-2001.
 PD 25-JUN-2001; 2001WO-US02455.
 XX
 PR 25-JAN-2000; 2000US-0491404.
 PR 02-MAY-2000; 2000US-0563786.
 XX
 PA (HYSE-) HYSEQ INC.
 PI Mize NK, Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C,
 PI Dymanc RT;
 XX WPI: 2001-483233/52.
 DR N-PSDB; AAH26343.
 XX
 PT Isolated human growth regulatory-like polypeptide useful for treating
 PT e.g. Alzheimer's disease, cancer, autoimmune disorders,
 PT hyperproliferative disorders, coagulation disorders, and nervous system
 PT disorders -
 XX
 PS Claim 10; Page 117; 119pp; English.
 XX
 CC The present sequence is that of a novel human growth regulatory-like
 CC polypeptide (GRLP) mature protein. The sequence is predicted from
 CC a novel assembled cDNA (see AAH26343) based on Hyseq clone number
 CC 16372272. The protein has a mol.wt. of 14 kDa unglycosylated. GRP
 CC belongs to the same protein family as growth regulatory proteins,
 CC growth factors, human melanoma derived growth regulatory protein
 CC precursor (64% similarity and 45% identity over 111 amino acids)
 CC or melanoma inhibitory protein (CD-RAP, 44% identity and 64%
 CC retinoic acid sensitive protein) and other retinoic acid-sensitive
 CC similarly over 126 amino acids) and other nucleotides of the invention
 CC proteins. GRP polypeptides and polynucleotides of the invention
 CC can be used in the prophylaxis, treatment (including gene therapy)
 CC and diagnosis of disorders and diseases caused by, or involving,
 CC cartilage development and maintenance, inhibition of melanoma cell
 CC growth and tumors, including neuroectodermal tumours such as
 CC gliomas. The polypeptides, which include the GRLP mature protein,
 CC may also have nutritional uses, cytokine and cell proliferation
 CC or differentiation activity, stem cell growth factor activity,
 CC hematopoiesis regulating activity, tissue growth activity,
 CC immunosuppressive or immunostimulant activity, activin/inhibin
 CC activity, chemoclastic/chemokinetic activity, haemostatic and
 CC thrombolytic activity, use in cancer diagnosis and therapy,
 CC drug screening, receptor/ligand activity, antiinflammatory,
 CC activity, and treatment of leukaemia, nervous system disorders,
 CC arthritis and inflammation.
 CC
 XX
 SQ Sequence 105 AA;
 XX
 Query Match 76.2%; Score 515; DB 22; Length 105;
 Best Local Similarity 89.5%; Pred. No. 5.3e-55;
 Matches 94; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
 XX
 QY 24 DKLSKKLCADEECYTTISLARAQEDYNAPDCRFINVKKGQIYVSKLVTEENGAGAFWA 83
 DB 1 DRLASKKLCADDECYTTISLAAQEDYNAPDCRFINVKKGQIYVSKLVTEENGAGAFWA 60
 XX
 QY 84 GSVYGDHDEMGIVGFPSNLVREQRYQEAATKE:PTTIDIDPFCE 128
 DB 61 GSVYGDGQDEMVGIVGFPSNLVREQRYQEAATKEVPTTIDIDPFCE 105
 XX
 RESULT 13
 AAAB69129
 ID AAAB69129 standard; Protein; 87 AA.
 AC AAAB69129;
 XX
 DT 23-APR-2001 (first entry)
 XX
 DE Rat MLP protein sequence SEQ ID NO:39.

XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
 KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
 KW cardiant; gene therapy; secretory cell function regulator; promoter;
 KW inhibitor.
 XX
 OS Rattus sp.
 XX
 PN WO200102564-A1.
 XX
 PD 11-JAN-2001.
 XX
 PF 29-JUN-2000; 2000WO-JP04278.
 XX
 PR 30-JUN-1999; 99JP-0186718.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Itch Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K,
 PI Tanaka H;
 XX
 DR WPI: 2001-159271/16.
 XX
 XX Safe, low-toxicity secretory cell function-regulatory protein and
 PT encoded DNA, applicable as drugs, in diagnosis and development of
 PT promoters and inhibitors for preventing or treating e.g. bone and joint
 PT diseases -
 XX
 PS Example 9; Page 103; 111pp; Japanese.
 XX
 CC The present invention describes novel MLP proteins and their encoding
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
 CC activities, and can be used in gene therapy and as secretory cell
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in
 CC the diagnosis and development of promoters and inhibitors for preventing
 CC or treating bone and joint diseases as well as pathologic angiogenesis.
 CC AAF59063 to AAF59099 and AA69122 to AA69132 represent sequences used
 CC in the exemplification of the present invention.
 CC
 XX
 SQ Sequence 87 AA;
 XX
 Query Match 68.3%; Score 462; DB 22; Length 87;
 Best Local Similarity 100.0%; Pred. No. 1.3e-48;
 Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 24 DKLSKKLCADEECYTTISLARAQEDYNAPDCRFINVKKGQIYVSKLVTEENGAGAFWA 83
 DB 1 DKLSKKLCADEECYTTISLARAQEDYNAPDCRFINVKKGQIYVSKLVTEENGAGAFWA 60
 XX
 QY 84 GSVYGDHDEMGIVGFPSNLVREQRY 110
 DB 61 GSVYGDHDEMGIVGFPSNLVREQRY 87
 XX
 RESULT 14
 AAAB69811
 ID AAAB69811 standard; Protein; 131 AA.
 AC AAAB69811;
 XX
 DT 25-MAR-2003 (updated)
 DT 26-OCT-1995 (first entry)
 XX
 DE Melanoma inhibiting protein (human).
 XX
 KW Melanoma; inhibition; cancer; melanoma; glioblastoma; neuroblastoma;
 KW small cell lung cancer; neuroectodermal tumours; immunosuppressant;
 KW phytohaemagglutinin; lymphocyte; interleukin 2; IL-2; detection;
 KW probe; fusion protein.
 XX
 OS Homo sapiens.
 XX
 PN WO9503328-A2.

```

XX 02-FEB-1995.
PD 19-JUL-1994; 94MO-EP02369.
XX 20-JUL-1993; 93DE-4324247.
XX (BOEF) BOEHRINGER MANNHEIM GMBH.
XX Bogdahn U, Buettner R, Kaluza B;
XX WPI: 1995-075191/10.
XX N-PSDB; AAQ84050, AAQ84051.
XX
XX New melanoma inhibiting protein and related nucleic acid -
XX vectors, transformed cells, antibodies etc., useful for treating
XX tumours and as immunosuppressant e.g. by gene therapy
XX
XX Claim 1; Page 54; 85pp; German.
XX
XX This protein has melanoma-inhibiting activity and can be used to
XX treat cancer (melanoma, glioblastoma, neuroblastoma, small cell
XX lung cancer, neuroectodermal tumours) or as an immunosuppressant
XX (it inhibits IL-2 or phytohemagglutinin induced proliferation of
XX peripheral blood lymphocytes). Antibodies raised against the
XX protein can be used to detect cell producing the protein and also
XX for protein purification. Probes derived from DNA encoding the
XX protein (AAQ84050, AAQ84051) can be used to detect sequences encoding
XX the protein or related proteins. The protein may be expressed as
XX a fusion protein (conjugated with dihydrofolate reductase (DHFR)).
XX (updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 131 AA:
SQ
XX
XX Query Match 40.8%; Score 275.5; DB 16; Length 131;
XX Best Local Similarity 44.4%; Pred. No. 1.7e-25;
XX Matches 60; Conservative 27; Mismatches 37; Indels 11; Gaps 6;
XX
XX 1 MARILILIGLVALLCA--GHGMF---MDKLSSKLCADBEVCYTISLABAQEDYNAPDC 55
XX 1 MARSLV-CLGVIIILSAFSGPGVGRGMPKLDRLKCADQECSPISMAVALQDYMAPDC 59
XX
XX 56 RFINVKGGQIYYYSKLVTEAG-APMAGSVYGDHDEMGI-VGYFPPSNLYREQRYOE 113
XX 60 RFLTIHRGQVVYVFSKL---KGRRLPFGSGVGGDYGGDLARLGYFPSSIVREDQTLKP 116
XX
XX 114 ATKEIPTDIDFCE 128
XX 117 GKVDVKTDMDFYCO 131
XX
XX Db
XX
XX RESULT 15
XX AAG65614
XX ID AAG65614 standard; Protein; 131 AA.
XX AC AAG65614;
XX DT 07-JAN-2002 (first entry)
XX
XX Human MIA protein sequence.
XX
XX MIA; melanoma inhibiting activity protein; antiinflammatory; human;
XX antiarthritic; antirheumatic; antithyroid; osteopathic; nephrotropic;
XX immunosuppressive; ophthalmological; dermatological; antidiabetic;
XX neuroprotective; immune tolerance; T-cell tolerance.
XX
XX Homo sapiens.
XX OS
XX PN W0200170253-A1.
XX PD 27-SEP-2001.
XX PF 15-MAR-2001; 2001MO-EP02391.

```

```

XX 23-MAR-2000; 2000EP-0201063.
XX (ALKT) AKZO NOBEL NV.
XX
XX Nelissen RLH, Verheijden GFM;
XX WPI: 2001-611446/70.
XX N-PSDB; AAH47783.
XX
XX Use of melanoma inhibiting activity protein or its derivatives as
XX immune modulatory agents for the treatment of inflammatory diseases,
XX specifically rheumatoid arthritis
XX
XX Example 4; Page 34; 41pp; English.
XX
XX The invention relates to the use of melanoma inhibiting activity (MIA)
XX protein and/or its fragments that have anti-inflammatory effects and
XX induce systemic immune tolerance or specific T-cell tolerance to MIA
XX antigen, for manufacturing a preparation against inflammatory diseases
XX and for induction of systemic immune tolerance or specific T-cell
XX tolerance in patients suffering from or susceptible to inflammatory
XX diseases. A fragment of MIA is useful as a therapeutic substance and is
XX useful for manufacture of pharmaceutical preparations against
XX inflammatory diseases such as an immune-cell mediated cartilage
XX destruction disease, specifically rheumatoid arthritis, autoimmune
XX diseases like Graves' disease, juvenile arthritis, primary
XX glomerulonephritis, polyarthritis, osteoarthritis, Sjogren's syndrome,
XX myasthenia gravis, Addison's disease, primary biliary sclerosis,
XX uveitis, systemic lupus erythematosus, inflammatory bowel disease,
XX multiple sclerosis or diabetes. The MIA polypeptides have specific
XX effect on the autoreactive T-cells thus leaving the other components of
XX the immune system intact as compared to the non-specific suppressive
XX effect of immunosuppressive drugs. The present sequence represents a
XX human MIA protein.
XX
XX Sequence 131 AA:
SQ
XX
XX Query Match 40.8%; Score 275.5; DB 22; Length 131;
XX Best Local Similarity 44.4%; Pred. No. 1.7e-25;
XX Matches 60; Conservative 27; Mismatches 37; Indels 11; Gaps 6;
XX
XX 1 MARILILIGLVALLCA--GHGMF---MDKLSSKLCADBEVCYTISLABAQEDYNAPDC 55
XX 1 MARSLV-CLGVIIILSAFSGPGVGRGMPKLDRLKCADQECSPISMAVALQDYMAPDC 59
XX
XX 56 RFINVKGGQIYYYSKLVTEAG-APMAGSVYGDHDEMGI-VGYFPPSNLYREQRYOE 113
XX 60 RFLTIHRGQVVYVFSKL---KGRRLPFGSGVGGDYGGDLARLGYFPSSIVREDQTLKP 116
XX
XX 114 ATKEIPTDIDFCE 128
XX 117 GKVDVKTDMDFYCO 131
XX
XX Db
XX
XX Search completed: December 29, 2003, 16:09:04
XX Job time : 26.098 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 29, 2003, 16:09:08 ; Search time 17.5686 Seconds
(without alignments)
1449.984 Million cell updates/sec

Title: US-10-019-455A-47

Perfect score: 676
Sequence: 1 MARILLILGLIWLACGHG.....RVYGEATKEIPTDIDFCE 128

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 724715 seqs, 199017464 residues

Total number of hits satisfying chosen parameters: 724715

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications-AA*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 600 | 88.8 | 128 | US-10-216-163-72 | Sequence 72, Appl |
| 2 | 600 | 88.8 | 128 | US-10-218-765-72 | Sequence 72, Appl |
| 3 | 600 | 88.8 | 128 | US-10-219-063-72 | Sequence 72, Appl |
| 4 | 600 | 88.8 | 128 | US-10-219-066-72 | Sequence 72, Appl |
| 5 | 600 | 88.8 | 128 | US-10-219-067-72 | Sequence 72, Appl |
| 6 | 600 | 88.8 | 128 | US-10-219-068-72 | Sequence 72, Appl |
| 7 | 600 | 88.8 | 128 | US-10-219-069-72 | Sequence 72, Appl |
| 8 | 600 | 88.8 | 128 | US-10-219-073-72 | Sequence 72, Appl |
| 9 | 600 | 88.8 | 128 | US-10-219-475-72 | Sequence 72, Appl |
| 10 | 600 | 88.8 | 128 | US-10-219-480-72 | Sequence 72, Appl |
| 11 | 600 | 88.8 | 128 | US-10-219-483-72 | Sequence 72, Appl |
| 12 | 600 | 88.8 | 128 | US-10-219-525-72 | Sequence 72, Appl |
| 13 | 600 | 88.8 | 128 | US-10-219-526-72 | Sequence 72, Appl |
| 14 | 600 | 88.8 | 128 | US-10-219-530-72 | Sequence 72, Appl |
| 15 | 600 | 88.8 | 128 | US-10-219-531-72 | Sequence 72, Appl |

| | | | | | |
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| 16 | 600 | 88.8 | 128 | US-10-219-532-72 | Sequence 72, Appl |
| 17 | 600 | 88.8 | 128 | US-10-219-533-72 | Sequence 72, Appl |
| 18 | 600 | 88.8 | 128 | US-10-223-081-360 | Sequence 360, App |
| 19 | 600 | 88.8 | 128 | US-10-230-437-72 | Sequence 72, Appl |
| 20 | 600 | 88.8 | 128 | US-10-232-228-72 | Sequence 72, Appl |
| 21 | 600 | 88.8 | 128 | US-10-223-082-360 | Sequence 360, App |
| 22 | 600 | 88.8 | 128 | US-10-227-884-72 | Sequence 72, Appl |
| 23 | 600 | 88.8 | 128 | US-10-230-163-72 | Sequence 72, Appl |
| 24 | 600 | 88.8 | 128 | US-10-230-338-72 | Sequence 72, Appl |
| 25 | 600 | 88.8 | 128 | US-10-218-631-72 | Sequence 72, Appl |
| 26 | 600 | 88.8 | 128 | US-10-230-414-72 | Sequence 72, Appl |
| 27 | 600 | 88.8 | 128 | US-10-216-159A-72 | Sequence 72, Appl |
| 28 | 600 | 88.8 | 128 | US-10-218-849-72 | Sequence 72, Appl |
| 29 | 600 | 88.8 | 128 | US-10-227-873-72 | Sequence 72, Appl |
| 30 | 600 | 88.8 | 128 | US-10-227-883-72 | Sequence 72, Appl |
| 31 | 600 | 88.8 | 128 | US-10-219-076-72 | Sequence 72, Appl |
| 32 | 600 | 88.8 | 128 | US-10-230-434-72 | Sequence 72, Appl |
| 33 | 600 | 88.8 | 128 | US-10-219-003-72 | Sequence 72, Appl |
| 34 | 600 | 88.8 | 128 | US-10-219-075-72 | Sequence 72, Appl |
| 35 | 600 | 88.8 | 128 | US-10-219-464-72 | Sequence 72, Appl |
| 36 | 600 | 88.8 | 128 | US-10-219-466-72 | Sequence 72, Appl |
| 37 | 600 | 88.8 | 128 | US-10-219-479-72 | Sequence 72, Appl |
| 38 | 600 | 88.8 | 128 | US-10-219-481-72 | Sequence 72, Appl |
| 39 | 600 | 88.8 | 128 | US-10-230-260-72 | Sequence 72, Appl |
| 40 | 600 | 88.8 | 128 | US-10-232-231-72 | Sequence 72, Appl |
| 41 | 600 | 88.8 | 128 | US-10-232-233-72 | Sequence 72, Appl |
| 42 | 600 | 88.8 | 128 | US-10-216-165-72 | Sequence 72, Appl |
| 43 | 600 | 88.8 | 128 | US-10-218-956-72 | Sequence 72, Appl |
| 44 | 600 | 88.8 | 128 | US-10-219-468-72 | Sequence 72, Appl |
| 45 | 600 | 88.8 | 128 | US-10-219-478-72 | Sequence 72, Appl |

ALIGNMENTS

RESULT 1
US-10-216-163-72
Sequence 72, Application US/10216163
Publication No. US20030149239A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P13
CURRENT APPLICATION NUMBER: US/10/216,163
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656

PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 72
LENGTH: 128
TYPE: PRT
ORGANISM: Homo Sapien
US-10-216-163-72

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Best Local Similarity 86.7%; Pred. No. 4.5e-65;
Matches 11; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

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Sequence 72, Application US/10218765
Publication No. US20030187201A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gettelsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gunney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530P1C19
CURRENT APPLICATION NUMBER: US/10/218,765
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
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PRIOR APPLICATION NUMBER: 60/119549
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/123618
PRIOR FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: 60/125259
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 60/125775
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 60/126773
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: 60/127887
PRIOR FILING DATE: 1999-04-05
PRIOR APPLICATION NUMBER: 60/130232
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/131022
PRIOR FILING DATE: 1999-04-26
PRIOR APPLICATION NUMBER: 60/131270
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131291
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131445
PRIOR FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 60/134287
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/140650
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/140723
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/141037
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 60/144758
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/145698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: 60/146222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: 60/146963
PRIOR FILING DATE: 1999-08-03
PRIOR APPLICATION NUMBER: 60/149320
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/149638
PRIOR FILING DATE: 1999-08-17

PRIOR APPLICATION NUMBER: 60/151733
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/164418
PRIOR FILING DATE: 1999-11-09
PRIOR APPLICATION NUMBER: 60/166361
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: 60/169445
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169495
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169835

Query Match 88.8%; Score 600; DB 12; Length 128;
Best Local Similarity 86.7%; Pred. No. 4.5e-65;
Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MARILLIGLVALDAGHGMFMDKSSKLLCDEECVYTTISLAPQEDYNAPDCRFINY 60
1 MARILLIFLGLVAVCAVHGFMDRLASKKLCADDECVYTTISLAPQEDYNAPDCRFINY 60
Db 61 KKGQIYVYSKLYTENGAGAFMGSVYGDHDEMGIYGFPSLVREORYCEATKEIPT 120
61 KKGQIYVYSKLYENAGAFMGSVYGDGDEMGVGIFPRULVKEQRYQATEKEVPT 120
Qy 121 TDIDFCE 128
Db 121 TDIDFCE 128

RESULT 3
US-10-219-063-72
Sequence 72, Application US/10219063
Publication No. US20030187202A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey J.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530P1C24
CURRENT APPLICATION NUMBER: US/10/219,063
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/076910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 72

LENGTH: 128
TYPE: PRT
ORGANISM: Homo Sapien
US-10-219-063-72

Query Match
Best Local Similarity 86.8%; Score 600; DB 12; Length 128;
Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 1 MARILLILGLVALCAGHGMFMDKLSKKLCADEECYTTISLAPQEDYNAPDCRFIV 60
DB 1 MARILLFLPLGLVAVCAVGI FMDRLASKKLCADCECYTTISLASAQEDYNAPDCRFIV 60
QY 61 KKGQOIYYSKLVTEENGAGAFMAGSVYGDQDEMGVGFPPNLVKEQRYQEAATKEVPT 120
DB 61 KKGQOIYYSKLVTEENGAGAFMAGSVYGDQDEMGVGFPPNLVKEQRYQEAATKEVPT 120
QY 121 TDIDFCE 128
DB 121 TDIDFCE 128

RESULT 4
US-10-219-066-72
Sequence 72, Application US/10219066
Publication No. US20030187203A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C27
CURRENT APPLICATION NUMBER: US/10/219,066
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 72
LENGTH: 128
TYPE: PRT
ORGANISM: Homo Sapien
US-10-219-066-72

Query Match
Best Local Similarity 86.8%; Score 600; DB 12; Length 128;
Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 1 MARILLILGLVALCAGHGMFMDKLSKKLCADEECYTTISLAPQEDYNAPDCRFIV 60
DB 1 MARILLFLPLGLVAVCAVGI FMDRLASKKLCADCECYTTISLASAQEDYNAPDCRFIV 60
QY 61 KKGQOIYYSKLVTEENGAGAFMAGSVYGDQDEMGVGFPPNLVKEQRYQEAATKEVPT 120
DB 61 KKGQOIYYSKLVTEENGAGAFMAGSVYGDQDEMGVGFPPNLVKEQRYQEAATKEVPT 120
QY 121 TDIDFCE 128
DB 121 TDIDFCE 128

RESULT 5
US-10-219-067-72
Sequence 72, Application US/10219067
Publication No. US20030187204A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C31
CURRENT APPLICATION NUMBER: US/10/219,067
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 72
LENGTH: 128
TYPE: PRT
ORGANISM: Homo Sapien
US-10-219-067-72

Query Match
Best Local Similarity 86.7%; Pred. No. 4.5e-65;
Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 1 MARILLILGLVALCAGHGMFMDKLSKKLCADEECYTTISLAPQEDYNAPDCRFIV 60
DB 1 MARILLFLPLGLVAVCAVGI FMDRLASKKLCADCECYTTISLASAQEDYNAPDCRFIV 60
QY 61 KKGQOIYYSKLVTEENGAGAFMAGSVYGDQDEMGVGFPPNLVKEQRYQEAATKEVPT 120

Db 61 KKGQIYVYSKLVKENGAGFWMAGSYVGGDQDENGIVGYFRPLVVEQRVYQATKEVPT 120
QY 121 TDIDFCE 128
Db 121 TDIDFCE 128

RESULT 6

US-10-219-068-72
Sequence 72, Application US/10219068
Publication No. US20030187205A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530PIC31
CURRENT APPLICATION NUMBER: US/10/219,068
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 72
LENGTH: 128
TYPE: PRT
ORGANISM: Homo Sapien
US-10-219-068-72

Query Match 88.8%; Score 600; DB 12; Length 128;
Best Local Similarity 86.7%; Pred. No. 4.5e-65;
Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 1 MARILLILGLVLAACAGHGMFMDKLSKKLCADEECVYTTISLAPQEDYNAPDCRFINV 60
Db 1 MARILLILFLPGLVAVCAVHGI FMDRLASKKLCADDECVYTTISLASAQEDYNAPDCRFINV 60
QY 61 KKGQIYVYSKLVKTENGAGAFWAGSYVGGDQDENGIVGYFRPSNLVREQRVYQATKEIPT 120
Db 61 KKGQIYVYSKLVKENGAGFWMAGSYVGGDQDENGIVGYFRPLVVEQRVYQATKEVPT 120
QY 121 TDIDFCE 128
Db 121 TDIDFCE 128

RESULT 7

US-10-219-069-72
Sequence 72, Application US/10219069
Publication No. US20030187206A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530PIC40
CURRENT APPLICATION NUMBER: US/10/219,069
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 72
LENGTH: 128
TYPE: PRT
ORGANISM: Homo Sapien
US-10-219-069-72

Query Match 88.8%; Score 600; DB 12; Length 128;
Best Local Similarity 86.7%; Pred. No. 4.5e-65;
Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 1 MARILLILGLVLAACAGHGMFMDKLSKKLCADEECVYTTISLAPQEDYNAPDCRFINV 60
Db 1 MARILLILFLPGLVAVCAVHGI FMDRLASKKLCADDECVYTTISLASAQEDYNAPDCRFINV 60
QY 61 KKGQIYVYSKLVKTENGAGAFWAGSYVGGDQDENGIVGYFRPSNLVREQRVYQATKEIPT 120
Db 61 KKGQIYVYSKLVKENGAGFWMAGSYVGGDQDENGIVGYFRPLVVEQRVYQATKEVPT 120
QY 121 TDIDFCE 128
Db 121 TDIDFCE 128

RESULT 8
US-10-219-073-72
Sequence 72, Application US/10219073
Publication No. US20030187207A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.


```

; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC52
; CURRENT APPLICATION NUMBER: US/10/219,073
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-073-72

Query Match      88.8%; Score 600; DB 12; Length 128;
Best Local Similarity 86.7%; Pred. No. 4.5e-65;
Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

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QY 1 MARILLLLGLVAVACAGHGMFMDKLSKKLCADEECVYTISLARAQEDYNAPDCRFINV 60
DB 1 MARILLFLPGIVAVCAVAGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINV 60
QY 61 KKGOQIYVYSKLVTEGAGAFWAGSVYGDHDEMGIVGFPSSNLVREQRYVQEAATKEIPT 120
DB 61 KKGOQIYVYSKLVTEGAGAFWAGSVYGDHDEMGIVGFPSSNLVREQRYVQEAATKEIPT 120
QY 121 TDIDFCE 128
DB 121 TDIDFCE 128

RESULT 9
US-10-219-475-72
; Sequence 72, Application US/10219475
; Publication No. US20030187208A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria

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; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC49
; CURRENT APPLICATION NUMBER: US/10/219,475
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-475-72

Query Match      88.8%; Score 600; DB 12; Length 128;
Best Local Similarity 86.7%; Pred. No. 4.5e-65;
Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

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QY 1 MARILLLLGLVAVACAGHGMFMDKLSKKLCADEECVYTISLARAQEDYNAPDCRFINV 60
DB 1 MARILLFLPGIVAVCAVAGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINV 60
QY 61 KKGOQIYVYSKLVTEGAGAFWAGSVYGDHDEMGIVGFPSSNLVREQRYVQEAATKEIPT 120
DB 61 KKGOQIYVYSKLVTEGAGAFWAGSVYGDHDEMGIVGFPSSNLVREQRYVQEAATKEIPT 120
QY 121 TDIDFCE 128
DB 121 TDIDFCE 128

RESULT 10
US-10-219-480-72
; Sequence 72, Application US/10219480
; Publication No. US20030187209A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC38
; CURRENT APPLICATION NUMBER: US/10/219,480

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; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-219-480-72

Query Match      88.8%; Score 600; DB 12; Length 128;
Best Local Similarity 86.7%; Pred. No. 4.5e-65;
Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 1 MARILLILGGVALCAGHGMFMDLSSKLCADDECVYTTISLAAQEDYNAPDCRFINV 60
   |||||
DB 1 MARILLFLPLGLVAVCAVHIFMDRLASKKLCADDECVYTTISLAAQEDYNAPDCRFINV 60
   |||||

QY 61 KKGQOIYVYSKLVTEKGAGFMAGSVYGDHODEMGIYGFPSNLVREORYOATKEIPT 120
   |||||
DB 61 KKGQOIYVYSKLVTEKGAGFMAGSVYGDHODEMGIYGFPSNLVREORYOATKEIPT 120
   |||||

QY 121 TDIDFCE 128
   |||||
DB 121 TDIDFCE 128
   |||||

RESULT 11
US-10-219-483-72
; Sequence 72, Application US/10219483
; Publication No. US20030187210A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Matanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC43
; CURRENT APPLICATION NUMBER: US/10/219,483
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-219-483-72

Query Match      88.8%; Score 600; DB 12; Length 128;
Best Local Similarity 86.7%; Pred. No. 4.5e-65;
Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 1 MARILLILGGVALCAGHGMFMDLSSKLCADDECVYTTISLAAQEDYNAPDCRFINV 60
   |||||
DB 1 MARILLFLPLGLVAVCAVHIFMDRLASKKLCADDECVYTTISLAAQEDYNAPDCRFINV 60
   |||||

QY 61 KKGQOIYVYSKLVTEKGAGFMAGSVYGDHODEMGIYGFPSNLVREORYOATKEIPT 120
   |||||
DB 61 KKGQOIYVYSKLVTEKGAGFMAGSVYGDHODEMGIYGFPSNLVREORYOATKEIPT 120
   |||||

QY 121 TDIDFCE 128
   |||||
DB 121 TDIDFCE 128
   |||||

RESULT 12
US-10-219-525-72
; Sequence 72, Application US/10219525
; Publication No. US20030187211A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Matanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC29
; CURRENT APPLICATION NUMBER: US/10/219,525
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
```

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; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO: 72
; LENGTH: 128
; TYPE: PRP
; ORGANISM: Homo Sapien
; US-10-219-525-72

Query Match      88.8%; Score 600; DB 12; Length 128;
Best Local Similarity 86.7%; Pred. No. 4.5e-65;
Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 1 MARILLIGLVALCAGHGMFMDKLSKKLCADEECVYTTISLAAQEDYNAPDCRFINV 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MARILLFLPGVAIVCAVHGIFMDRLASKKLCADDECVYTTISLAAQEDYNAPDCRFINV 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 KKGOIIVYSKLVTEKGAGAFWAGSVYGDHDEMGIIVGFPSNLVREQRYVQEAATKEIPT 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 KKGOIIVYSKLVTEKGAGAFWAGSVYGDHDEMGIIVGFPSNLVREQRYVQEAATKEIPT 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 TDIDFCE 128
   |||||:|||||
Db 121 TDIDFCE 128
   |||||:|||||

RESULT 13
US-10-219-526-72
; Sequence 72, Application US/10219526
; Publication No. US20030187212A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC54
; CURRENT APPLICATION NUMBER: US/10/219,526
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069673
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO: 72
; LENGTH: 128
; TYPE: PRP
; ORGANISM: Homo Sapien
; US-10-219-530-72
```

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; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO: 72
; LENGTH: 128
; TYPE: PRP
; ORGANISM: Homo Sapien
; US-10-219-526-72

Query Match      88.8%; Score 600; DB 12; Length 128;
Best Local Similarity 86.7%; Pred. No. 4.5e-65;
Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 1 MARILLIGLVALCAGHGMFMDKLSKKLCADEECVYTTISLAAQEDYNAPDCRFINV 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MARILLFLPGVAIVCAVHGIFMDRLASKKLCADDECVYTTISLAAQEDYNAPDCRFINV 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 KKGOIIVYSKLVTEKGAGAFWAGSVYGDHDEMGIIVGFPSNLVREQRYVQEAATKEIPT 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 KKGOIIVYSKLVTEKGAGAFWAGSVYGDHDEMGIIVGFPSNLVREQRYVQEAATKEIPT 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 TDIDFCE 128
   |||||:|||||
Db 121 TDIDFCE 128
   |||||:|||||

RESULT 14
US-10-219-530-72
; Sequence 72, Application US/10219530
; Publication No. US20030187213A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC54
; CURRENT APPLICATION NUMBER: US/10/219,530
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069673
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO: 72
; LENGTH: 128
; TYPE: PRP
; ORGANISM: Homo Sapien
; US-10-219-530-72
```


Db 1 MARSLV-CLGVILLSAFSGPGVAGGPMPLADRLCADQECSPHISMVAVALDYNAADC 59
QY 56 RFIWKKGGQIYYVSKLVTENGAG-AFWAGSVYGDHODEMGI-VGYFPSNLVREQRYOE 113
Db 60 RFLTHGGQVYVFSKL--KGRGLFWGGSVQGDYDGLAARLGYFPSSIVREDDTLKP 116
QY 114 ATKEIPTDIDFCE 128
Db 117 GKVDKTDKMFYCO 131

RESULT 2
US-08-578-649-5
; Sequence 5, Application US/08578649
; Patent No. 5770366
; GENERAL INFORMATION:
; APPLICANT: Ulrich Bogdan
; APPLICANT: Reinhard Butner
; APPLICANT: Brigitte Kaluza
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESS: Felite & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/578,649
; FILING DATE: 29-July-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 24 247.2
; FILING DATE: 20-July-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Andrew L. Tiajoloief
; REGISTRATION NUMBER: 31,575
; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-578-649-5

Query Match 36.5%; Score 247; DB 1; Length 130;
Best Local Similarity 43.0%; Pred. No. 2e-23;
Matches 55; Conservative 22; Mismatches 41; Indels 10; Gaps 4;

QY 8 LLGGVALACAGHG---MFMDKLSKKLCADEECVYISLARQEDYNAAPDCFFINVKK 62
Db 6 VLLGIVLVSFSGSRARAPKPLADWLCLADECSHISMAVALQDYVAPDCFFLIYR 65
QY 63 GQOIYVSKLVTENGAG-AFWAGSVYGDHODEMGI-VGYFPSNLVREQRYOEATKEIPT 120
Db 66 GQVYVFSKL--KGRGLFWGGSVQGDYDGLAARLGYFPSSIVREDDTLKP 122
QY 121 TDIDFCE 128
Db 123 DQWDFYCO 130
RESULT 3

US-07-646-537B-2
; Sequence 2, Application US/07646537B
; Patent No. 534864
; GENERAL INFORMATION:
; APPLICANT: Barbacid, Mariano
; TITLE OF INVENTION: Vav Proto-Oncogene Protein
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company
; STREET: P.O. Box 4000
; CITY: Princeton
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 08543-4000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/646,537B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaul, Timothy J.
; REGISTRATION NUMBER: 33,111
; REFERENCE/DOCKET NUMBER: DC10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 921-5901
; TELEFAX: (609) 921-4526
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 844 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-646-537B-2

Query Match 13.8%; Score 93.5; DB 1; Length 844;
Best Local Similarity 32.9%; Pred. No. 0.0079;
Matches 23; Conservative 14; Mismatches 20; Indels 13; Gaps 3;

QY 44 ARAQEDYNAADCFINVKKGQIYYVSKLVTENGAGAFWAGSVYGDHODEMGI-VGYFPSN 103
Db 786 AKARYDFCARDSSELSLEGDII---KLUNKKGQGWRRGETYGR-----IGMPSN 834
QY 104 LVRECRYOE 113
Db 835 YVEED--YSE 842

RESULT 4
US-09-346-510B-21
; Sequence 21, Application US/09346510B
; Patent No. 6281014
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Wang, Yinxiang
; TITLE OF INVENTION: SH3-containing Protein, DNA and Uses Thereof
; FILE REFERENCE: D6221CIP
; CURRENT APPLICATION NUMBER: US/09/346,510B
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: 08/871,732
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 21
; LENGTH: 54
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; NAME/KEY: Domain
; OTHER INFORMATION: amino acid sequence of Vav SH3 domain
; US-09-346-510B-21

Query Match 12.5%; Score 84.5; DB 3; Length 54;
Best Local Similarity 32.3%; Pred. No. 0.002;
Matches 20; Conservative 13; Mismatches 18; Indels 11; Gaps 2;

QY 46 AQEYNNPDRFRIVKKGQOQIYVSKVLTENGAGAFMAGSVYGDHDEMIGVYFSPNLV 105
DB 1 ARYDFCARDRSELKSGDII---KILNKKGGQGWRRGEIYGR-----VGMFPANV 49

QY 106 RE 107
DB 50 EE 51

RESULT 5

US-09-356-952-4
Sequence 4, Application US/09356552
Patent No. 611763
GENERAL INFORMATION:
APPLICANT: Boriack-Sjodin, Ann
APPLICANT: Margalit, S. M.
APPLICANT: Bor-Sogil, Dafna
APPLICANT: Cole, Philip
APPLICANT: Kuriyan, John
TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE
FILE REFERENCE: 600-1-228N
CURRENT APPLICATION NUMBER: US/09/356,952
CURRENT FILING DATE: 1999-07-19
EARLIER APPLICATION NUMBER: 60/093,631
EARLIER FILING DATE: 1998-07-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 1589
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-09-356-952-4

Query Match 12.2%; Score 82.5; DB 3; Length 1589;
Best Local Similarity 28.1%; Pred. No. 0.49;
Matches 25; Conservative 18; Mismatches 35; Indels 11; Gaps 4;

QY 26 LSSKKLACDECCYVITISLARAQEDYNAP----DCRFINKKGQOQIYVSKVLTENGAGA 80
DB 45 LSSPSPSELSTIRPIGIVAAVFNPIKDDSSQLSLVQGGFTIILNK---NSSG- 99

QY 81 FMAGSVYGDHDEMIGVYFSPNLVREOR 109
DB 100 WMDGLVTDSDSGKVN-RGMFPQNGRPLR 127

RESULT 6

US-09-346-5108-24
Sequence 24, Application US/093465108
Patent No. 6281014
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Wang, Yinxiang
TITLE OF INVENTION: SH3-Containing Protein, DNA and Uses Thereof
FILE REFERENCE: D6221CIP
CURRENT APPLICATION NUMBER: US/09/346,5108
CURRENT FILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: 08/871,732
PRIOR FILING DATE: 1997-06-09
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 24
LENGTH: 48
TYPE: PRT
ORGANISM: unknown
FEATURE:
NAME/KEY: Domain
LOCATION: 2...49

OTHER INFORMATION: amino acid sequence of Yav SH3 domain at position 2
OTHER INFORMATION: through position 49 of SEQ ID No. 6281014 21
US-09-346-5108-24

Query Match 11.3%; Score 76.5; DB 3; Length 48;
Best Local Similarity 31.6%; Pred. No. 0.018; 16; Indels 11; Gaps 2;
Matches 18; Conservative 12; Mismatches 16; Indels 11; Gaps 2;

QY 49 DYNAPDRFRIVKKGQOQIYVSKVLTENGAGAFMAGSVYGDHDEMIGVYFSPNLV 105
DB 3 DFCARDRSELKSGDII---KILNKKGGQGWRRGEIYGR-----VGMFPANV 48

RESULT 7

US-08-164-839-4
Sequence 4, Application US/08164839
Patent No. 5514573
GENERAL INFORMATION:
APPLICANT: YASUEDA, HISASHI
APPLICANT: NAKANISHI, KAZUO
APPLICANT: MOTOKI, MASAO
APPLICANT: NAGASE, KAZUO
APPLICANT: MATSUI, HIROSHI
TITLE OF INVENTION: GENE ENCODING TRANSGLUTAMINASE DERIVED
TITLE OF INVENTION: FROM FISH
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: OELON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/164,839
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/004,729
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: O'Brien, No. 5514573man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-599-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 412-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 694 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-164-839-4

Query Match 10.9%; Score 74; DB 1; Length 694;
Best Local Similarity 26.2%; Pred. No. 1.8;
Matches 21; Conservative 21; Mismatches 28; Indels 10; Gaps 3;

QY 49 DYNAPDRFRIVKKGQOQIYVSKVLTENGAGAFMAGSVYGDHDEMIGVYFSPNLV 105
DB 392 EVNADPTIYIVQKDGOR---RKITEDHASYGKNISTKSYGNHREDVTLLHYKYPESQ 446
QY 106 REORVYQEAETKEI--PTTDI 123
DB 447 KERIVYKKAAGRVRTEPSNEI 466

RESULT 8
US-08-583-799-4
Sequence 4, Application US/08583799
Patent No. 5607849
GENERAL INFORMATION:
APPLICANT: YASUEDA, HISASHI
APPLICANT: NAKANISHI, KAZUO
APPLICANT: MOTOKI, MASAO
APPLICANT: NAGASE, KAZUO
APPLICANT: MATSUI, HIROSHI
TITLE OF INVENTION: GENE ENCODING TRANSGLUTAMINASE DERIVED
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,799
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/004,729
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5607849man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-599-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)412-3000
TELEFAX: (703)413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 694 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-583-799-4

Query Match 10.9%; Score 74; DB 1; Length 694;
Best Local Similarity 26.2%; Pred. No. 1.8;
Matches 21; Conservative 21; Mismatches 28; Indels 10; Gaps 3;

QY 49 DYNAPDCRFIVKKGQIYVSKLVTEGAGA---FMAGSYGDHDEMGIVGYPNSLV 105
DB 392 EVNADTIYWIYQKDCGR-----RKITEDHASVGNISTKSVYGNHREDVTLHYKYPEGSG 446

QY 106 REORVYQATKEI--PTTDI 123
DB 447 KEREVYKXAGRRVTEPSNEI 466

RESULT 9
US-08-164-839-6
Sequence 6, Application US/08164839
Patent No. 5514573
GENERAL INFORMATION:
APPLICANT: YASUEDA, HISASHI
APPLICANT: NAKANISHI, KAZUO
APPLICANT: MOTOKI, MASAO
APPLICANT: NAGASE, KAZUO
APPLICANT: MATSUI, HIROSHI

APPLICANT: MATSUI, HIROSHI
TITLE OF INVENTION: GENE ENCODING TRANSGLUTAMINASE DERIVED
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/164,839
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/004,729
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5514573man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-599-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)412-3000
TELEFAX: (703)413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 695 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-164-839-6

Query Match 10.9%; Score 74; DB 1; Length 695;
Best Local Similarity 26.2%; Pred. No. 1.8;
Matches 21; Conservative 21; Mismatches 28; Indels 10; Gaps 3;

QY 49 DYNAPDCRFIVKKGQIYVSKLVTEGAGA---FMAGSYGDHDEMGIVGYPNSLV 105
DB 393 EVNADTIYWIYQKDCGR-----RKITEDHASVGNISTKSVYGNHREDVTLHYKYPEGSG 447

QY 106 REORVYQATKEI--PTTDI 123
DB 448 KEREVYKXAGRRVTEPSNEI 467

RESULT 10
US-08-583-799-6
Sequence 6, Application US/08583799
Patent No. 5607849
GENERAL INFORMATION:
APPLICANT: YASUEDA, HISASHI
APPLICANT: NAKANISHI, KAZUO
APPLICANT: MOTOKI, MASAO
APPLICANT: NAGASE, KAZUO
APPLICANT: MATSUI, HIROSHI
TITLE OF INVENTION: GENE ENCODING TRANSGLUTAMINASE DERIVED
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.

ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,799
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/004,729
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5607849man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-599-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)412-3000
TELEFAX: (703)413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 695 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-583-799-6

Query Match 10.9%; Score 74; DB 1; Length 695;
Best Local Similarity 26.2%; Pred. No. 1.8;
Matches 21; Conservative 21; Mismatches 28; Indels 10; Gaps 3;

QY 49 DYNAPDGRFINVKGGQIIVYSKLVTEHGAGA---FWAGSVGDHODEMKIVGIFSNLY 105
DB 393 EVNADITWIVQKXGQR---RKITEDHASVGKNISTKSVGNHREDVTLHYKYEBSQ 447

QY 106 REGRVQOATKEI--PTTDI 123
DB 448 KEREVYKAGRGRTVEPSNEI 467

RESULT 11
US-08-467-603-89
Sequence 89, Application US/08467603
Patent No. 5843672
GENERAL INFORMATION:
APPLICANT: Morgenstern, Jay P.
APPLICANT: Kanieczny, Andrzey
APPLICANT: Bizindaukas, Christine B.
APPLICANT: Brauer, Andrew W.
TITLE OF INVENTION: Allergenic Proteins and
TITLE OF INVENTION: Peptides from Dog
NUMBER OF INVENTION: Dander and Uses Therefor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII-text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,603
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/156,549

FILING DATE: 07/999,712
APPLICATION NUMBER:
FILING DATE: 31-Dec-92
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 1M1-026CP (IPC-048CP)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 182 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: Internal
US-08-467-603-89

Query Match 10.9%; Score 73.5; DB 2; Length 182;
Best Local Similarity 24.7%; Pred. No. 0.29;
Matches 37; Conservative 11; Mismatches 39; Indels 63; Gaps 6;

QY 1 MARILILLGLVALCAGH-----GMFYDKL-----SSK----- 29
DB 1 MRLILLGLGLILVCGHAEANSEKGNLDVCKLNGDMFSLIVASNKRKIEKNGSMRV 60

QY 30 -----KLCADK-ECYTTISLAPADYDNPDC-----RFINVK 62
DB 61 FMQHDIVLNSLGFCLCKENGECKRLYSVA-----YTPKIGEYFLYDGGNTFTILKT 115

QY 63 GQGIIVYSKLVTEHGAGAFWAGSVGDHOD 92
DB 116 DYERYMFLVAVNNGEAFLQMLMELYGRTRD 145

RESULT 12
US-08-466-793-89
Sequence 89, Application US/08466793
Patent No. 5891716
GENERAL INFORMATION:
APPLICANT: Morgenstern, Jay P.
APPLICANT: Kanieczny, Andrzey
APPLICANT: Bizindaukas, Christine B.
APPLICANT: Brauer, Andrew W.
TITLE OF INVENTION: Allergenic Proteins and
TITLE OF INVENTION: Peptides from Dog
NUMBER OF INVENTION: Dander and Uses Therefor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII-text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,793
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/156,549
FILING DATE: 22-NOV-1993
APPLICATION NUMBER: 07/999,712
FILING DATE: 31-Dec-92
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207

QY 1 MetAlaArgIleLeuLeuLeuLeuLeuLeuLeuLeuValAlaLeuCysAlaGlyHisGly 20
 Db 1 ATGGCAAGATATGATTTCTTTGCTGGGGCCCTTGCTGATATGATGCGGCGATGCT 60
 QY 21 MetPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysValTyrThr 40
 Db 61 GATTTATGATTAACCTTCTTCTTAAGAAAGTGTGTGGGAGATGAGAGATGCTATACT 120
 QY 41 IleSerLeuAlaArgAlaGlnGlnAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
 Db 121 ATTTCTGTGGCAAGACAGACAGAAATTAACAATGCCCACTGATGATCATCATGTC 180
 QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGlnAsnGlyAlaGlyAla 80
 Db 181 AAGAAAGGGCAGCAGATCTATGTTTACTCCAGCTGTGAACAGAAACGAGCTGGAGAG 240
 QY 81 PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
 Db 241 TTTTGGCTGGCAGATGTTATGTGACCAACGAGATGAGATGGAAATGTAGCTTATTTTC 300
 QY 101 ProSerAsnLeuValArgGlnGlnArgValTyrGlnGlnAlaThrLysGluIleProThr 120
 Db 301 CCCAGCACTGTGTGAAGAGCAGCGTGTATACAGAGAGCCACCAAGAGATCCCAACC 360
 QY 121 ThrAspIleAspPhePheCysGlu 128
 Db 361 ACGGATATTGACTTCTTCTGTGAA 384
 RESULT 5
 AF243504 929 bp mRNA linear ROD 26-DEC-2000
 LOCUS Mus musculus fibrocyte-derived protein (Fdp) mRNA, complete cds.
 ACCESSION AF243504
 VERSION AF243504.1 GI:11991841
 KEYWORDS
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 929)
 Cohen-salmon, M., Frenz, D., Verpy, E., Voegelings, S. and Petit, C.
 Fdp, a new fibrocyte-derived protein related to MIA/CD-RAP, has an
 in vitro effect on the early differentiation of the inner ear
 mesenchyme
 J. Biol. Chem. 275 (51), 40036-40041 (2000)
 PUBMED 10998416
 MEDLINE 20568254
 JOURNAL 10998416
 REFERENCE 2 (bases 1 to 929)
 AUTHORS Cohen-salmon, M., Frenz, D., Verpy, E., Voegelings, S. and Petit, C.
 TITLE Direct Submission
 JOURNAL Submitted (09-MAR-2000) Biotechnologies, Institut Pasteur, 25 rue
 du Dr. Roux, Paris 75015, France
 FEATURES
 source
 1..929
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="BALB/c"
 /db_xref="taxon:10090"
 /chromosome="2"
 1..929
 /gene="Fdp"
 9..395
 /gene="Fdp"
 /codon_start=1
 /product="fibrocyte-derived protein"
 /protein_id="AA042355.1"
 /db_xref="GI:11991842"
 /translation="MARILILLGLVLCAGVGVMDKSLKSLCADEECVYTLIA
 RAGDYNAPCRFIDYKAGQIYVSKLVTEENGAGFEWASVYGDHDEMGIVGYFSP
 NLVKECVYOEATKEIPTDIDFCE"
 BASE COUNT 260 a 156 c 220 g 293 t

ORIGIN
 Alignment Scores:
 Pred. No.: 4,66e-69 Length: 929
 Score: 655.00 Matches: 123
 Percent Similarity: 98.44% Conservative: 3
 Best Local Similarity: 96.09% Mismatches: 2
 Query Match: 96.89% Indels: 0
 DB: 10 Gaps: 0
 US-10-019-455a-47 (1-128) x AF243504 (1-929)
 QY 1 MetAlaArgIleLeuLeuLeuLeuLeuLeuLeuValAlaLeuCysAlaGlyHisGly 20
 Db 9 ATGGCAAGATATGATTTCTTTGCTGGGGCCCTTGCTGATATGATGCGGCGATGCT 68
 QY 21 MetPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysValTyrThr 40
 Db 69 GATTTATGATTAACCTTCTTCTTAAGAAAGTGTGTGGGAGATGAGAGATGCTATACT 128
 QY 41 IleSerLeuAlaArgAlaGlnGlnAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
 Db 129 ATTTCTGTGGCAAGACAGACAGAAATTAACAATGCCCACTGATGATCATCATGTC 188
 QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGlnAsnGlyAlaGlyAla 80
 Db 189 AAGAAAGGGCAGCAGATCTATGTTTACTCCAGCTGTGAACAGAAACGAGCTGGAGAG 248
 QY 81 PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
 Db 249 TTTTGGCTGGCAGATGTTATGTGACCAACGAGATGAGATGGAAATGTAGCTTATTTTC 308
 QY 101 ProSerAsnLeuValArgGlnGlnArgValTyrGlnGlnAlaThrLysGluIleProThr 120
 Db 309 CCCAGCACTGTGTGAAGAGCAGCGTGTATACAGAGAGCCACCAAGAGATCCCAACC 368
 QY 121 ThrAspIleAspPhePheCysGlu 128
 Db 369 ACGGATATTGACTTCTTCTGTGAA 392
 RESULT 6
 BD010821 947 bp DNA linear PAT 31-JAN-2002
 LOCUS Novel polypeptide and DNA thereof.
 ACCESSION BD010821
 VERSION BD010821.1 GI:18639194
 KEYWORDS JP 2001069994-A/22.
 SOURCE Mus sp.
 ORGANISM Mus sp.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 947)
 Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
 Yoshimura, K. and Tanaka, H.
 Novel polypeptide and DNA thereof
 Patent: JP 2001069994-A 22 21-MAR-2001;
 JOURNAL TAKEDA CHEMICAL INDUSTRIES LTD
 COMMENT OS Mus sp. (mouse)
 EN JP 2001069994-A/22
 PD 21-MAR-2001
 PF 29-JUN-2000 JP 2000195911
 PR
 PI YASUAKI ITO, KAZUMORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI
 SHINICHI MOGI,
 PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
 PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC
 A61P19/08,
 PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC
 G01N33/53//
 PC C12P21/08, C12N15/00, A61K37/02, C12N5/00
 CC
 FH Key Location/Qualifiers
 FT source 1..947

Db 256 TTGTGGGCTGCGAGTGTATGATGACCAACAGATGAGATGGAAATTGATTATTC 317

Qy 101 ProserasleuValArgGluGlnArgValTyrGlnGlnAlaThrGluGluLeuProThr 120

Db 318 CCCACCACTTGTGTGAGCAGCGGTATACACAGAGCCACCAAGAGATCCCAACC 377

Qy 121 ThrAspIleAspPhePheCysGlu 128

Db 378 ACCGATATTGACTTCTTCTGTGAA 401

RESULT 10

BD010802 384 bp DNA linear PAT 31-JAN-2002

LOCUS Novel polypeptide and DNA thereof.

DEFINITION BD010802

ACCESSION BD010802.1 GI:18639175

VERSION JP 2001069994-A/3.

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 384)

AUTHORS Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y., Yoshimura, K. and Tanaka, H.

TITLE Novel polypeptide and DNA thereof

JOURNAL Patent: JP 2001069994-A 3 21-MAR-2001; TAKEDA CHEMICAL INDUSTRIES LTD

COMMENT OS Homo sapiens (human)

PN JP 2001069994-A/3

PD 21-MAR-2001

PF 29-JUN-2000 JP 2000195911

PR

PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI SHINICHI MOGI,

PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA

PC C12N15/09, A61K48/00, A61K45/00, A61K46/00, A61P9/00, A61P19/02, PC A61P19/08,

PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC G01N33/53//

PC C12P21/08, C12N15/00, A61K37/02, C12N5/00

CC

CC Key Location/Qualifiers

FT source 1..384

FT /organism='Homo sapiens (human)'

FT Location/Qualifiers

1..384

/organism='Homo sapiens'

/mol_type='genomic DNA'

/db_xref='taxon:9606'

BASE COUNT 99 a 70 c 106 g 109 t

ORIGIN

Alignment Scores:

Pred. No.: 7.09e-63 Length: 384

Score: 600.00 Matches: 111

Percent Similarity: 93.75% Conservative: 9

Best Local Similarity: 86.72% Mismatches: 8

Query Match: 88.76% Indels: 0

DB: 6 Gaps: 0

US-10-019-455A-47 (1-128) x BD010802 (1-384)

Qy 1 MetaIaArgIleuLeuLeuLeuGlyGlyLeuValAlaLeuCysAlaGlyHisGly 20

Db 1 AAGGCAAGAAATATTGTTACTTTTCTCCCGGAGCTTGTGCTGATGCTGTGATGGA 60

Qy 21 MetPheMetAspIysLeuSerSerIysIysLeuCysAlaAspGluGlnCysValTyrThr 40

Db 61 AATATTATGACCGCTGCTTACTTCCCTCCCGGAGCTTGTGCTGATGCTGTGATGGA 120

Qy 41 IleserLeuAlaArgIleuGlnuAspTyrAsnAlaProAspCysArgPheIleAsnVal 60

Db 121 ATTTCCTGCTAGTGCCTCAAGAGATTAATAGCCCCGAGCTGTAGATTCACTTAACGT 180

Qy 61 LysIleGlyGlnGlnIleuTyrValTyrSerLysLeuValThrGluGlnGlyAla 80

Db 181 AAAAAAGGCGACGAGATCTATGTGTTACTCAAGGTGTAAAGAAAAATGAGCTGGAGAA 240

Qy 81 PheTPrAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100

Db 241 TTGTGGGCTGCGAGTGTATTATGATGATGCGCAGAGACAGATGAGAGCTGCGGATTATTC 300

Qy 101 ProserasleuValArgGluGlnArgValTyrGlnGlnAlaThrGluGluLeuProThr 120

Db 301 CCCAGCAACTTGTGCAAGAAACGCTGTGTACCAAGAGCTACCAAGAGATTCCACC 360

Qy 121 ThrAspIleAspPhePheCysGlu 128

Db 361 ACCGATATTGACTTCTTCTGTGAA 401

RESULT 11

BD093103 384 bp DNA linear PAT 27-AUG-2002

LOCUS Novel polypeptide and ite DNA.

DEFINITION BD093103

ACCESSION BD093103.1 GI:22638691

VERSION WO 0102564-A/3.

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 384)

AUTHORS Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y., Yoshimura, K. and Tanaka, H.

TITLE Novel polypeptide and ite DNA

JOURNAL Patent: WO 0102564-A 3 11-JAN-2001; TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA

COMMENT OS Homo sapiens (human)

PN WO 0102564-A/3

PD 11-JAN-2001

PF 29-JUN-2000 WO 2000JP004278

PR 30-JUN-1999 JP 99P 186718

PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI MOGI,

PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA

PC C12N15/12, C12N5/10, C12P21/02, C07K14/47, C07K16/18, A61K45/00, PC A61K38/17,

PC A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/7088// (C12P21/02, C12R1:19)

CC

CC Key Location/Qualifiers

FT source 1..384

FT /organism='Homo sapiens'

/mol_type='genomic DNA'

/db_xref='taxon:9606'

BASE COUNT 99 a 70 c 106 g 109 t

ORIGIN

Alignment Scores:

Pred. No.: 7.09e-63 Length: 384

Score: 600.00 Matches: 111

Percent Similarity: 93.75% Conservative: 9

Best Local Similarity: 86.72% Mismatches: 8

Query Match: 88.76% Indels: 0

DB: 6 Gaps: 0

US-10-019-455A-47 (1-128) x BD093103 (1-384)

Qy 1 MetaIaArgIleuLeuLeuLeuGlyGlyLeuValAlaLeuCysAlaGlyHisGly 20

Db 1 AAGGCAAGAAATATTGTTACTTTTCTCCCGGAGCTTGTGCTGATGCTGTGATGGA 60

QY 21 MetPheMetAspLysLeuSerSerLysLysLeuCyAlaAspGluGluCysValTyrThr 40
 DB 61 ATATTATTAGACCGCTTACCTTCCAGAAAGCTGTGCGAGATGATGAGTGTCTTAACT 120
 QY 41 lIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
 DB 121 ATTTCCTGGCTAGCTCTCAAGAAATTAATGCCCCGAGCTGTAAGATTCACTTAACGTT 180
 QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAspGlyIleValAla 80
 DB 181 AAAAAAGGCGACGACATCTATGTGACTCAAAAGCTGTAAAGAAATGAGCTGAGAGAA 240
 QY 81 PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValAlaGlyTyrPhe 100
 DB 241 TTTTGGCTGGCGAGCTTTTATGTGATGCGCCAGAGACGATGGAGTCTGTGGATTATTC 300
 QY 101 ProSerAsnLeuValArgGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120
 DB 301 CCAGAGACTTGTCTCAAGAAACGCGTGTGTACCAAGAAAGTACCAAGAAAGTCCACAC 360
 QY 121 ThrAspIleAspPhePheCysGlu 128
 DB 361 ACGGATATTGACTTCTCTGCGAG 384
 RESULT 12
 AX358818 521 bp DNA linear PAT 13-FEB-2002
 LOCUS
 DEFINITION Sequence 71 from Patent WO0193983.
 ACCESSION AX358818
 VERSION AX358818.1 GI:18675310
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS 1 Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,
 Godowski, P.J., Grimaldi, J.C., Gunney, A.L., Smith, V., Stephan, J.P.,
 Watanabe, C.K. and Wood, W.I.
 TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
 the same
 JOURNAL Patent: WO 0193983-A 71 13-DEC-2001;
 Genentech Inc. (US)
 FEATURES
 source Location/Qualifiers
 1..521
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 BASE COUNT 167 a 86 c 131 g 137 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 9.85e-63 Length: 521
 Score: 600.00 Matches: 111
 Percent Similarity: 93.75% Conservative: 9
 Best Local Similarity: 86.72% Mismatches: 8
 Query Match: 88.76% Indels: 0
 DB: 6 Gaps: 0
 US-10-019-455a-47 (1-128) x AX358818 (1-521)
 QY 1 MetAlaArgIleLeuIleLeuLeuGlyGlyLeuValAlaLeuCysAlaGlyHisGly 20
 DB 38 ATGGCAAGAAATATTGTAATTTCTCCCGGCTTGTGCTGATGCTGTGCAATGA 97
 QY 21 MetPheMetAspLysLeuSerSerLysLysLeuCyAlaAspGluGluCysValTyrThr 40
 DB 98 ATATTATTAGACCGCTTACCTTCCAGAAAGCTGTGCGAGATGATGAGTGTCTTAACT 157
 QY 41 lIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
 DB 158 ATTTCTGGCTAGCTCTCAAGAAATTAATGCCCCGAGCTGTAAGATTCACTTAACGTT 217

QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyIleValAla 80
 DB 218 AAAAAAGGCGACGACATCTATGTGACTCAAAAGCTGTAAAGAAATGAGAGCTGAGAA 277
 QY 81 PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValAlaGlyTyrPhe 100
 DB 278 TTTTGGCTGGCGAGCTTTTATGTGATGCGCCAGAGACGATGGAGTGTGGATTATTC 337
 QY 101 ProSerAsnLeuValArgGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120
 DB 338 CCAGAGACTTGTCTCAAGAAACGCGTGTGTACCAAGAAAGTACCAAGAAAGTCCACAC 397
 QY 121 ThrAspIleAspPhePheCysGlu 128
 DB 398 ACGGATATTGACTTCTCTGCGAG 421
 RESULT 13
 AX362311 521 bp DNA linear PAT 15-FEB-2002
 LOCUS
 DEFINITION Sequence 71 from Patent WO208288.
 ACCESSION AX362311
 VERSION AX362311.1 GI:18694613
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS 1 Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,
 Godowski, P.J., Grimaldi, J.C., Gunney, A.L., Smith, V., Stephan, J.P.,
 Watanabe, C.K. and Wood, W.I.
 TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
 the same
 JOURNAL Patent: WO 0208288-A 71 31-JAN-2002;
 Genentech, Inc. (US)
 FEATURES
 source Location/Qualifiers
 1..521
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 BASE COUNT 167 a 86 c 131 g 137 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 9.85e-63 Length: 521
 Score: 600.00 Matches: 111
 Percent Similarity: 93.75% Conservative: 9
 Best Local Similarity: 86.72% Mismatches: 8
 Query Match: 88.76% Indels: 0
 DB: 6 Gaps: 0
 US-10-019-455a-47 (1-128) x AX362311 (1-521)
 QY 1 MetAlaArgIleLeuIleLeuLeuGlyGlyLeuValAlaLeuCysAlaGlyHisGly 20
 DB 38 ATGGCAAGAAATATTGTAATTTCTCCCGGCTTGTGCTGATGCTGTGCAATGA 97
 QY 21 MetPheMetAspLysLeuSerSerLysLysLeuCyAlaAspGluGluCysValTyrThr 40
 DB 98 ATATTATTAGACCGCTTACCTTCCAGAAAGCTGTGCGAGATGATGAGTGTCTTAACT 157
 QY 41 lIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
 DB 158 ATTTCTGGCTAGCTCTCAAGAAATTAATGCCCCGAGCTGTAAGATTCACTTAACGTT 217
 QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyIleValAla 80
 DB 218 AAAAAAGGCGACGACATCTATGTGACTCAAAAGCTGTAAAGAAATGAGAGCTGAGAA 277
 QY 81 PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValAlaGlyTyrPhe 100
 DB 278 TTTTGGCTGGCGAGCTTTTATGTGATGCGCCAGAGACGATGGAGTGTGGATTATTC 337

| | | | | |
|--|--|--|---|------------------------|
| OY | | 101 | ProSeRAsnIeuValAArgGluGlnAryValTYrGInGlnAlaThrLysGluLePProThr | 120 |
| Db | | 338 | CCAGGAACCTGGCTCAAGAAACAAGGTGTATGCCAGAAGCTACCAGAAAGTTCCACC | 357 |
| OY | | 121 | ThiASPIeasPhPePheCysGlu | 128 |
| Db | | 398 | ACCGATATTGCATCTTCTTCGCCAG | 421 |
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| | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euleleostomi; | | | |
| | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | |
| REFERENCE | | | | |
| AUTHORS | Baker,K.P., Ferrara,N., Gerber,H., Gertitsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L., Hillan,K.J., Masters,S.A., Pan,J., Pearl,N.F., Stephan,D.P., Watanabe,C.K., Williams,P.M., Wood,W.I. and Ye,W. | | | |
| TITLE | Compositions and methods for the diagnosis and treatment of disorders involving angiodogenesis: Patent: WO 0208284-A 359 31-JAN-2002; Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone (US) ; Gerber, Hanspeter (US) ; Gertitsen, Mary E. (US) ; Goddard, Andrew (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ; Hillan, Kenneth J. (US) ; Masters, Scot A. (US) ; Pan, James (US) ; Pearl, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ; Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William I. (US) | | | |
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| Best Local Similarity: | 86.72% | Mismatches: | 8 | |
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| Db | 38 | ATGGCAGAAATATGTACTTTCTCCCGGCTGTGGCTGATGCTGTCGACGGA | 97 | |
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| Db | 98 | ATATTATATGACCGCTTACCTTCCAAGAACCTCTGTGACATGATGATGCTGTATACT | 157 | |
| OY | 41 | IleSerIeuAlaArgAlaGlnGluIuAspTyraAnaIaProAspCysArgPheIleAsnVal | 60 | |
| Db | 158 | ATTTCCTCGCTAGTGCTCANAGAAATTAATAATGCCCGACGTAGATTCATTAAAGTT | 217 | |
| OY | 61 | LysLysGlyGlnGlnIleTyralTyserLysLsuValIthrGuangGlyAlaGlyala | 80 | |
| Db | 218 | AAAAAGGGCAGCAGATCATATGTATCTCAAAGCTGTAAAGAAAATGAGCTGGAGAA | 277 | |
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| KEYWORDS | | | |
| SOURCE | | | |
| ORGANISM | Homo sapiens (human) | | |
| REFERENCE | Homo sapiens | | |
| AUTHORS | Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euleleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | |
| TITLE | Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L., Hillan,K.J., Masters,S.A., Pan,J., Pooni,N.P., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I. and Ye,W. | | |
| JOURNAL | Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis | | |
| FEATURES | Patent: WO 0200690-A 359 03-JAN-2002; Genentech, Inc. (US) | | |
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| Alignment Scores: | | | |
| Pred. No.: | 9.85e-63 | Length: | 521 |
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| Percent Similarity: | 93.75% | Conservative: | 9 |
| Best Local Similarity: | 86.72% | Mismatches: | 8 |
| Query Match: | 88.76% | Indels: | 0 |
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| US-10-019-455A-47 (1-128) x AX491252 (1-521) | | | |
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| Qy | 21 | MeCHeMeCAspLySLeuSeRSeLySbLyLeuCyAlaAspG1uG1yCyValTyThr | 40 |
| Db | 98 | ATATTATGACCGCTACGCTCCAGAACCTCTGTGCACATGATGATGTGTACT | 157 |
| Qy | 41 | 1leSeRleuAlaG1aG1aG1uAspTyRAsnAlaProAspCyAspGHe1leAsnVal | 60 |
| Db | 158 | ATTTCCTGGCTAGTGCTCAAGAGATTAAATGCCCCGACGTGATTCATTAAAGTT | 217 |
| Qy | 61 | LyS1yS1yG1aG1n1leTyValTyRSeLySLeuValThrg1uAeG1yAlaG1yAla | 80 |
| Db | 218 | AAAAAAGGAGCAGCACTATGTGTACTCAAAGCTGTAAAGAAATGAGCTCGAGAA | 277 |
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| Db | 278 | TTTGGGCTGGCAAGTGTATATGGATGCGCAGAGCAGATGGAGTCGTGGATTATTC | 337 |
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Tue Dec 30 10:20:49 2003

us-10-019-455a-47.rge

Page 10

Search completed: December 29, 2003, 19:57:22
Job time : 2108.98 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 29, 2003, 16:23:14 ; Search time 1324.28 Seconds
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Searched: 22781352 seqs, 12152238056 residues
Total number of hits satisfying chosen parameters: 45562784

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 21 | 360.5 | 53.3 | 677 | 13 BQ563227 | BQ563227 g101a05.Y |
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VERSION BQ570035.1 GI:21473352
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 398)

AUTHORS Kachar, B.
TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
JOURNAL Unpublished
COMMENT Contact: Kachar, B.
 Structural Cell Biology
 National Institute of Deafness and other Communication Disorders
 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
 Tel: 301-402-1599
 Fax: 301-402-1765
 Email: kacharbenidcd.nih.gov
 Plate: 143 row: b column: 10
 Seq primer: M13Rpl reverse primer (ABI).
 Location/Qualifiers

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 /note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 23721, Stratagene) and Uni-Zap XR GigaPack III Gold Cloning Kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and Phase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predestined with EcoR I and Xho I. The phagemid was packaged with GigaPack III Gold and, upon titration on XL1 Blue MRF⁺ cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's Exassis interference resistance helper phage (catalogue # 211903) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from universal M13 reverse primer (CAGGAAACAGTATGAC) and 25th strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster

City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in Genbank and have known function; 23% have hits in Genbank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified.

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 Pred. No.: 2,41e-80 Length: 398
 Score: 655.00 Matches: 123
 Percent Similarity: 98.44% Conservative: 3
 Best Local Similarity: 96.09% Mismatches: 2
 Query Match: 96.89% Indels: 0
 DB: 13 Gaps: 0

US-10-019-455a-47 (1-128) x BQ570035 (1-398)

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 Db 13 ATGGCAAGATATGATGATTTGCTGGGACCTTGTGCTTATGTCGCCGATGAT 72
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 QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGly 80
 Db 193 AAGAAAGGCGAGCAGATCTATGTTTACTCCAGCTGTAAACGAAACGAGCTGGAGAG 252
 QY 81 PheThrAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
 Db 253 TTTTGAGCTGGCGATTTATGATGTCACCCAGAGATGAGATGGAAATGTAGTTATTC 312
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 VERSION BQ564607.1 GI:21467924
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
 1 (bases 1 to 488)
 Kachar, B.
AUTHORS EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
TITLE Unpublished
JOURNAL Contact: Kachar, B.
 Structural Cell Biology
 National Institute of Deafness and other Communication Disorders
 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
 Tel: 301-402-1599
 Fax: 301-402-1765
 Email: kacharbenidcd.nih.gov
 Plate: 19 row: b column: 02
 Seq primer: M13Rpl reverse primer (ABI).

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Location/Qualifiers
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/note="Organ: Organ of Corti; Vector: pluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR GigaPack III Gold Cloning Kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly, 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with GigaPack III Gold and, upon titration on XL1 Blue XRF⁺ cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's Express II⁺ Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAAACAGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA) and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 143 a 83 c 135 g 127 t
ORIGIN

Alignment Scores:
Pred. No.:
Score:
Percent Similarity:

3.25e-80 Length: 488
655.00 Matches: 123
98.44% Conservative: 3

Best Local Similarity: 96.09% Mismatches: 2
Query Match: 96.89% Indels: 0
DB: 13 Gaps: 0

US-10-019-455a-47 (1-128) x BQ564607 (1-488)

QY 1 MetAlaArgIleLeuIleLeuLeuLeuGlyGlyLeuValAlaLeuGlyAlaGly 20
DB 7 ATGGCAAGATATTGATCTTTTGGCTGGGGCCCTTGCTGTTCTATGTCGCCGGCATGCT 66
QY 21 MetPheMetAspIleLeuSerSerIleValLeuGlyAlaAspGluGluCysValTyrThr 40
DB 67 GATTATTGATGATAAATTCTTCTTAAGAGTGTGTGCGATGAGAGAGTGTCTATACT 126
QY 41 IleSerLeuAlaArgAlaGluIleAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
DB 127 ATTTCTGTGGCAAGACACAGGAGATTCATGCCCCGACTGTAGTTTCATGCTATGTC 186
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerIleValThrGluAsnGlyAlaGlyAla 80
DB 187 AGAAAGGCGACAGATCTATGTTTACTCAAGCTGTACAGAAACGAGCTGGAGAG 246
QY 81 PheTTPAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyTyrIleValGlyTyrPhe 100
DB 247 TTTTGGCTGGCAGATCTTATGTCACCCAGCATGAGATGGAAATGTAGTTATTTC 306
QY 101 ProSerAsnLeuValAlaGlnGlnIleArgValTyrGlnGlnAlaThrIleGlnIleProThr 120
DB 307 CCAGCAACTTGTGTAGAGAGAGCGGTATACAGAGCCAGAGCCAGAGAGATCCACAC 366
QY 121 ThrAspIleAspPhePheCysGlu 128
DB 367 ACGATATTGACTTCTTCTGTGAA 390

RESULT 3
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LOCUS g119h02.y1 Mouse Organ of Corti cDNA pluescript Mus musculus CDNA
DEFINITION
VERSION BQ568498.1 GI:21471815
KEYWORDS EST.
ORGANISM Mus musculus (house mouse)
MUS musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 514)
REFERENCE
AUTHORS Kachar B.
TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
JOURNAL Unpublished
COMMENT
CONTACT: Kachar, B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: kacharb@nidcd.nih.gov
Plate: 109 row: c column: 02
Seq primer: M13Rpl reverse primer (ABI).
FEATURES
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/strain="BALB/c"
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/clone="g119h02"
/sex="male and female"
/dev_stage="Post natal day 5 to 13"
/clone_lib="Mouse Organ of Corti cDNA pluescript"
/note="Organ: Organ of Corti; Vector: pluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72

from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR GigaPack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with GigaPack III Gold and, upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's EXaseist interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concerto6 (TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from Carlsbad, CA) as instructed by the manufacturer. ESTs from Maltham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in Genbank and have known function; 23% have hits in Genbank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 147 a 85 c 143 g 139 t
ORIGIN

Alignment Scores:
Pired. No.: 3,52e-80 Length: 514
Score: 655.00 Matches: 123
Percent Similarity: 98.44% Conservative: 3
Best Local Similarity: 96.09% Mismatches: 2
Query Match: 96.89% Indels: 0
DB: 13 Gaps: 0

US-10-019-455A-47 (1-128) x BQ568498 (1-514)

QY 1 MetAlaArgIleLeuIleLeuLeuGlyGlyLeuValAlaLeuCyAaIlyHisGly 20
DB 5 ATGGGAGAGATATGATTTCTTGTGGGCGCTTGCTCTATGTCGCCGCGATGCT 64
QY 21 MetPheMetAspLysLeuSerSerLysLysLysCysAlaAspGluGluCysValLyrThr 40
DB 65 GTATTATGATTAACCTTCTCTTAAGAACTGCTGCGAGTGGAGAGTGTCTTACT 124

QY 41 ILeSerLeuAlaArgAlaGlnGluAspLysAsnAlaProAspCysArpPheIleAsnVal 60
DB 125 ATTTCTTGCGACAGACAGACAGAAATTAACATGCCAGACTGTACGTTCACTCATGTC 184
QY 61 LysLysGlyGlnGlnIleTyValTySerLysLeuValThrGluGlnGlyAla 80
DB 185 AAGAAAGGAGGAGAGATCTATGTTTACTCCAGCTGTACAGAAAAACGAGCTGAGAG 244
QY 81 PheTrpAlaGlySerValTyTyGlyAspHisGlnAspGluMetGlyIleValGlyTyPhe 100
DB 245 TTTTGCGCTGCGAGTGTATTATGTCACCCAGAGATGAGATGGAAATTGACGTTATTC 304
QY 101 ProSerLeuValAlaArgGluGlnArgValTyTyGlnGluAlaThrLysGluIleProThr 120
DB 305 CCCGACACTTGAGGAGAGCGAGCGATATACAGAGGCGACAGAGGATCCAGACC 364
QY 121 ThrAspIleAspPhePheCysGlu 128
DB 365 ACGGATATTGACTTCTTCTGTGAA 388
RESULT 4
BQ564134 534 bp mRNA linear EST 19-JUN-2002
LOCUS g11d01.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA
DEFINITION
ACCESSION BQ564134
VERSION BQ564134.1 GI:21467451
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Kachar,B.
TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
JOURNAL Unpublished
COMMENT Contact: Kachar,B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: kachar@nidcd.nih.gov
Plate: 11 row: d column: 01
Seq primer: M13Rpl reverse primer (ABI).
FEATURES
Source
Location/Qualifiers
1..534
/organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
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/dev_stage="Post natal day 5 to 13"
/clone_lib="Mouse Organ of Corti cDNA pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5-72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR GigaPack III Gold Cloning kit (catalog # 237612), both

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BASE COUNT 155 a 87 c 148 g 144 t
ORIGIN

Alignment Scores:

Pred. No.: 3 72e-80 Length: 534
Score: 655.00 Matches: 123
Percent Similarity: 98.44% Conservative: 3
Best Local Similarity: 96.09% Mismatches: 2
Query Match: 96.89% Indels: 0
DB: 13 Gaps: 0

US-10-019-455a-47 (1-128) x BQ564134 (1-534)

QY 1 MetAlaArgIleLeuIleLeuLeuLeuGlyGlyLeuValAlaLeuCysAlaGlyIleGly 20
DB 3 ATGGCAGAGATATGATTCTTTGCTTGGGGGCTTGTGCTCTATGTCGCCGAGATGTT 62
QY 21 MetPheMetAspIleuSerSerIleValLeuCysAlaAspGluGluCysValIleThr 40
DB 63 GTATTATGATTAACCTTCTCTTAAGAGTGTGCGGATGAGAGAGTGTCTATACT 122
QY 41 IleserLeuAlaArgIleGluGluAspIleAspAlaProAspCysAspPheIleAsnAl 60
DB 123 ATTTCTTGGCAGACACGAGAAATTCATATCCCACTGTTAGTTCATCGATGTC 182
QY 61 LysLeuGlyGlnGlnIleIleValIleSerIleValIleThrGluAsnGlyAlaGlyAla 80
DB 183 AAAAAGGCGAGAGATCTATGTTTCTCAAGCTGTAAACAGAAACCGACTGGAGAG 242
QY 81 PheTIPAlaGlySerValIleGlyAspHISGlnAspGluMetGlyIleValGlyIlePhe 100
DB 243 TTTGGCTGGCGAGTGTATTATGTTGACCAACGAGATGAGATGGAATTGTAGTATTTC 302

QY 101 ProSerAsnLeuValArgIleGlnIleValIleThrIleGlnIleProThr 120
DB 303 CCCAGCACTTGTGTAAGAGCAGCGTGTATACAGAGGCCACCAAGAGATCCCAAC 362
QY 121 ThrAspIleAspPhePheCysGlu 128
DB 363 ACCGATATGACTTCTCTGTGAA 386
RESULT 5
BQ569741 560 bp mRNA linear EST 19-JUN-2002
LOCUS g135f01.Y1 Mouse Organ of Corti cDNA plucscript Mus musculus cDNA
DEFINITION clone g135f01 5', mRNA sequence.
ACCESSION BQ569741 GI:21473058
VERSION BQ569741.1
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 560)
REFERENCE
AUTHORS Kachar,B.
TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
JOURNAL Unpublished
COMMENT Contact: Kachar,B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: kachar@nidcd.nih.gov
Plate: 135 row: f column: 01
Seq primer: M13RPL reverse primer (ABI).
FEATURES
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
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/db_xref="taxon:10090"
/clone="g135f01"
/sex="male and female"
/dev_stage="Post natal day 5 to 13"
/clone_lib="Mouse Organ of Corti cDNA plucscript"
/note="Organ: Organ of Corti; Vector: plucscript; The Organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5, 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro FastTrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Reverse transcription was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMuV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA)

columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XL1 Blue MRF⁺ cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExaSelect Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAAACGCTATGAC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 160 a 92 c 154 g 153 t 1 others
ORIGIN

Alignment Scores:

Pred. No.: 4e-80 Length: 560
Score: 655.00 Matches: 123
Percent Similarity: 98.44% Conservative: 3
Best Local Similarity: 96.09% Mismatches: 2
Query Match: 96.89% Gaps: 0
DB: 13

US-10-019-455a-47 (1-128) x B0569741 (1-560)

QY 1 MetAlaArgIleLeuLeuLeuGlyGlyLeuValAlaLeuCysAlaGlyHisGly 20
DB 6 ATGGCAAGATATGATCTTTGCTGGGGCCCTTGTGCTTCATGTCGGGCAATGCT 65
QY 21 MetMetLeuAlaPheLeuSerSerLeuValLeuValAlaPheGluGluCysVal 40
DB 66 GTATTATGATTAACCTTCTTAAAGAGTGTGTGGAGTGGAGTGTGTACT 125
QY 41 IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheLeuVal 60
DB 126 ATTCTCTGCAAGACACAGAGATTACATGCCAGAGCTGTAAGTTCATCGATGTC 155
QY 61 LysLysGlnGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGly 80
DB 186 AAGAAAGGCGACGATCTATGTTACTCCAACTGCTAAACAGAAACGAGCTGAGAG 245
QY 81 PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
DB 246 TTTTGGGCTGGCAGTGTATGATGGACACACAGATAGATGAGAAATGATGATTTTC 305
QY 101 ProSerAsnLeuValArgGlnGlnArgValTyrGlnGlnAlaThrLysGlnIleProThr 120
DB 306 CCCAGCAACTGCTGTAAGAGACACGCTATACACAGAGGCGACCAAGAGATGCCAAC 365
QY 121 ThrAspIleAspPhePheCysGlu 128
DB 366 ACGGATATGACTTCTCTGAA 389

RESULT 6
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LOCUS B0564944
DEFINITION g127909.Y1 Mouse Organ of Corti cDNA pb1uescript Mus musculus cDNA
clone g127909 5', mRNA sequence.

ACCESSION B0564944
VERSION B0564944.1 GI:21468261
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 608)
REFERENCE
AUTHORS Kachar, B.
TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
JOURNAL Unpublished
COMMENT Contact: Kachar, B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: kachar@nidcd.nih.gov
Plate: 27 row: 9 column: 09
Seq primer: M13R1 reverse primer (ABI).
FEATURES
source
1..608
/organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="g127909"
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/clone_lib="Mouse Organ of Corti cDNA pb1uescript"
/note="Organ: Organ of Corti; Vector: pb1uescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XL1 Blue MRF⁺ cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExaSelect Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen,


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Db 144 ATTTCTGGCAGAGCAGACAGATACATGCCAGACTGAGCTTCATGATGTC 203
Qy 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 80
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Qy 81 PheTPAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
Db 264 TTTTGGCTGGAGAGCTTATGTCACACAGAGTGAAGATGGGATTTGATTTATTC 323
Qy 101 ProSerAsnLeuValArgGlnGlnArgValTyrGlnGlnAlaThrLysGlnIleProThr 120
Db 324 CCCAGCACTTGTTGTAAGAGCAGCGTGTATACAGAGAGCCACCAAGAGATCCCAAC 383
Qy 121 ThrAspIleAspPhePheCysGlu 128
Db 384 ACGGATATTGACTTCTCTGTGAA 407

RESULT 9
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VERSION B0565637
KEYWORDS B0565637.1 GI:21468954
SOURCE EST
ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
1 (bases 1 to 474)
REFERENCE Kachar.B.
AUTHORS EST analysis of gene expression in the mouse Organ of Corti at the
TITLE onset of hearing
JOURNAL Unpublished
COMMENT Contact: Kachar.B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: kachar@nidcd.nih.gov
Plate: 42 row: G Column: 03
Seq primer: MJ3P1 reverse primer (ABI).
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/mol_type="mRNA"
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/clone_lib="Mouse Organ of Corti cDNA pBluescript"
/note="Organ: Organ of Corti; Vector: pBluescript; The
Organ of Corti (OC) was fine dissected from a total of 386
OC as follows: 102 samples from post-natal (P) day 5; 72
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
14 from P12 and 24 from P13. After killing animals by
cervical dislocation followed by decapitation, the bulla
was removed and opened in Leibowitz medium. The bony
capsule of the cochlea was chipped away, stria vascularis
and spiral ligament were removed and the sensory
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(catalog # K1593-02; Invitrogen, Carlsbad, CA) according
to manufacturer's instructions. Reverse transcription and
library construction were carried out with the Uni-Zap XR
vector kit (catalog # 237211, Stratagene) and Uni-Zap XR
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manufacturer's instructions. Briefly: 1.5 ug mRNA was

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that contains an Xho I site. First strand synthesis was
primed with the linker-primer and transcribed using
Moloney murine leukemia virus reverse transcriptase
(MMLV-RT) and 5-methyl dCTP. The second strand was
synthesized with DNA polymerase and RNase H. Complementary
DNA was blunt ended with Pfu DNA polymerase, ligated with
EcoR I adapters in the presence of ligase and digested
with Xho I. The cDNA was sequentially size fractionated
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, respectively. The cDNA was then directionally ligated to
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recombinants. Stratagene's ExAssist Interference
resistance helper phage (catalogue # 211203) was adopted
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rescued library, individual cDNA clones were selected and
grown in 96-well, 2 ml growth plate. Plasmid DNA was
purified from 200 ul of saturated culture with the
Concert96(TM) plasmid purification kit (Invitrogen,
Carlsbad, CA) as instructed by the manufacturer. ESTs from
the 5' end of the cDNA clones were generated with the
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strength BigDye terminator sequencing chemistry (Applied
Biosystems, Foster City, CA). Sequencing reactions were
performed on MJ Tetrad thermal cyclers (MJ Research,
Watham, MA), and analyzed on 3700 automated capillary
sequencers using POP5 polymer (Applied Biosystems, Foster
City, CA). The frequency distribution of the library is
as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10;
1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of
genes are present in GenBank and have know function; 23%
have hits in GenBank, but do not have assigned function;
12% are uncharacterized ESTs and 20% are unidentified."
BASE COUNT 145 a 78 c 131 g 120 t
ORIGIN
Alignment Scores:
Pred. No.: 1,54e-79 Length: 474
Score: 650.00 Matches: 122
Percent Similarity: 97.66% Conservative: 3
Best Local Similarity: 95.31% Mismatches: 3
Query Match: 96.15% Indels: 0
DB: 13 Gaps: 0
US-10-019-455A-47 (1-128) x B0565637 (1-474)
Qy 1 MetAlaArgIleLeuIleLeuLeuGlyGlyLeuValAlaLeuCysAlaGlyHisGly 20
Db 14 ATGGCAAGATATTGATTTCTTTGGTGGGCGCTTGTTGTTATGTCGGCGCATGCT 73
Qy 21 MetPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGlnGluCysValTyrThr 40
Db 74 GATATTATGATTAACCTTTCTTCTTAATAGTTGTGTGCGGATGAGAGTGTCTATACT 133
Qy 41 IleSerLeuAlaArgAlaGlnGlnAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
Db 134 ATTTCTGGCAGAGCAGACAGAAATTACAAAGCCCGACGTAAGTTCATCAGATGTC 193
Qy 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 80
Db 194 AAGAAAGGACAGACATCTATGTTTCTCAAGCTGTTACAGAAACGAGCTGAGAG 253
Qy 81 PheTPAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
Db 254 TTTTGGCTGGAGAGCTTATGTCACACAGAGTGAAGATGGGATTTGATTTATTC 313
Qy 101 ProSerAsnLeuValArgGlnGlnArgValTyrGlnGlnAlaThrLysGlnIleProThr 120

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Db 314 CCCAGCACTTGTCAGAGCAGCGGTATACAGAGCCAGCAGAGATCCCAACC 373

Qy 121 ThrAspIleAspPheCysGlu 128

Db 374 ACGGATATTGACTTCTCTGTGAA 397

RESULT 10

LOCUS B0563768

DEFINITION g106c09.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA

ACCESSION B0563768

VERSION B0563768.1 GI:21466749

KEYWORDS EST

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 684)

AUTHORS Kachar, B.

TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing

JOURNAL Unpublished

COMMENT Contact: Kachar, B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/429 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: kachar@nidcd.nih.gov
Plate: 06 row: c column: 09
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
1..684
/organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
/db_xref="taxon:10090"
/clone="g106c09"
/sex="male and female"
/dev_stage="Post natal day 5 to 13"
/note="Organ: Organ of Corti. Vector: pBluescript. The organ of Corti (OC) was fine dissected from a total of 366 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR GigaPack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and Phasex H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to

the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with GigaPack III Gold and, upon titration on XL1 Blue MRF⁺ cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExSist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96 (TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCTATGAC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in Genbank and have known function; 23% have hits in Genbank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 194 a 120 c 178 g 192 t

ORIGIN

Alignment Scores:

Pred. No.: 5,01e-79 Length: 684

Score: 648.00 Matches: 122

Percent Similarity: 97.66% Conservative: 3

Best Local Similarity: 95.31% Mismatches: 3

Query Match: 95.86% Indels: 0

DB: 13 Gaps: 0

US-10-019-455a-47 (1-128) x B0563768 (1-684)

Qy 1 MeChAArgIleuLeuIleuLeuLeuGlyIleuValAlaLeuCysAlaGlyHisGly 20

Db 13 ATGGCAGGATATGATTTCTTGGTGGGGGCTTGTTGTTATGTCGGGCATAGT 72

Qy 21 MetPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysValIYrThr 40

Db 73 GTATTTCGATTAACCTTTCTTCAAGATTGTGCGGATGAGAGTGTCTTACT 112

Qy 41 ILeSerLeuAlaArgAlaGluGluAspIYrAsnAlaProAspCysArgPheIleAsnVal 60

Db 133 ATTTCCTGGCAGAGCAGCAGGAATTACAAATGCCCGACAGTGTGATCATCATGTC 192

Qy 61 LysLysGlyGluGluIleIYrValIYrSerLysLeuValThrGluGluAlaGlyAla 80

Db 193 AACGAAGCGCAGCAGATCTATGTTTCTCCAACTGCTTAACAAACGAGCGTGGAGAG 252

Qy 81 PheTrpAlaGlySerValIYrGlyAspHisGluAspGluMetGlyIleValGlyIYrPhe 100

Db 253 TTTTGAGCTGACGATGTTATGATGACACACAGAGAGAGAGTGAATGTAGGTATTTTC 312

Qy 101 ProSerAsnLeuValArgGluGluArgValIYrGluGluAlaThrLysGluIleProThr 120

Db 313 CCCAGCACTTGTCAGAGCAGCGGTATACAGAGCCAGCAGAGATCCCAACC 372

Qy 121 ThrAspIleAspPheCysGlu 128

Db 373 ACGGATATTGACTTCTCTGTGAA 396

RESULT 11

LOCUS B0566932

DEFINITION g173g09.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA

ACCESSION B0566932

VERSION B0566932.1 GI:21470249

KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE 1 (bases 1 to 409)
COMMENT EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
JOURNAL Unpublished
CONTACT: Kachar, B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: kachar@nidcd.nih.gov
Plate: 73 row: 9 column: 09
Seq primer: M13RPI reverse primer (ABI).
Location/Qualifiers
1..409
/organism="Mus musculus"
/mol_type="mRNA"
/strain="BABy/c"
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/clone="g173g09"
/sex="male and female"
/dev_stage="Post natal day 5 to 13"
/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR GigaPack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with GigaPack III Gold and, upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist interference resistance helper phage (catalogue # 21103) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the

universal M13 reverse primer (CAGGAAAGCTATGACC) and 25x strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 102 a 75 c 121 g 111 t
ORIGIN

Alignment Scores:

| Pred. No.: | Score: | Percent Similarity: | Best Local Similarity: | Query Match: | DB: | Length: | Matches: | Conservative: | Mismatches: | Indels: | Gaps: |
|------------|--------|---------------------|------------------------|--------------|-----|---------|----------|---------------|-------------|---------|-------|
| 3,58e-76 | 625.00 | 96.09% | 93.75% | 92.46% | 13 | 409 | 120 | 3 | 4 | 1 | 0 |

US-10-019-455a-47 (1-128) x B0566932 (1-409)

| | | | |
|----|-----|--|-----|
| Qy | 1 | MetAlaArgIleLeuIleLeuLeuLeuGlyLeuValAlaLeuGlyAlaGlyHisGly | 20 |
| Db | 27 | ATGGCAAGATATTGATTTCTTTGCTGGGGCGCTTGCTTATGTGCGGGCATGTG | 86 |
| Qy | 21 | MetPheMetAspIleuSerSerIleValLeuGlyAla-AspGluGluCysValIleTyr | 40 |
| Db | 87 | GATTTTATGATTAACCTTCTTAAAGAGTTGCTTGAGAGAGAGTGTCTATAC | 146 |
| Qy | 40 | IleIleSerLeuAlaArgAlaGluGluAspTyrAsnAlaProAspCysArgPheIleAsn | 60 |
| Db | 147 | TATTTCTTGGCAAGACAGCAAGAAATTAACATGCCCCAGCTGATGCTTATCATG | 206 |
| Qy | 60 | IleValGlyGluGluIleTyrValTyrSerIleLeuValIleGluAsnGlyAlaGly | 80 |
| Db | 207 | CAAGAAAGGCGACGACATCTATGTTTATCTCAAGCTGTTACAGAAACGAGCTGAGA | 266 |
| Qy | 80 | AlaPheTyrAlaGlySerValTyrGlyAspHisGluAspGluIleValGlyTyrPhe | 100 |
| Db | 267 | GTTTGGCTGGCAGAGTGTATGATGATCCACCGAGATGAGATGGAATTTAGCTATTT | 326 |
| Qy | 100 | eProSerAsnLeuValArgGluGluArgValTyrGluGluAlaThrIleGluIleProth | 120 |
| Db | 327 | CCCCAGCACTTGATGTGAGAGAGAGCGTGTATACCGAGAGCCACAGAGATCCCAAC | 386 |
| Qy | 120 | rThrAspIleAspPhePheCys | 127 |
| Db | 387 | CACGGCTATGACTTCTTCTGT | 408 |

RESULT 12

B0565411

490 bp mRNA linear EST 19-JUN-2002

LOCUS

g137b12.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA

DEFINITION

clone g137b12 5', mRNA sequence.

ACCESSION

B0565411

GI:21468728

VERSION

B0565411.1

GI:21468728

KEYWORDS

EST.

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

1 (bases 1 to 490)

AUTHORS

Kachar, B.

EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing

TITLE

Unpublished

JOURNAL

Contact: Kachar, B.

COMMENT

Structural Cell Biology
National Institute of Deafness and other Communication Disorders

50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
 Tel: 301-402-1599
 Fax: 301-402-1765
 Email: kachar@denied.nih.gov
 Plate: 37 row: b column: 12
 Seq primer: M13Rpl reverse primer (ABI)
 Location/Qualifiers

FEATURES

1..490
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 /mol_type="mRNA"
 /strain="BALB/c"
 /db_xref="taxon:10090"
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 /sex="male and female"
 /dev_stage="Post natal day 5 to 13"
 /clone_1b="Mouse Organ of Corti cDNA pbluescript"
 /note="Organ: Organ of Corti; Vector: pbluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (p) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro FastTrack Kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and the Uni-Zap XR Glaspick III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Glaspick III Gold and, upon titration on XL1 Blue MRF⁺ cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's EXassist interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGGAACGCGTATGAC) and 25x strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT

191 a 77 c 109 g 112 t 1 others

ORIGIN

Alignment Scores:
 Pred. No.: 9.2e-72
 Score: 594.00
 Percent Similarity: 95.97%
 Best Local Similarity: 89.52%
 Query Match: 87.87%
 DB: 13
 Gaps: 0

US-10-019-455A-47 (1-128) x B0565411 (1-490)

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 99 TTGATTCCTTTGTTGGGGGCGCTTGGGTTTATGTCGGGCAATGATTTATGAT 158
 25 LysLeuSerSerLysLysLeuCysAlaAspGluGluCysValTyrThrIleSerLeuAla 44
 159 AAATTCCTCTTAAAAAATTGTCGGGATPAGAGATGTGCTACTATTCTCTGCA 218
 45 ArgAlaGluGluAspTyrAsnAlaProAspCysAspPheIleAsnValLysGlyGln 64
 219 AGAGCAGCAGGAAATTAACAAATGCCCAACTGATGTTCAATGATGCAAAAAAGGCGAG 278
 65 GlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyAlaPheTyrPAlaGly 84
 279 CAAATCTATGTTTCTCCAGCTGTACCAAAAAACGAGCTGAAAGTTTGGGCTGGC 338
 339 AGCTGTTATGGGACCAACAGATGAATGGGATTTAGGTTATTTCCCACTTG 398
 105 ValArgGluGlnArgValTyrGlnGluAlaThrLysGluIlePheThrThrAsp 124
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 125 PhePheCysGlu 128
 459 TTCTTCTGGGAA 470

RESULT 13
 LOCUS BY232622
 DEFINITION BY232622 RIKEN full-length enriched, adult inner ear Mus musculus
 cDNA clone F33002620 5', mRNA sequence.
 ACCESSION BY232622
 VERSION BY232622.1 GI:26413732
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 365)
 Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nishida, I., Otsu, N., Saito, R., Suzuki, H., Yamana, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gogobori, T., Baldarelli, R., Hill, D. P., Butt, C., Hume, D. A., Gucekubush, J., Schmitt, L. M., Kanapin, A., Matuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusci, V., Chochia, C., Forrest, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawai, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Malais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Perera, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, D. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, J. U., Reid, J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Sempke, C. A., Setou, M., Shinada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wyszynski, B. S., Zhan, Y., Zhan, Y., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A.,

Carminci, P., Hayatsu, N., Hirozane-Kikihawa, T., Konno, H., Nakamura, M., Sakizume, N., Sato, K., Shiraki, T., Maki, K., Kawai, U., Aizawa, T., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imocani, K., Ishii, Y., Ichigawa, M., Kagawa, T., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shiga, M., A., Yasunishi, A., Yoshino, M., Waterson, R., Lander, E. S., Rogers, U., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation

JOURNAL
MEDLINE
PUBMED
COMMENT

Nature 420, 563-573 (2002)
22354683
12466851

FEATURES

1.365

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609 110 5

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| ORIGIN | | | | |

Alignment Scores:

Pred. No.:

Score:

Percent Similarity
Post-Treatment Comparison

Best Local Similarity Match:

QUELY MARCII:
DB.

DB:

US-10-019-455A-47 (1-128) X BY232622 (1-365)

QY 1 MetAlaArgIleLeuIleLeuLeuGlyGlyLeuValAlaLeuCysAlaGlyHisGly 20
Db 24 ATGGCAAGGATATTGATCTTTGGCTTGGGGCCTTGTTGCTTCATGTGCCGGGCATGGT 83

[illegible]

| | |
|------------|---|
| RESULT 14 | |
| B0567343 | |
| LOCUS | B0567343 |
| DEFINITION | 604 bp mRNA linear EST 19-JUN-2002 |
| ACCESSION | g186dd08.Y1 Mouse Organ of Corti cDNA pBluescript Mus musculus CDNA clone g186dd08 5', mRNA sequence. |
| VERSION | B0567343 |
| KEYWORDS | B0567343.1 GI:21470660 EST. |
| SOURCE | Mus musculus (house mouse) |
| ORGANISM | Mus musculus |

FEATURES

1.604

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manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of 1 ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack II Gold and, upon titration on XL1 Blue MRF⁺ cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's EXassist interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACGCTATGACC) and 25X strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function, 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified.

BASE COUNT 178 a 108 c 152 g 166 t
ORIGIN

Alignment Scores:
Pred. No.: 4.51e-62 Length: 604
Score: 525.00 Matches: 97
Percent Similarity: 99.00% Conservative: 2
Best Local Similarity: 97.00% Mismatches: 1
Query Match: 77.66% Indels: 0
DB: 13 Gaps: 0

US-10-019-455a-47 (1-128) x B0567343 (1-604)

QY 29 LysLysLeuGlyAlaAspGluGlyValThrThrLeuSerLeuAlaArgAlaGlnGlu 48
DB 1 AAGAGAGTTGTGGAGAGTGTGTATACCAATTCCTGGCAAGACAGACAGGAA 60
QY 49 AspTyrAsnAlaProAspCysArgPheLeuAsnValLysLysGlyGlnGlnIleTyrVal 68
DB 61 GATTACATGCCCAAGCTGTAGCTTCATGATGATCAAGAAAGGAGCAGATCATGTT 120
QY 69 TyrSerLysLeuValThrGluAsnGlyAlaGlyAlaPheTyrAlaGlySerValTyrGly 88
DB 121 TACTCCAGCTGTAAACAGAAACGAGCTGAGAGATTGTGGCTGGCAGTTTATGCT 180
QY 89 AsnHisGlnAspGluMetGlyIleValGlyTyrPheProSerAsnLeuValArgGluGln 108
DB 181 GACCAACGAGATAGAGGAAATGTAAGTTATTTCCACGAACTTGGAAGAGGACG 240
QY 109 ArgValTyrGlnGlnAlaThrLysGlnIleProThrThrAspIleAspPhePheCysGlu 128
DB 241 CGGTATACCAAGAGGCCCAAGAGATCCCAACGATTTATTCATCTTTCTGTGA 300
RESULT 15

BE236443
LOCUS BE236443 527 bp mRNA linear EST 25-APR-2001
DEFINITION 14645 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE236443
VERSION BE236443.1 GI:9021161
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 527)
REFERENCE Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casaes,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,
G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-Hackow,C.G.,
Pettea,G., Holt,I., Karamecheva,S., Liang,F., Quackenbush,J. and
Keefe,J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
11282978
PUBMED

TITLE JOURNAL MEDLINE
COMMENT USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smithth@mail.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -mnscore 18
and -mismatch 12 options.
PCR primers
FORWARD: AGGAACGCTATGACCAT
BACKWARD: GTTCCAGTCACGACG
Plate: 54 row: C column: 18
Seq primer: ATTAGGTGACACATATAG.
Location/Qualifiers

FEATURES
source 1..527
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_id="MARC 4BOV"
/note="Vector: pCMV SPORT6, Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from day 20 and day 40
embryos."
Location/Qualifiers

BASE COUNT 173 a 94 c 126 g 134 t
ORIGIN

Alignment Scores:
Pred. No.: 3.83e-58 Length: 527
Score: 496.00 Matches: 96
Percent Similarity: 82.95% Conservative: 11
Best Local Similarity: 74.42% Mismatches: 8
Query Match: 73.37% Indels: 14
DB: 10 Gaps: 2

US-10-019-455a-47 (1-128) x BE236443 (1-527)

QY 1 MetaArgIleLeuIleLeuLeuLeuGlyGlyLeuValAlaLeuCysAlaGlyHisGly 20
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QY 21 MetPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGlyCysValTyrThr 40
DB 95 ATATTATGACACAGACTGTGTTCCAGAGCTGTGTCAAGATGATGATGCTATACT 154
QY 41 ILeSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheLeuVal 60
DB 155 ATTCTCTGGCCAGAGCTCAAGAGATTTACATGCTCGGACGTATATTCATTAAAGTT 214
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyAla 80

```
Db      215 AAAAAAAAAAGGACAGGAGATCTATGTTTACTCAAAAGCTG----- 250
Qy      81 PhETTPAlaGlySerValTyrGlyAspHis---GlnAspGluMetGlyIleValGlyTyr 99
Db      251 -----GTTCTATGCAATCAGCTCTGAGAGATGAATGGAAACCGTGGGTTAT 295
Qy      100 PheProSerAsnLeuValArgGluGlnArgValTyrGlnGluAlaThrIleGluIlePro 119
Db      296 TTTCAGCACTTGTCCAGGACACATGTGTACCAAGAACCCACAGGAGATTCCT 355
Qy      120 ThrThrAspIleAspPhePheCysGlu 128
Db      356 ACCACGATATTGACTTTTCTGCGAG 382
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Search completed: December 29, 2003, 22:00:52
Job time : 1326.28 secs

GenCore version 5.1.6
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OK protein - nucleic search, using frame_plus_p2n model

Run on: December 29, 2003, 16:10:49 ; Search time 154.353 Seconds
(without alignments)
2238.558 Million cell updates/sec

Title: US-10-019-455a-47
Perfect score: 676
Sequence: 1 MARILLILGLVALCAGHC.....RVYGEATKEIPTTDIPFCE 128

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=bl0sum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pro -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO MAP -LARGESUBSTR -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.

and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|-----------|---------------------|
| 1 | 676 | 100.0 | 384 | 22 | AAFS9098 | Rat MLP nucleotide |
| 2 | 655 | 96.9 | 384 | 22 | AAFS9068 | Mouse MLP nucleoti |
| 3 | 655 | 96.9 | 947 | 22 | AAFS9084 | Mouse MLP nucleoti |
| 4 | 600 | 88.8 | 384 | 22 | AAFS9065 | Human MLP nucleoti |
| 5 | 600 | 88.8 | 387 | 24 | AA517583 | DNA encoding novel |
| 6 | 600 | 88.8 | 426 | 22 | AAH26341 | Human growth regul |
| 7 | 600 | 88.8 | 521 | 24 | ABL95740 | Human angiogenesis |
| 8 | 600 | 88.8 | 521 | 24 | ABL88251 | Human PRO9873 cDNA |
| 9 | 600 | 88.8 | 521 | 24 | ABK33571 | cDNA encoding huma |
| 10 | 600 | 88.8 | 891 | 22 | AAH98228 | Human EST-derived |
| 11 | 600 | 88.8 | 891 | 22 | AAH26342 | Human growth regul |
| 12 | 600 | 88.8 | 923 | 22 | AAFS9083 | Human MLP nucleoti |
| 13 | 600 | 88.8 | 1201 | 22 | AAH26343 | Human growth regul |
| 14 | 591 | 87.4 | 330 | 22 | AAFS9099 | Rat MLP nucleotide |
| 15 | 574 | 84.9 | 330 | 22 | AAFS9080 | Mouse MLP nucleoti |
| 16 | 541 | 80.0 | 330 | 22 | AAFS9079 | Human MLP nucleoti |
| 17 | 525 | 77.7 | 307 | 22 | AAFS9093 | Rat MLP nucleotide |
| 18 | 458 | 67.8 | 261 | 22 | AAFS9092 | Rat MLP nucleotide |
| 19 | 275.5 | 40.8 | 459 | 16 | AAQ84050 | Sequence encoding |
| 20 | 275.5 | 40.8 | 459 | 22 | AAI70083 | Melanoma inhibitor |
| 21 | 275.5 | 40.8 | 459 | 22 | AAH47832 | Human antisense ol |
| 22 | 273.5 | 40.5 | 433 | 22 | AAH47833 | Recombinant human |
| 23 | 265.5 | 39.3 | 442 | 24 | ABL63602 | Breast cancer rela |
| 24 | 265.5 | 39.3 | 442 | 24 | ABL64012 | Breast cancer rela |
| 25 | 264.5 | 39.1 | 330 | 16 | AAQ84061 | Sequence encoding |
| 26 | 264.5 | 39.1 | 555 | 23 | ABV59229 | Human prostate exp |
| 27 | 247 | 36.5 | 581 | 16 | AAQ84052 | Sequence encoding |
| 28 | 222.5 | 32.9 | 305 | 16 | AAQ84055 | Amplified fragment |
| 29 | 215 | 31.8 | 1060 | 22 | AAFP92140 | Human PRO19670 cDN |
| 30 | 215 | 31.8 | 1060 | 24 | AB574460 | Human cDNA encodin |
| 31 | 215 | 31.8 | 1060 | 24 | ABL95738 | Human angiogenesis |
| 32 | 215 | 31.8 | 1060 | 24 | ABL88249 | Human PRO19670 cDN |
| 33 | 215 | 31.8 | 1060 | 25 | ACA57963 | Human PRO19670 cDN |
| 34 | 215 | 31.8 | 1060 | 25 | ACA58892 | cDNA encoding huma |
| 35 | 215 | 31.8 | 1060 | 25 | ACA60445 | Novel human secret |
| 36 | 215 | 31.8 | 1060 | 25 | ACA63455 | cDNA encoding huma |
| 37 | 215 | 31.8 | 1060 | 25 | ABX98433 | Human cDNA encodin |
| 38 | 215 | 31.8 | 1060 | 25 | ABX98935 | Novel human secret |
| 39 | 215 | 31.8 | 1060 | 25 | ACA05980 | Human secreted/cita |
| 40 | 215 | 31.8 | 1060 | 25 | ABX98024 | Human PRO polynuci |
| 41 | 215 | 31.8 | 1060 | 25 | ABX78808 | Human PRO polynuci |
| 42 | 215 | 31.8 | 1060 | 25 | ABX75821 | Human cDNA encodin |
| 43 | 215 | 31.8 | 1060 | 25 | ABX77026 | Human PRO polynuci |
| 44 | 215 | 31.8 | 1060 | 25 | ABX16866 | Human cDNA encodin |
| 45 | 215 | 31.8 | 1061 | 22 | AA546205 | Human DNA encoding |

ALIGNMENTS

RESULT 1
AAFS9098
ID AAF59098 standard; DNA; 384 BP.
AC AAF59098;
DT 23-APR-2001 (first entry)
XX
XX Rat MLP nucleotide sequence SEQ ID NO:46.
XX
XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
XX joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
XX cardiant; gene therapy; secretory cell function regulator; promoter;
XX inhibitor; ds.
XX
XX Rattus sp.
XX

EN WO200102564-A1.
 XX 11-JAN-2001.
 PD 29-JUN-2000; 2000WO-JP04278.
 XX 30-JUN-1999; 99JP-0186718.
 PR (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Itch Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
 XX Tanaka H;
 DR WPI; 2001-159271/16.
 DR P-PSDB; AAB69130.
 XX
 PT Safe, low-toxicity secretory cell function-regulatory protein and
 PT encoded DNA, applicable as drugs, in diagnosis and development of
 PT promoters and inhibitors for preventing or treating e.g. bone and joint
 PT diseases -
 XX
 PS Claim 13; Page 105-106; 111pp; Japanese.
 XX
 CC The present invention describes novel MLP proteins and their encoding
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
 CC activities, and can be used in gene therapy and as secretory cell
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in
 CC the diagnosis and development of promoters and inhibitors for preventing
 CC or treating bone and joint diseases as well as pathologic angiogenesis.
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
 CC in the exemplification of the present invention.
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 SQ Sequence 384 BP; 98 A; 72 C; 109 G; 105 T; 0 other;
 Alignment Scores:
 Pred. No.: 1,1e-84 Length: 384
 Score: 676.00 Matches: 128
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0
 US-10-019-455A-47 (1-128) x AAF59099 (1-384)
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 DB 1 ATGGCAAGAAATATGATCTTTGCTTGCGGGGCTTGCTGCTGCTGCGGGCAATGCG 60
 QY 21 MetPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysValTyrThr 40
 DB 61 ATGTTATGATGAATAAATTCTTCTTAAGAAAGTTGTGTGCAAGATGAGAGTGTCTATATCC 120
 QY 41 IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
 DB 121 ATTTCTCTGGCAAGACGACAGAAAGACTACATGCCCCGAGCTGATGATCATCAATGTC 180
 QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyAla 80
 DB 181 AAGAAAGGGGACAGATCTATGTTATTCCAAAGCTGTAACGAAATGAGAGCTGGGCA 240
 QY 81 PheTPAAGLysSerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
 DB 241 TTCTGGGCTGGCAGCTTATGTCGACCAACAGATGAGATGGGAATTTGCGTATATTC 300
 QY 101 ProSerAsnLeuValArgGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120
 DB 301 CCGACCACTGCTGTAGAGAGCAAGAGTGTACCGAGAGCCACCAAGAGATTCACACC 360
 QY 121 ThrAspIleAspPhePheCysGlu 128
 DB 361 ACGGATATGACTTCTTCTGTGAA 384
 RESULT 2

AAF59068
 ID AAF59068 standard; DNA; 384 BP.
 XX
 AC AAF59068;
 XX
 XX 23-APR-2001 (first entry)
 DT
 DT Mouse MLP nucleotide sequence SEQ ID NO:10.
 DE
 XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
 XX joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
 KM cardiant; gene therapy; secretory cell function regulator; promoter;
 KM inhibitor; ds.
 XX
 OS Mus musculus.
 XX
 PN WO200102564-A1.
 XX 11-JAN-2001.
 PD 29-JUN-2000; 2000WO-JP04278.
 XX 30-JUN-1999; 99JP-0186718.
 PR (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Itch Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
 XX Tanaka H;
 DR WPI; 2001-159271/16.
 DR P-PSDB; AAB69125.
 XX
 PT Safe, low-toxicity secretory cell function-regulatory protein and
 PT encoded DNA, applicable as drugs, in diagnosis and development of
 PT promoters and inhibitors for preventing or treating e.g. bone and joint
 PT diseases -
 XX
 PS Claim 11; Page 93; 111pp; Japanese.
 XX
 CC The present invention describes novel MLP proteins and their encoding
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
 CC activities, and can be used in gene therapy and as secretory cell
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in
 CC the diagnosis and development of promoters and inhibitors for preventing
 CC or treating bone and joint diseases as well as pathologic angiogenesis.
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
 CC in the exemplification of the present invention.
 XX
 SQ Sequence 384 BP; 98 A; 68 C; 111 G; 107 T; 0 other;
 Alignment Scores:
 Pred. No.: 9,27e-82 Length: 384
 Score: 655.00 Matches: 123
 Percent Similarity: 98.44% Conservative: 3
 Best Local Similarity: 96.09% Mismatches: 2
 Query Match: 96.89% Indels: 0
 DB: 22 Gaps: 0
 US-10-019-455A-47 (1-128) x AAF59068 (1-384)
 QY 1 MetAlaArgIleLeuIleLeuLeuLeuGlyGlyLeuValAlaLeuCysAlaGlyHisGly 20
 DB 1 ATGGCAAGAAATATGATCTTTGCTTGCGGGGCTTGCTGCTGCTGCGGGCAATGCG 60
 QY 21 MetPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysValTyrThr 40
 DB 61 GATTTATGATGAATAAATTCTTCTTAAGAAAGTTGTGTGCAAGATGAGAGTGTCTATATCT 120
 QY 41 IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
 DB 121 ATTTCTCTGGCAAGACGACAGAAAGACTACATGCCCCGAGCTGATGATCATCAATGTC 180
 QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyAla 80


```

Db      181 AAGAAAGGGCAGCATCTATTACTCCAAAGCTGTAACAGAAACGAGCTGGAGAG 240
Qy      81 PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
Db      241 TTTGGGCTGGCAGATGTTTATGTGACCAAGATAGATGGAATTTGATGTTATTC 300
Qy      101 ProSerAsnLeuValArgGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120
Db      301 CCCAGCAACTGTGTGAAGAGCAGCGTGTATACCAAGAGGCCACCAAGAGATCCCAACC 360
Qy      121 ThrAspIleAspPhePheCysGlu 128
Db      361 ACGGATATTGACTTCTCTGTGAA 384

RESULT 3
AAFS9084
ID      AAFS9084 standard; DNA; 947 BP.
XX
AC      AAFS9084;
XX
DT      23-APR-2001 (first entry)
XX
DB      Mouse MLP nucleotide sequence SEQ ID NO:30.
XX
KW      MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
KW      joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
KW      cardiant; gene therapy; secretory cell function regulator; promoter;
KW      inhibitor; ds.
XX
XX      Mus musculus.
XX      OS
XX      MO200102564-A1.
XX      PN
XX      11-JAN-2001.
XX      PD
XX      29-JUN-2000; 2000MO-JP04278.
XX      PF
XX      30-JUN-1999; 99JP-0186718.
XX      PR
XX      (TAKE ) TAKEDA CHEM IND LTD.
XX      PA
XX      Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
XX      Tanaka H;
XX      PI
XX      WPI; 2001-159271/16.
XX      DR
XX      Safe, low-toxicity secretory cell function-regulatory protein and
XX      PT encoded DNA, applicable as drugs, in diagnosis and development of
XX      PT promoters and inhibitors for preventing or treating e.g. bone and joint
XX      PT diseases -
XX
XX      Example 2; Page 100-101; 11pp; Japanese.
XX
XX      The present invention describes novel MLP proteins and their encoding
XX      CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
XX      CC activities, and can be used in gene therapy and as secretory cell
XX      CC function regulators. The MLP proteins and DNAs can be used in drugs, in
XX      CC the diagnosis and development of promoters and inhibitors for preventing
XX      CC or treating bone and joint diseases as well as pathologic angiogenesis.
XX      CC AAFS9063 to AAFS9099 and AAB69122 to AAB69132 represent sequences used
XX      CC in the exemplification of the present invention.
XX
XX      SQ Sequence 947 BP; 279 A; 158 C; 221 G; 289 T; 0 other;
XX
Alignment Scores:
Pred. No.: 3,378-81 Length: 947
Score: 655.00 Matches: 123
Percent Similarity: 98.44% Conservative: 3
Best Local Similarity: 96.09% Mismatches: 2
Query Match: 96.89% Indels: 0
DB: 22 Gaps: 0

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US-10-019-455a-47 (1-128) x AAFS9084 (1-947)
Qy      1 MetAlaArgIleLeuIleLeuLeuLeuGlyGlyLeuValAlaLeuCysAlaGlyHisGly 20
Db      11 ATGGCAAGATATATGATTTCTTTGGCTGGGGCCCTTGTTGTTCTATGTCGGGCAATGGT 70
Qy      21 MetPheMetAspIleLeuSerSerIleValLeuCysAlaAspGluGluCysValTyrThr 40
Db      71 GATTTATGATTAATCTTCTTAAGAAAGTTGTGTGCGGATGAGAGAGTGTCTACTACT 130
Qy      41 IleSerLeuAlaArgAlaGlnGlnIleTyrValTyrSerIleValThrGlyLysGlyAlaGly 60
Db      131 ATTTCTCTGACAGACAGACAGAAAGTTACAAATGCCCTGACTGTAGTTCAATCGATGTC 190
Qy      61 LysLysGlyGlnGlnIleTyrValTyrSerIleValThrGlyLysGlyAlaGly 80
Db      191 AAGAAAGGGCAGCATCTATTACTCCAAAGCTGTAACAGAAACGAGCTGGAGAG 250
Qy      81 PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
Db      251 TTTGGGCTGGCAGATGTTTATGTGACCAAGATAGATGGAATTTGATGTTATTC 310
Qy      101 ProSerAsnLeuValArgGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120
Db      311 CCCAGCAACTGTGTGAAGAGCAGCGTGTATACCAAGAGGCCACCAAGAGATCCCAACC 370
Qy      121 ThrAspIleAspPhePheCysGlu 128
Db      371 ACGGATATTGACTTCTCTGTGAA 394

RESULT 4
AAFS9065
ID      AAFS9065 standard; DNA; 384 BP.
XX
AC      AAFS9065;
XX
DT      23-APR-2001 (first entry)
XX
DB      Human MLP nucleotide sequence SEQ ID NO:4.
XX
XX      Homo sapiens.
XX      OS
XX      MO200102564-A1.
XX      PN
XX      11-JAN-2001.
XX      PD
XX      29-JUN-2000; 2000MO-JP04278.
XX      PF
XX      30-JUN-1999; 99JP-0186718.
XX      PR
XX      (TAKE ) TAKEDA CHEM IND LTD.
XX      PA
XX      Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
XX      Tanaka H;
XX      PI
XX      WPI; 2001-159271/16.
XX      DR
XX      P-PSDB; AAB69123.
XX      DR
XX      Safe, low-toxicity secretory cell function-regulatory protein and
XX      PT encoded DNA, applicable as drugs, in diagnosis and development of
XX      PT promoters and inhibitors for preventing or treating e.g. bone and joint
XX      PT diseases -
XX
XX      Example 1; Page 91; 11pp; Japanese.
XX
XX      The present invention describes novel MLP proteins and their encoding
XX      CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
XX      CC activities, and can be used in gene therapy and as secretory cell

```

CC function regulators. The WIP proteins and DNAs can be used in drugs, in
 CC the diagnosis and development of promoters and inhibitors for preventing
 CC or treating bone and joint diseases as well as pathologic angiogenesis.
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
 CC in the exemplification of the present invention.

XX Sequence 384 BP, 99 A; 70 C; 106 G; 109 T; 0 other;

Alignment Scores:

| Pred. No.: | 4,298-74 | Length: | 384 |
|------------------------|----------|---------------|-----|
| Score: | 600.00 | Matches: | 111 |
| Percent Similarity: | 93.75% | Conservative: | 9 |
| Best Local Similarity: | 86.72% | Mismatches: | 8 |
| Query Match: | 88.76% | Indels: | 0 |
| DB: | 22 | Gaps: | 0 |

US-10-019-455A-47 (1-128) x AAF59065 (1-384)

```

QY 1 MetAlaArgIleLeuIleLeuLeuGlyGlyLeuValAlaLeuCysAlaGlyHisGly 20
DB 1 ATGGCAAGATATTTGTTACTTTCTCCCGGCTTGTGCGTATGCTGCGATGGA 60
QY 21 MetPheMetAspLysLeuSerSerLysLeuCysAlaAspGluGluCysValTyrThr 40
DB 61 ATATTATGGACCGCTAGCTTCCAGAGCTCTGTGAGATGATGATGTTCTATACT 120
QY 41 IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
DB 121 ATTCTCTGCTAGTACGCTCAAGATTTAATGCCCGGACTGAGATTATTAACGTT 180
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyAla 80
DB 181 AAAAAAGGCGACAGATCTATGTCTACTCAAGCTGTGTAAGAAAAATGAGCTGAGAA 240
QY 81 PheTTPAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
DB 241 TTTTGGGCTGGCAGGTTTATGTATGTCGCGAGCGAGATGGGATGTGTGTTATTTTC 300
QY 101 ProSerAsnLeuValArgGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120
DB 301 CCCAGGAACCTTGCTCAAGAACAGCGTGTGTACCGAAGACTTCCAGAGAACTTCCACC 360
QY 121 ThrAspIleAspPhePheCysGlu 128
DB 361 ACGGATTTGACTTCTTCTGCGAG 384

```

RESULT 5

AA517583
 ID AAS17583 standard; cDNA; 387 BP.

AC AAS17583;

DE 26-FEB-2002 (first entry)

XX DNA encoding novel secreted protein #12.

XX Secreted protein; cytosolic; immunosuppressive; vulnary; vaccine;
 KW antiinflammatory; neuroprotective; nephrotropic; cardiovascular;
 KW human; cancer; autoimmune disease; wound healing disorder; infection;
 KW haematopoietic disorder; inflammatory disorder; infertility;
 KW neurological disease; psychiatric disease; cardiovascular disease;
 KW respiratory disease; renal; gastrointestinal; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..387

FT /tag= a

FT /product= "Human secreted protein"

XX WO200179454-A1.

XX PD 25-OCT-2001.

XX 11-APR-2001; 2001WO-US11797.
 XX 13-APR-2000; 2000US-196603P.
 XX 24-APR-2000; 2000US-199417P.

XX (SMIK) SMITHKLINE BEECHAM CORP.
 XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;

XX WPI: 2002-061975/08.

XX DR P-PSDB; AAU09871.

XX New secreted proteins or polypeptides, useful for treating e.g. cancer,
 PT autoimmune diseases, wound healing disorder, infections, haematopoietic
 PT disorders, inflammatory disorders, infertility, cancer -

XX Claim 2, Page 44; 92pp; English.

XX The invention relates to an isolated novel secreted polypeptide (I) and
 CC polynucleotide (II). (I) and (II) are useful for treating cancer,
 CC autoimmune diseases, wound healing disorder, infections, haematopoietic
 CC disorders, inflammatory disorders, infertility, neurological and
 CC psychiatric diseases, cardiovascular diseases, respiratory diseases,
 CC renal diseases, or gastrointestinal diseases. These may also be used to
 CC treat diseases, abnormalities and disorders caused by abnormal
 CC expression, production, function and/or metabolism of the genes, as
 CC vaccines for inducing immunological response in a mammal, and in the
 CC screening methods for detecting the effect of added compounds on the
 CC production of mRNA and polypeptide in cells. The polypeptides can be used
 CC as immunogens to produce antibodies immunospecific for the polypeptides,
 CC and to identify membrane-bound or soluble receptors. The polynucleotides
 CC may be used as diagnostic reagents, in chromosome localisation studies,
 CC and in tissue expression studies. The present sequence represents the
 CC coding sequence of novel human secreted protein #12.

XX Sequence 387 BP, 101 A; 70 C; 106 G; 110 T; 0 other;

Alignment Scores:

| Pred. No.: | 4,338-74 | Length: | 387 |
|------------------------|----------|---------------|-----|
| Score: | 600.00 | Matches: | 111 |
| Percent Similarity: | 93.75% | Conservative: | 9 |
| Best Local Similarity: | 86.72% | Mismatches: | 8 |
| Query Match: | 88.76% | Indels: | 0 |
| DB: | 24 | Gaps: | 0 |

US-10-019-455A-47 (1-128) x AAS17583 (1-387)

```

QY 1 MetAlaArgIleLeuIleLeuLeuGlyGlyLeuValAlaLeuCysAlaGlyHisGly 20
DB 1 ATGGCAAGATATTTGTTACTTTCTCCCGGCTTGTGCGTATGCTGCGATGGA 60
QY 21 MetPheMetAspLysLeuSerSerLysLeuCysAlaAspGluGluCysValTyrThr 40
DB 61 ATATTATGGACCGCTAGCTTCCAGAGCTCTGTGAGATGATGATGTTCTATACT 120
QY 41 IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
DB 121 ATTCTCTGCTAGTACGCTCAAGATTTAATGCCCGGACTGAGATTATTAACGTT 180
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyAla 80
DB 181 AAAAAAGGCGACAGATCTATGTCTACTCAAGCTGTGTAAGAAAAATGAGCTGAGAA 240
QY 81 PheTTPAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
DB 241 TTTTGGGCTGGCAGGTTTATGTATGTCGCGAGCGAGATGGGATGTGTGTTATTTTC 300
QY 101 ProSerAsnLeuValArgGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120
DB 301 CCCAGGAACCTTGCTCAAGAACAGCGTGTGTACCGAAGACTTCCAGAGAACTTCCACC 360

```

QY 121 ThrAspIleaspPhepCysGlu 128
 |||||
 DB 361 ACGGATATGACTTCTTCTCGCAG 384

RESULT 6

AAH26341
 ID AAH26341 standard; cDNA; 426 BP.

XX AAH26341;

XX 02-OCT-2001 (first entry)

XX Human growth regulatory-like polypeptide clone 16372272.

XX Growth regulatory-like polypeptide; human; cartilage; melanoma;

KM neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;

XX ss.

OS Homo sapiens.

XX WO200155332-A2.

XX 02-AUG-2001.

XX 25-JAN-2001; 2001WO-US02455.

XX 25-JAN-2000; 2000US-0491404.

XX 02-MAY-2000; 2000US-0563786.

XX (HYSE-) HYSEQ INC.

PI Mike NK, Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C;

PI Drmanac RT;

PT Isolated human growth regulatory-like polypeptide useful for treating

PT e.g. Alzheimer's disease, cancer, autoimmune disorders,

PT hyperproliferative disorders, coagulation disorders, and nervous system

PT disorders -

XX

XX

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XX

Example 1; Page 114, 119pp; English.

The present sequence is that of Hyseq clone identification number 16372272, which was obtained from a human thymus cDNA library using standard PCR with primers specific for vector sequences flanking the inserts, sequencing by hybridisation sequence signature analysis, and Sanger sequencing techniques. This expressed sequence tag was used in the assembly of a full-length cDNA sequence (see AAH26343) encoding a novel human growth regulatory-like polypeptide (GRLP, see AAH2671). The GRLP belongs to the same protein family as growth regulatory proteins, growth factors, human melanoma derived growth regulatory protein precursor (64% similarity and 45% identity over 111 amino acids) or melanoma inhibitory activity, cattle cartilage-derived retinoic acid sensitive protein (CD-RAP, 44% identity and 64% similarity over 126 amino acids) and other retinoic acid-sensitive proteins. GRLP polypeptides and polynucleotides of the invention can be used in the prophylaxis, treatment (including gene therapy) and diagnosis of disorders and diseases caused by, or involving, cartilage development and maintenance, inhibition of melanoma cell growth and tumours, including neuroectodermal tumours such as gliomas. The polynucleotides can also be used to design probes and primers, for chromosome and gene mapping, in the recombinant production of protein, in the generation of antisense, ribozyme and peptide-nucleic acid molecules, and to produce transgenic animals.

Sequence 426 BP; 119 A; 73 C; 113 G; 120 T; 1 other;

Alignment Scores:

Pred. No.: 4.96e-74

Score: 600.00

Percent Similarity: 93.75%

Length: 426

Matches: 111

Conservative: 9

Best Local Similarity: 86.72%
 Query Match: 88.76%
 DB: 22
 Gaps: 0

US-10-019-455a-47 (1-128) x AAH26341 (1-426)

QY 1 MetAlaArgIleLeuIleLeuLeuGlyGlyLeuValAlaLeuCysAlaGlyHisGly 20

DB 19 ATGGCAGAAATATTGTACTTTCTCCCGGCTCTGGCTGTATGCTGTGCATGCA 78

QY 21 MetPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGlyCysValTyrThr 40

DB 79 ATATTATGACCGCTACCTTCAAGAGCTTGTGACATGATGATGATGATGATGATGAT 138

QY 41 IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60

DB 139 ATTCTCTGCTAGTGTCTCAAGAGATTATATGCCCGGACTGTATGATTTAACGTT 198

QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyAla 80

DB 199 AAAAAAGGACAGACATCTATCTCAAGCTGTAAAGAAATGACAGCTGACAGAA 258

QY 81 PheTTPAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100

DB 259 TTTGGGCTGGCAGATGTTATGTGTATGGCCGACGAGATGGAGTCTGTGGTATTTTC 318

QY 101 ProSerAsnLeuValArgGlnGlnArgValTyrGlnGlnAlaThrLysGlnIleProThr 120

DB 319 CCAGGAACTTGTGTCAAGAACAGCGGTGTTCACGAGAGCTCAACAGAGAGTCCACCC 378

QY 121 ThrAspIleaspPhepCysGlu 128

DB 379 ACGGATATGACTTCTTCTCGCAG 402

RESULT 7

ABL95740
 ID ABL95740 standard; cDNA; 521 BP.

XX ABL95740;

XX 19-JUL-2002 (first entry)

XX Human angiogenesis related cDNA PRO9873 SEQ ID NO: 359.

KM Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;

KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;

KM cardiac; cytosolic; antiangiogenic; hypotensive; vulnereary;

XX antiarteriosclerotic; gene; ss.

OS Homo sapiens.

XX WO200208284-A2.

XX 31-JAN-2002.

XX 09-JUL-2001; 2001WO-US21735.

XX 20-JUL-2000; 2000US-219556P.

XX 25-JUL-2000; 2000US-220624P.

XX 28-JUL-2000; 2000WO-US20710.

XX 02-AUG-2000; 2000US-222695P.

XX 17-AUG-2000; 2000US-0643657.

XX 23-AUG-2000; 2000WO-US23522.

XX 07-SEP-2000; 2000US-230978P.

XX 15-SEP-2000; 2000US-000000P.

XX 18-SEP-2000; 2000US-0646410.

XX 18-SEP-2000; 2000US-0665350.

XX 24-OCT-2000; 2000US-242922P.

XX 08-NOV-2000; 2000US-0709238.

XX 08-NOV-2000; 2000WO-US30952.

XX 10-NOV-2000; 2000WO-US30873.

PR 20-DEC-2000; 2000WO-US34956.
 PR 22-JAN-2001; 2001US-0767609.
 PR 28-FEB-2001; 2001US-0796498.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0808689.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 30-MAY-2001; 2001US-0870574.
 PR 30-MAY-2001; 2001WO-US17443.
 PR 01-JUN-2001; 2001WO-US17800.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 XX
 DR WPI; 2002-090516/12.
 DR P-PSDB; ABB84996.
 XX
 PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal -
 XX
 PS Claim 2; Fig 359; 565pp; English.
 XX
 CC ABB88072 to ABB88258 encode the PRO proteins given in ABB84817 to
 CC ABB85003. The PRO proteins and polynucleotides have cardiac, cytosolic,
 CC antiangiogenic, hypotensive, vulnary and antiarteriosclerotic
 CC activities, and can be used in gene therapy. The PRO polynucleotides,
 CC proteins, agonists and antagonists are useful for treating or diagnosing
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal,
 CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular
 CC degeneration, atherosclerosis, hypertension, arterial restenosis,
 CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
 CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
 CC carcinoma) and wound healing. The PRO polynucleotides have applications
 CC in molecular biology, including use as hybridisation probes, and in
 CC chromosome and gene mapping. ABB88259 to ABB88267 represent primers and
 CC probes used in the exemplification of the present invention.
 CC
 XX
 SQ Sequence 521 BP; 167 A; 86 C; 131 G; 137 T; 0 other;
 XX
 Alignment Scores:
 Pred. No.: 6.62e-74 Length: 521
 Score: 600.00 Matches: 111
 Percent Similarity: 93.75% Conservative: 9
 Best Local Similarity: 86.72% Mismatches: 8
 Query Match: 88.76% Indels: 0
 DB: 24 Gaps: 0
 US-10-019-455A-47 (1-128) X ABB88251 (1-521)
 QY 1 MetAlaATGtLeuLeuLeuLeuLeuGlyGlyLeuValAlaLeuCysAlaGlyValGly 20
 DB 38 ATGGCAGATATTTCTTCTTCTCCCGGCTTTGGCTGTATGCTGTCATGCA 97
 QY 21 MetPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysValTyrThr 40
 DB 98 ATATTATGACCGCTGCTTCCACAGAGCTGTGTGACATGATGATGCTTACT 157
 QY 41 TLeuLeuAlaAlaGluGluGluGluAspTyrAsnAlaProAspCysAlaGluPheLeuAsnVal 60
 DB 158 ATTCTCTGGCTTACGTCCAGAGATTATATATCCCGGCTTAAATTCATTACGTT 217
 QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyAla 80

DB 218 AAAAAGGGCAGCAGATCTATGTACTCAAAAGCTGTAAAAAATGAGCTGAGCA 277
 QY 81 PheTPrAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyTLeValGlyTyrPhe 100
 DB 278 TTTGGGCTGGCAGCTTTATGTTATGCGCAGAGCAGATAGGAGTCTGGGTTATTC 337
 QY 101 ProSerAsnLeuValAlaGluGluGluValTyrGlnGluAlaThrLysGluLeuProThr 120
 DB 338 CCCAGGAACTTGCTGACAGAGACGCGTGTACAGAGAGCTACCAAGAGAGTCCACCC 397
 QY 121 ThrAspTLeAspPhePheCysGlu 128
 DB 398 ACGGATATTGACTTCTTCTGCGAG 421
 RESULT 9
 ABBK3571
 ID ABBK3571 standard; cDNA; 521 BP.
 AC
 XX ABBK3571;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE cDNA encoding human PRO protein. Seq ID No 71.
 XX
 KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
 KW breast cancer; prostate tumour; liver tumour;
 KW pericyte cell proliferation; chondrocyte cell proliferation;
 KW tumour necrosis factor-alpha; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WC0200208288-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 29-JUN-2001; 2001WO-US21066.
 XX
 PR 20-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220585P.
 PR 25-JUL-2000; 2000US-220605P.
 PR 25-JUL-2000; 2000US-220607P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 25-JUL-2000; 2000US-220638P.
 PR 25-JUL-2000; 2000US-220664P.
 PR 25-JUL-2000; 2000US-220666P.
 PR 26-JUL-2000; 2000US-220893P.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 28-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 15-SEP-2000; 2000US-000000P.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 28-NOV-2000; 2000US-253646P.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000US-074725P.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001WO-US17092.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX
 DR WPI; 2002-172001/22.
 DR P-PSDB; AUB3627.
 XX
 PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful for treating a PRO related disorder and for diagnosing tumours
 PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
 PT tumour or liver tumour -
 XX

PS Claim 2; Figure 71; 35pp; English.

XX The invention relates to one hundred and twenty two nucleic acids
CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
CC agonists and antagonists are useful for treating a PRO related disorder.
CC The PRO polypeptides are useful for diagnosing tumours, especially lung
CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
CC liver tumour. The PRO polypeptides are useful for stimulating the
CC proliferation of, or gene expression, in pericyte cells, for stimulating
CC the proliferation or differentiation of chondrocyte cells, for
CC stimulating the release of tumour necrosis factor-alpha from human blood,
CC for stimulating or inhibiting the proliferation of normal human dermal
CC fibroblast cells. The PRO polypeptide may also be used as molecular
CC weight markers and for tissue typing. The PRO nucleic acids have
CC applications in molecular biology, including use as hybridisation probes,
CC and in chromosome and gene mapping. ABK3356-ABK33657 represent human
CC PRO protein coding sequences of the invention.

XX Sequence 521 BP; 167 A; 86 C; 131 G; 137 T; 0 other;

Alignment Scores:

| Pred. No.: | Length: | Matches: | 521 |
|-------------------------------|----------|---------------|-----|
| Score: 600.00 | 6,62e-74 | Conservative: | 111 |
| Percent Similarity: 93.758 | | Mismatches: | 9 |
| Best Local Similarity: 86.728 | | Indels: | 0 |
| Query Match: 88.764 | | Gaps: | 0 |

US-10-019-455A-47 (1-128) x ABK33571 (1-521)

QY 1 MetAlaArgIleLeuIleLeuLeuGlyGlyLeuValAlaLeuCysAlaGlyHisGly 20
DB 38 ATGGCAGAAATATGTTACTTTCCCGGGCTTGTGGCTGTATGCTGATGATGA 97
QY 21 MetPheMetAspIleuSerSerIleuValLeuCysAlaAspGluGluCysValIleThr 40
DB 98 AATATTATGACCGCTTACTTCTCCAGAGAGCTGTGCGAGAGAGAGTGTCTTACT 157
QY 41 IleSerLeuAlaArgIleLeuValAspIleuValAlaProAspCysArgPheIleAsnVal 60
DB 158 ATTCTCTGGCTAGTCTCAAGAGATTTAATGCCCGAGCTGATGATCTTAACTT 217
QY 61 LysLysGlyGlnGlnIleIleValIleValIleValIleValIleValIleValIleVal 80
DB 218 AAAAAAGGCGAGAGATCTATGCTATGCTCAAAAGCTGTAAAGAAATGAGAGCTGAGAA 277
QY 81 PheTIPAlaGlySerValIleValIleValIleValIleValIleValIleValIleVal 100
DB 278 TTTTGGCTGGCAGAGTGTATGCTGTGCTGAGAGAGATGAGAGTGTGCTTATTTTC 337
QY 101 ProSerAsnLeuValArgValIleValIleValIleValIleValIleValIleValIle 120
DB 338 CCGAGAACTTGGTCAAGAGACGCTGTGTACAGAGAGCTTCAAGAGAGCTTCCACC 397
QY 121 ThrAspIleAspPhePheCysGlu 128
DB 398 ACGGATATTGACTTCTTCTGCGAG 421

RESULT 10

AAH98228 standard; cDNA; 891 BP.

XX AAH98228;

DT 12-OCT-2001 (first entry)

XX Human EST-derived coding sequence SEQ ID NO: 85.

KM Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;

KM tomato; monkey; dog; sea urchin; expressed sequence tag; EST;

KM diagnostics; forensic test; gene mapping; genetic disorder;

KM biodiversity; gene therapy; nutrition; ss.

XX Homo sapiens.

XX WO200154477-A2.

XX 02-AUG-2001.

XX 25-JAN-2001; 2001WO-US02667.

XX 25-JAN-2000; 2000US-0491404.

XX 17-JUL-2000; 2000US-0617746.

XX 03-AUG-2000; 2000US-0631451.

XX 15-SEP-2000; 2000US-0663870.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;

XX Cao Y, Drmanac RA, Zhang J, Werhman T;

XX WPI; 2001-476164/51.

XX P-PSDB; AAM23569.

XX Isolated polypeptide for treatment of diseases, diagnostics, raising

XX antibodies and research use -

XX Claim 1; Page 236; 1275pp; English.

XX The present invention provides the protein and coding sequences of novel

XX proteins from a variety of organisms, including human, dog, cat, horse,

XX cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea (ESTs)

XX from the organism of interest. They can be used in diagnostics,

XX forensics, gene mapping, identification of mutations, to assess

XX biodiversity and for nutritional purposes. The present sequence is a cDNA

XX of the invention.

XX Sequence 891 BP; 272 A; 146 C; 214 G; 259 T; 0 other;

XX Alignment Scores:

XX Pred. No.:

XX Score: 600.00

XX Percent Similarity: 93.758

XX Best Local Similarity: 86.728

XX Query Match: 88.764

XX DB: 22

XX Gaps: 0

XX US-10-019-455A-47 (1-128) x AAH98228 (1-891)

QY 1 MetAlaArgIleLeuIleLeuLeuGlyGlyLeuValAlaLeuCysAlaGlyHisGly 20
DB 19 ATGGCAGAAATATGTTACTTTTCCCGGGCTTGTGGCTGTATGCTGATGATGA 78
QY 21 MetPheMetAspIleuSerSerIleuValLeuCysAlaAspGluGluCysValIleThr 40
DB 79 AATATTATGACCGCTTACTTCTCCAGAGAGCTGTGCGAGAGAGTGTCTTACT 138
QY 41 IleSerLeuAlaArgIleLeuValAspIleuValAlaProAspCysArgPheIleAsnVal 60
DB 139 ATTCTCTGGCTAGTCTCAAGAGATTTAATGCCCGAGCTGATGATCTTAACTT 198
QY 61 LysLysGlyGlnGlnIleIleValIleValIleValIleValIleValIleValIleVal 80
DB 199 AAAAAAGGCGAGAGATCTATGCTGTGCTGAGAGAGATGAGAGTGTGCTTATTTTC 258
QY 81 PheTIPAlaGlySerValIleValIleValIleValIleValIleValIleValIleVal 100
DB 259 TTTTGGCTGGCAGAGTGTATGCTGTGCTGAGAGAGATGAGAGTGTGCTTATTTTC 318
QY 101 ProSerAsnLeuValArgValIleValIleValIleValIleValIleValIleValIle 120
DB 319 CCGAGAACTTGGTCAAGAGACGCTGTGTACAGAGAGCTTCAAGAGAGCTTCCACC 378
QY 121 ThrAspIleAspPhePheCysGlu 128

CC activities, and can be used in gene therapy and as secretory cell
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in
 CC the diagnosis and development of promoters and inhibitors for preventing
 CC or creating bone and joint diseases as well as pathologic angiogenesis.
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
 CC in the exemplification of the present invention.

XX Sequence 923 BP; 303 A; 147 C; 213 G; 260 T; 0 other;

Alignment Scores:

| Pred. No.: | Length: | Matches: | Conservative: | Mismatches: | Indels: | Gaps: |
|-------------------------------|---------|----------|---------------|-------------|---------|-------|
| Score: 600.00 | 923 | 111 | 9 | 8 | 0 | 0 |
| Percent Similarity: 93.75% | | | | | | |
| Best Local Similarity: 86.72% | | | | | | |
| Query Match: 88.76% | | | | | | |

US-10-019-455a-47 (1-128) x AAF59063 (1-923)

```

OY 1 MetAlaArgIleLeuIleLeuLeuGlyGlyLeuValAlaLeuCysAlaGlyHisGly 20
DB 34 ATGGCAGAAATATGTTACTTCTCCCGGCTTGTGTGCTGATGCTGTGCATGGA 93
OY 21 MetPheMetAspLysLeuSerSerLysLeuCysAlaAspGluGluCysValThr 40
DB 94 ATATTATGACCCGCTTACCTTCCAGAAAGCTCTGTGCATGATGATGCTGTACT 153
OY 41 ILeSerLeuAlaArgAlaGluGluAspLysAsnAlaProAspCysArgPheIleAsnVal 60
DB 154 ATTTCCTGGCTAGAGGCTCAGAAAGATATATATGCCCGGACTGTATACATTACCTT 213
OY 61 LysLysGlyGluGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGly 80
DB 214 AAAAAGGCGCAGCATATGATGTACTCAAAAGCTGTAAAGAAATGAGCTGGAGAA 273
OY 81 PheTTPAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
DB 274 TTTTGGCTGGCAGGTTTATGATGATGCGCAGACGAGATGGAGTCTGGGTTATTC 333
OY 101 ProSerAsnLeuValArgGluGluArgValTyrGlnGluAlaThrLysGluIleProThr 120
DB 334 CCCAGGAAGCTTGTCACAGAACACGGCTGTACACAGGAGAGTACCAAGAAAGTCCAC 393
OY 121 ThrAspIleAspPhePheCysGlu 128
DB 394 ACGGATATTGACTTCTCTCGCAG 417

```

RESULT 13

AAH26343
 ID AAH26343 standard; cDNA; 1201 BP.

AC AAH26343;

XX 02-OCT-2001 (first entry)

XX Human growth regulatory-like polypeptide cDNA.

XX Growth regulatory-like polypeptide; human; cartilage; melanoma;

XX neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;

XX ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 33..419

XX sig_peptide 33..101

XX mat_peptide 102..416

XX /*tag= c

XX WO200155332-A2.

PD 02-AUG-2001.

XX 25-JAN-2001; 2001WO-US02455.

XX 25-JAN-2000; 2000US-0491404.

XX 02-MAY-2000; 2000US-0563786.

XX (HYSE-) HYSEQ INC.

XX Mize NK, Boyle BJ, Ford JB, Atterburn MC, Tang YT, Liu C;

XX Drmanac RT;

XX WPI; 2001-48323/52.

XX P-PDSB; AAB82671.

XX Isolated human growth regulatory-like polypeptide useful for treating

XX e.g. Alzheimer's disease, cancer, autoimmune disorders,

XX hyperproliferative disorders, coagulation disorders, and nervous system

XX disorders -

XX Claim 1, Page 115-116; 119pp; English.

XX The present sequence is that of a novel nucleic acid encoding

XX human growth regulatory-like polypeptide (GRLP, see AAB82671).

XX The sequence was assembled using human thymus cDNA library-derived

XX Hyseq clone identification number 16372272 (see AAB26341) as seed,

XX using software programs to pull additional sequences from Hyseq's

XX proprietary database containing expressed sequence tag sequences,

XX and by gel sequencing using primers to extend both 5' and 3' ends.

XX The predicted protein has a mol.wt. of 14 kDa unglycosylated. GRLP

XX belongs to the same protein family as growth regulatory proteins.

XX growth factors, human melanoma derived growth regulatory protein

XX precursor (64% similarity and 45% identity over 111 amino acids)

XX or melanoma inhibitory activity, cattle cartilage-derived

XX retinoic acid sensitive protein (CD-RAP, 44% identity and 64%

XX similarity over 126 amino acids) and other retinoic acid-sensitive

XX proteins. GRLP polypeptides and polynucleotides of the invention

XX can be used in the prophylaxis, treatment (including gene therapy)

XX and diagnosis of disorders and diseases caused by, or involving,

XX cartilage development and maintenance, inhibition of melanoma cell

XX growth and tumours, including neuroectodermal tumours such as

XX gliomas. The polynucleotides can also be used to design probes

XX and primers, for chromosome and gene mapping, in the recombinant

XX production of protein, in the generation of antisense, ribozyme, and

XX peptide-nucleic acid molecules, and to produce transgenic animals.

XX They may also have cytokine and cell proliferation or

XX cell differentiation activity, stem cell growth factor activity,

XX haematopoiesis, regulating activity, tissue growth activity,

XX immunosuppressive or immunostimulant activity, activin/inhibin

XX activity, chemotactic/chemokinetic activity, haemostatic and

XX thrombolytic activity, use in cancer diagnosis and therapy,

XX drug screening, receptor/ligand activity, anti-inflammatory

XX activity, and treatment of leukaemia, nervous system disorders,

XX arthritis and inflammation.

SQ Sequence 1201 BP; 357 A; 188 C; 275 G; 381 T; 0 other;

Alignment Scores:

| Pred. No.: | Length: | Matches: | Conservative: | Mismatches: | Indels: | Gaps: |
|-------------------------------|---------|----------|---------------|-------------|---------|-------|
| Score: 2,196-73 | 1201 | 111 | 9 | 8 | 0 | 0 |
| Percent Similarity: 93.75% | | | | | | |
| Best Local Similarity: 86.72% | | | | | | |
| Query Match: 88.76% | | | | | | |

US-10-019-455a-47 (1-128) x AAH26343 (1-1201)

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OY 1 MetAlaArgIleLeuIleLeuLeuGlyGlyLeuValAlaLeuCysAlaGlyHisGly 20
DB 33 ATGGCAGAAATATGTTACTTCTCCCGGCTTGTGTGCTGATGCTGTGCATGGA 92
OY 21 MetPheMetAspLysLeuSerSerLysLeuCysAlaAspGluGluCysValThr 40

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Db 93 ATATTATGACCGCTAGCTCCAGAGCTCTGTGCAGATGATGATGCTTACT 152
 Qy 41 TLeSerLeuAlaGAlaGlnGluAspDyrAspAlaProAspCysArgPheIleAsnVal 60
 Db 153 ATTCTCTGGTGTAGTGTCTCAAGAGATTATATATCCCCGGAGCTGTATATTCAATTCGTT 212
 Qy 61 LysTlsgLgInGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 80
 Db 213 AAAAAAGGCGACGATCTATGTCTACTCAAGCTGTAAAGAAATGAGAGCTGGAGAA 272
 Qy 81 PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
 Db 273 TTTGGGTGGTCAGATGTTATGTGATGGCCAGACAGATGGAGATGGAGCTGGATTATTC 332
 Qy 101 ProSerAsnLeuValArgGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120
 Db 333 CCCAGAACTTGGTCAGAGGAGACAGCTGTGTACCGAGAGCTACCAAGAAAGTTCCACCC 392
 Qy 121 ThrAspIleAspPhePheCysGlu 128
 Db 393 ACGGATATTGACTTCTTCTGCGAG 416
 RESULT 14
 AAF59099
 ID AAF59099 standard; DNA; 330 BP.
 AC AAF59099;
 DT 23-APR-2001 (first entry)
 DE Rat MLP nucleotide sequence SEQ ID NO:48.
 XX
 KM MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
 KM joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
 KM cardiant; gene therapy; secretory cell function regulator; promoter;
 KM inhibitor; ds.
 XX
 OS Rattus sp.
 PN WO200102564-A1.
 PD 11-JAN-2001.
 PF 29-JUN-2000; 2000WO-JP04278.
 PR 30-JUN-1999; 99JP-0186718.
 PA (TAKE) TAKEDA CHEM IND LTD.
 PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K,
 PI Tanaka H;
 DR WPI: 2001-159271/16.
 DR P-PDB; AAB69131.
 XX
 PT Safe, low-toxicity secretory cell function-regulatory protein and
 PT encoded DNA, applicable as drugs, in diagnosis and development of
 PT promoters and inhibitors for preventing or treating e.g. bone and joint
 PT diseases -
 XX
 PS Claim 12; Page 107; 11pp; Japanese.
 CC The present invention describes novel MLP proteins and their encoding
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
 CC activities, and can be used in gene therapy and as secretory cell
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in
 CC the diagnosis and development of promoters and inhibitors for preventing
 CC or treating bone and joint diseases as well as pathologic angiogenesis.
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
 CC in the exemplification of the present invention.
 XX
 SQ Sequence 330 BP; 91 A; 62 C; 91 G; 86 T; 0 other;

Alignment Scores:
 Pred. No.: 6,19e-73 Length: 330
 Score: 591.00 Matches: 110
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 87.43% Indels: 0
 DB: 22 Gaps: 0
 US-10-019-455a-47 (1-128) x AAF59099 (1-330)
 Qy 19 HisGlyMetPheMetCaspLysLeuSerSerLysLeuCysAlaAspGluLucySerVal 38
 Db 1 CATGGCATTTTATGATTAACCTTTCTTCTAAGAAAGTTGTGTGCAGATGAGAGTGTGTC 60
 Qy 39 TyrThrIleSerLeuAlaArgAlaGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 58
 Db 61 TATACCATTTCTCTGGCAAGACACAGAACTCAATGATGAGAGCTGTGATTC 120
 Qy 59 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 78
 Db 121 AATGTCAAGAAAGGCGACGATCTATGTTATTCACAGCTGTAAAGAAATGGAGCT 180
 Qy 79 GlyAlaPheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 98
 Db 181 GGGGCATTTCTGGGCTGCGAGTGTATGAGTACCAACAGATGAGATGGGAATTCGGGT 240
 Qy 99 TyrPheProSerAsnLeuValArgGluGlnArgValTyrGlnGluAlaThrLysGluIle 118
 Db 241 TATTTCCCGACAACTTGTTAGAGGACAGATGTACCGAGAGGCCACAAAGAGATT 300
 Qy 119 ProThrThrAspIleAspPhePheCysGlu 128
 Db 301 CCNACCAAGATATTGACTTCTTCTGTGA 330
 RESULT 15
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 ID AAF59080 standard; DNA; 330 BP.
 AC AAF59080;
 DT 23-APR-2001 (first entry)
 DE Mouse MLP nucleotide sequence SEQ ID NO:25.
 XX
 KM MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
 KM joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
 KM cardiant; gene therapy; secretory cell function regulator; promoter;
 KM inhibitor; ds.
 XX
 OS Mus musculus.
 PN WO200102564-A1.
 PD 11-JAN-2001.
 PF 29-JUN-2000; 2000WO-JP04278.
 PR 30-JUN-1999; 99JP-0186718.
 PA (TAKE) TAKEDA CHEM IND LTD.
 PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K,
 PI Tanaka H;
 DR WPI: 2001-159271/16.
 DR P-PDB; AAB69127.
 XX
 PT Safe, low-toxicity secretory cell function-regulatory protein and
 PT encoded DNA, applicable as drugs, in diagnosis and development of
 PT promoters and inhibitors for preventing or treating e.g. bone and joint
 PT diseases -
 XX
 PS Claim 10; Page 98; 11pp; Japanese.

XX The present invention describes novel MLP proteins and their encoding
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
 CC activities, and can be used in gene therapy and as secretory cell
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in
 CC the diagnosis and development of promoters and inhibitors for preventing
 CC or treating bone and joint diseases as well as pathologic angiogenesis.
 CC AAF59063 to AAF59099 and AAB59122 to AAB59132 represent sequences used
 CC in the exemplification of the present invention.

XX
 SQ Sequence 330 BP; 91 A; 60 C; 92 G; 87 T; 0 other;

Alignment Scores:

| | | | |
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| Score: | 574.00 | Matches: | 106 |
| Percent Similarity: | 99.09% | Conservative: | 3 |
| Best Local Similarity: | 96.36% | Mismatches: | 1 |
| Query Match: | 84.91% | Indels: | 0 |
| DB: | 22 | Gaps: | 0 |

US-10-019-455A-47 (1-128) x AAF59080 (1-330)

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| QY | 19 | HISGLYMETPHEMETASPLYSEUSESESLYSLEUCYSAIASPGIUGIUCYVAL | 38 |
| DB | 1 | CATGGTGTATTATGATTAACCTTCTCTAAGAGTTGTGTGCGATGAGGAGTGTCTC | 60 |
| QY | 39 | TYRTHRILESELEUALAARGAAGINGIUAAPITYRASNALAPROASPCYEAIRPHEILE | 58 |
| DB | 61 | TATACATTTCTCTGCGACAGCACAGAGATTACAAATGCCCGACTGTAGGTTCAATC | 120 |
| QY | 59 | ASNVALIVSESLVSGIUGINGIULETYRVALITYRSESLYSLEUVALTHRGIUASNGIYALA | 78 |
| DB | 121 | GATGTCAGAGAAAGGCGACGATCTATGTTTCTCCAGCTGTGTAACAGAAAACGAGCT | 180 |
| QY | 79 | GIYALAPHETIPALAGIYSEVALTYRGIIYASPHISGINASPGIUMETGLYLEVALGIY | 98 |
| DB | 181 | GGAGAGTTTGGGCTGGCAGTGTATGTGTACCAACAGATGATGGGAATTGTAGCT | 240 |
| QY | 99 | TYRPHETPSEASINLEUVALARGIUGIARGVALTYRGINGIUALATHIRIYSGIUILE | 118 |
| DB | 241 | TATTTCCCGACCACTTGTGAAGAGCGCGGTATACCAAGAGGCCACCAAGAGAGATC | 300 |
| QY | 119 | PROTHRTHRASPILASPPHEPCYSGIU | 128 |
| DB | 301 | CCAAACCGAGATATTGACTTCTTCTGTGAA | 330 |

Search completed: December 29, 2003, 16:41:14
 Job time : 157.353 secs

Tue Dec 30 10:20:49 2003

us-10-019-455a-47.rnpb

Page 1

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 29, 2003, 19:57:30 ; Search time 287.193 Seconds
(without alignments)
1527.048 Million cell updates/sec

Title: US-10-019-455a-47

Perfect score: 676

Sequence: 1 NARIILLGLGVALCAGHG.....RYGQATKPTPTDIDFCE 128

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| Ygapop 10.0 , Ygapext 0.5 | |
| Fgapop 6.0 , Fgapext 7.0 | |
| Delop 6.0 , Delext 7.0 | |

Searched: 2244575 seqs, 173117285 residues

Total number of hits satisfying chosen parameters: 4489150

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-TRANS-human40.cai -LIST=45 -DOCALLIGN=200 -THR.SCORE=pct -THR.MAX=100
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Database: Published Applications NA:

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| 2: | /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq: |
| 3: | /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq: |
| 4: | /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq: |
| 5: | /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq: |
| 6: | /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq: |
| 7: | /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq: |
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| 9: | /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq: |
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Pred. No. is the number of results predicted by change to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
|------------|-------|-------------|--------|----|-------------|

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| 1 | 600 | 88.8 | 426 | 15 | US-10-216-038-1 | Sequence 1, Appl |
| 2 | 600 | 88.8 | 521 | 13 | US-10-216-163-71 | Sequence 71, Appl |
| 3 | 600 | 88.8 | 521 | 13 | US-10-218-765-71 | Sequence 71, Appl |
| 4 | 600 | 88.8 | 521 | 13 | US-10-219-063-71 | Sequence 71, Appl |
| 5 | 600 | 88.8 | 521 | 13 | US-10-219-066-71 | Sequence 71, Appl |
| 6 | 600 | 88.8 | 521 | 13 | US-10-219-067-71 | Sequence 71, Appl |
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| 9 | 600 | 88.8 | 521 | 13 | US-10-219-073-71 | Sequence 71, Appl |
| 10 | 600 | 88.8 | 521 | 13 | US-10-219-475-71 | Sequence 71, Appl |
| 11 | 600 | 88.8 | 521 | 13 | US-10-219-480-71 | Sequence 71, Appl |
| 12 | 600 | 88.8 | 521 | 13 | US-10-219-483-71 | Sequence 71, Appl |
| 13 | 600 | 88.8 | 521 | 13 | US-10-219-525-71 | Sequence 71, Appl |
| 14 | 600 | 88.8 | 521 | 13 | US-10-219-526-71 | Sequence 71, Appl |
| 15 | 600 | 88.8 | 521 | 13 | US-10-219-530-71 | Sequence 71, Appl |
| 16 | 600 | 88.8 | 521 | 13 | US-10-219-531-71 | Sequence 71, Appl |
| 17 | 600 | 88.8 | 521 | 13 | US-10-219-532-71 | Sequence 71, Appl |
| 18 | 600 | 88.8 | 521 | 13 | US-10-219-533-71 | Sequence 71, Appl |
| 19 | 600 | 88.8 | 521 | 13 | US-10-223-081-359 | Sequence 359, App |
| 20 | 600 | 88.8 | 521 | 13 | US-10-230-437-71 | Sequence 71, Appl |
| 21 | 600 | 88.8 | 521 | 13 | US-10-232-228-71 | Sequence 71, Appl |
| 22 | 600 | 88.8 | 521 | 13 | US-10-223-082-359 | Sequence 359, App |
| 23 | 600 | 88.8 | 521 | 15 | US-10-227-884-71 | Sequence 71, Appl |
| 24 | 600 | 88.8 | 521 | 15 | US-10-230-163-71 | Sequence 71, Appl |
| 25 | 600 | 88.8 | 521 | 15 | US-10-230-338-71 | Sequence 71, Appl |
| 26 | 600 | 88.8 | 521 | 15 | US-10-218-631-71 | Sequence 71, Appl |
| 27 | 600 | 88.8 | 521 | 15 | US-10-230-414-71 | Sequence 71, Appl |
| 28 | 600 | 88.8 | 521 | 15 | US-10-216-159a-71 | Sequence 71, Appl |
| 29 | 600 | 88.8 | 521 | 15 | US-10-218-849-71 | Sequence 71, Appl |
| 30 | 600 | 88.8 | 521 | 15 | US-10-227-873-71 | Sequence 71, Appl |
| 31 | 600 | 88.8 | 521 | 15 | US-10-227-883-71 | Sequence 71, Appl |
| 32 | 600 | 88.8 | 521 | 15 | US-10-219-076-71 | Sequence 71, Appl |
| 33 | 600 | 88.8 | 521 | 15 | US-10-230-434-71 | Sequence 71, Appl |
| 34 | 600 | 88.8 | 521 | 15 | US-10-219-003-71 | Sequence 71, Appl |
| 35 | 600 | 88.8 | 521 | 15 | US-10-219-075-71 | Sequence 71, Appl |
| 36 | 600 | 88.8 | 521 | 15 | US-10-219-464-71 | Sequence 71, Appl |
| 37 | 600 | 88.8 | 521 | 15 | US-10-219-466-71 | Sequence 71, Appl |
| 38 | 600 | 88.8 | 521 | 15 | US-10-219-479-71 | Sequence 71, Appl |
| 39 | 600 | 88.8 | 521 | 15 | US-10-219-481-71 | Sequence 71, Appl |
| 40 | 600 | 88.8 | 521 | 15 | US-10-230-260-71 | Sequence 71, Appl |
| 41 | 600 | 88.8 | 521 | 15 | US-10-232-331-71 | Sequence 71, Appl |
| 42 | 600 | 88.8 | 521 | 15 | US-10-232-333-71 | Sequence 71, Appl |
| 43 | 600 | 88.8 | 521 | 15 | US-10-216-163-71 | Sequence 71, Appl |
| 44 | 600 | 88.8 | 521 | 15 | US-10-218-956-71 | Sequence 71, Appl |
| 45 | 600 | 88.8 | 521 | 15 | US-10-219-468-71 | Sequence 71, Appl |

ALIGNMENTS

RESULT 1
US-10-216-038-1
Sequence 1, Application US/10216038
Publication No. US20030124573A1
GENERAL INFORMATION:
APPLICANT: Mize, Nancy K
APPLICANT: Boyle, Bryan J
APPLICANT: Ford, John E
APPLICANT: Aretburn, Matthew C
APPLICANT: Tang, Y Tom
APPLICANT: Liu, Chenghua
APPLICANT: Drmanac, Radoje T
APPLICANT: Song, Yong
APPLICANT: Sjaastad, Michael
TITLE OF INVENTION: Methods and Materials Relating to No. US20030124573A1 Growth R
FILE REFERENCE: HYS-7C1P
CURRENT FILING DATE: 2002-08-08
PRIOR APPLICATION NUMBER: US 09/563,786
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR FILING DATE: 2000-01-25
NUMBER OF SEQ ID NOS: 8

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 426
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (426)..(426)
; OTHER INFORMATION: n = A, T, G, or C
US-10-216-038-1

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Alignment Scores:
Pred. No.: 1,47e-83 Length: 426
Score: 600.00 Matches: 111
Percent Similarity: 93.75% Conservative: 9
Best Local Similarity: 86.72% Mismatches: 8
Query Match: 88.76% Indels: 0
DB: Gaps: 0

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US-10-019-455a-47 (1-128) x US-10-216-038-1 (1-426)

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QY 1 MetAlaArgIleuLeuLeuLeuGlyLeuValAlaLeuCysAlaGlyHisGly 20
DB 19 ATGGCAGATATTGTACTTTCTCCCGGCTTGCTGCTGATGCTGTCATGGA 78
QY 21 MetPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysValIYrThr 40
DB 79 ATATTATGACCGCTAGCTTCCAGAGAGCTCTGTCCAGATATGATGCTGTCTACT 138
QY 41 ILeSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
DB 139 ATTCTCTGCTAGCTGCTCAGAGATTAATATGCCCCGAGCTGATTCATTAAAGTT 198
QY 61 LysIleGlyGlnGlnIleTyrValIYrSerLysLeuValThrGluAsnGlyAlaGlyAla 80
DB 199 AAAAAAGGCGACGATCTATGCTACTCAAGCTGTTAAAGAAATGAGCTGGAGAA 258
QY 81 PheTyrAlaGlySerValIYrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
DB 259 TTTGGGCTGGCAGCTGTTATGATGATGCGCAGAGACAGATGGAGCTGCGGTTATTTC 318
QY 101 ProSerAsnLeuValArgGluGlnArgValIYrGlnGluAlaThrLysGluIleProThr 120
DB 319 CCCAGGAAGCTGTGCAAGAACACGGTGTACCAAGAGCTACCAAGAGTTCCACCC 378
QY 121 ThrAspIleAspPhePheCysGlu 128
DB 379 ACGGATATTGACTTCTCTCGCAG 402

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RESULT 2

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US-10-216-163-71
; Sequence 71, Application US/10216163
; Publication No. US20030149239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Macanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C3
; CURRENT APPLICATION NUMBER: US/10/216,163
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113

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; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-216-163-71

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Alignment Scores:
Pred. No.: 1.98e-83 Length: 521
Score: 600.00 Matches: 111
Percent Similarity: 93.75% Conservative: 9
Best Local Similarity: 86.72% Mismatches: 8
Query Match: 88.76% Indels: 0
DB: Gaps: 0

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US-10-019-455a-47 (1-128) x US-10-216-163-71 (1-521)

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QY 21 MetPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysValIYrThr 40
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QY 81 PheTyrAlaGlySerValIYrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
DB 278 TTTGGGCTGGCAGCTGTTATGATGATGCGCAGAGACAGATGGAGCTGCGGTTATTTC 337
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RESULT 3

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; Sequence 71, Application US/10218765
; Publication No. US20030187201A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.

```

APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Matanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P530P1C19
CURRENT APPLICATION NUMBER: US/10/218,765
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/086392
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089905
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090691
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/095302
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/095318
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/095916
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/096146
PRIOR FILING DATE: 1998-08-11
PRIOR APPLICATION NUMBER: 60/096791
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 60/097986
PRIOR FILING DATE: 1998-08-26

PRIOR APPLICATION NUMBER: 60/098544
PRIOR FILING DATE: 1998-08-31
PRIOR APPLICATION NUMBER: 60/099596
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099598
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099803
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099811
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099812
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099816
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/100038
PRIOR FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: 60/100385
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100390
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100627
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100848
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/100919
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/101477
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101738
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101741
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101786
PRIOR FILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: 60/101916
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101922
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/106464
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 60/106178
PRIOR FILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: 60/106248
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 60/106464
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 60/106905
PRIOR FILING DATE: 1998-11-03
PRIOR APPLICATION NUMBER: 60/108787
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/108801
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/108849
PRIOR FILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: 60/112422
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/113296
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/113605
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113621
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/115558
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115565
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115733
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/119549
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/123618
PRIOR FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: 60/125259
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/125775

QY 1 MetAlaArgIleLeuLeuLeuLeuLeuGlyGlyLeuValAlaLeuCysAlaGlyHisGly 20
Db 38 ATGGCAAGAAATTATTGTTACTTTTCTCCCGGGTCTTGCGCTGTATGTGCTGTCATGCA 97
QY 21 MetPheMetAspLysLeuSerSerLysLeuCysAlaAspGluGluCysValTyrThr 40
Db 98 ATATTTTATGACCGCTCAGCTTCACAAAGAGCTGTGGCAGATGAGAGTGTCTATACT 157
QY 41 ILeSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
Db 158 ATTCTCTGCTGAGTGGCTCACAAGATTATTAATGCCCGAGCTGTAGATTATTAAAGCTT 217
QY 61 LysIleGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyAla 80
Db 218 AAAAAGGCGACGATCTATGTGTACTAAAGCTGTGTAAGAAGAAATGAGACTGGAGAA 277

| | | | |
|----|-----|---|-----|
| Db | 38 | ATGGCAGAAATATATTGTTACTTTTCTCTCCCGGGTCTTGAGGCTGATAGCTGCATCGA | 97 |
| Qy | 21 | MetPheMetAspLysLeuSerSerLysLysLeuCySalaaapglugluCySalValTYrThr | 40 |
| | ... | ... | ... |
| Db | 98 | ATATTATATGACCGCTTACTTCTTCAAGAAAGCTCTGTGCAGATGATGATGTGTATACT | 157 |
| Qy | 41 | ILSerLeuLuarargLagLingluAspTYrAsnAlaPcoAspCySarGpPheILAsnVal | 60 |
| Db | 158 | ATTTCCTGGCTAGTGTCTCAAGAAAGTATTAATGCCCGGAGCTGTAGATTATTAAAGCTT | 217 |
| Qy | 61 | LysLysglYngLinglinIeTYrValTYrSerLysLeuValIthrgluAsnGlyAlaGlyAla | 80 |
| Db | 218 | AAAAAAGGACACAGATCTATGTGTACTCAAAAGCTGTATAAAGAAAAATGGAGCTGGAGAA | 277 |
| Qy | 81 | PheTYrAlaGlySerValTYrGlyAspHisGlnaapglumetGlyIleValGlyTYrPhe | 100 |
| Db | 278 | TTTTGGGCTGGCAGTGTTATGTGTATGGCCAGACGAGATGGAGTGCTGGGTATTTC | 337 |
| Qy | 101 | ProSerLysnLeuValIarGluGlnaGValTYrGlnGlnuAlaIthLysGluIleProThr | 120 |
| Db | 338 | CCCGAGAACTTGGTCACAGGAACGCTGTGTATCCAGGAAGTCAACCAAGAAATTCCAC | 397 |
| Qy | 121 | ThrAspIleAspPhePheCysGlu | 128 |
| Db | 398 | ACGGATATTAAGCTTTCTTCTGCGAG | 421 |

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PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 71
LENGTH: 521
TYPE: DNA
ORGANISM: Homo Sapien
US-10-019-067-71

Alignment Scores:
Pred. No.: 1,98e-83 Length: 521
Score: 600.00 Matches: 111
Percent Similarity: 93.75% Conservative: 9
Best Local Similarity: 86.72% Mismatches: 8
Query Match: 88.76% Indels: 0
Gaps: 0
DB: 13

US-10-019-455a-47 (1-128) x US-10-219-067-71 (1-521)
QY 1 MetAlaArgIleLeuIleLeuLeuGlyLeuValAlaLeuCysAlaGlyHisGly 20
DB 38 ATGGCAAGATATTTTACTTTCTCCCGGCTTGCTGATGCTGTCATGGA 97
QY 21 MetPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysValIleThr 40
DB 98 ATATTATGACCGCTGATGCTTCCCAAGAGCTTGTCAGATGATGATGCTATACT 157
QY 41 IleserLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
DB 158 ATTTCTGCTGCTAGCTCTCAAGAGATTAATATGCCCCGAGCTGTAGATTCAATTAAGCTT 217
QY 61 LysLysGlyGlnGlnIleTyrValIleTyrSerLysLeuValIleGluAsnGlyAlaGlyAla 80
DB 218 AAAAAAGGCGACGATCTATGTGCTCAAGAGCTGTGTAAGAAATGAGAGCTGGAGAA 277
QY 81 PheTyrAlaGlySerValIleTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
DB 278 TTTTGGCTGCGACGATTTATGCTATGCGCCAGAGAGATGCGAGTGTGGTATTTCC 337
QY 101 ProSerAsnLeuValAlaGlnGluIleArgValIleTyrGlnGluAlaThrLysGluIleProThr 120
DB 338 CCCAGAGACTTGCTGCAAGAGACGCTGTGTACCCAGAGAGCTTACCAAGAGATTCCACC 397
QY 121 ThrAspIleAspPhePheCysGlu 128
DB 398 ACGGATATTGACTTTCTTCCGAG 421

RESULT 7
US-10-219-068-71
Sequence 71, Application US/10219068
Publication No. US20030187205A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerltsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C31

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CURRENT APPLICATION NUMBER: US/10/219,068
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 71
LENGTH: 521
TYPE: DNA
ORGANISM: Homo Sapien
US-10-219-068-71

Alignment Scores:
Pred. No.: 1,98e-83 Length: 521
Score: 600.00 Matches: 111
Percent Similarity: 93.75% Conservative: 9
Best Local Similarity: 86.72% Mismatches: 8
Query Match: 88.76% Indels: 0
Gaps: 0
DB: 13

US-10-019-455a-47 (1-128) x US-10-219-068-71 (1-521)
QY 1 MetAlaArgIleLeuIleLeuLeuGlyLeuValAlaLeuCysAlaGlyHisGly 20
DB 38 ATGGCAAGATATTTTACTTTCTCCCGGCTTGCTGATGCTGTCATGGA 97
QY 21 MetPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysValIleThr 40
DB 98 ATATTATGACCGCTGATGCTTCCCAAGAGCTTGTCAGATGATGATGCTATACT 157
QY 41 IleserLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
DB 158 ATTTCTGCTGCTAGCTCTCAAGAGATTAATATGCCCCGAGCTGTAGATTCAATTAAGCTT 217
QY 61 LysLysGlyGlnGlnIleTyrValIleTyrSerLysLeuValIleGluAsnGlyAlaGlyAla 80
DB 218 AAAAAAGGCGACGATCTATGTGCTCAAGAGCTGTGTAAGAAATGAGAGCTGGAGAA 277
QY 81 PheTyrAlaGlySerValIleTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
DB 278 TTTTGGCTGCGACGATTTATGCTATGCGCCAGAGAGATGCGAGTGTGGTATTTCC 337
QY 101 ProSerAsnLeuValAlaGlnGluIleArgValIleTyrGlnGluAlaThrLysGluIleProThr 120
DB 338 CCCAGAGACTTGCTGCAAGAGACGCTGTGTACCCAGAGAGCTTACCAAGAGATTCCACC 397
QY 121 ThrAspIleAspPhePheCysGlu 128
DB 398 ACGGATATTGACTTTCTTCCGAG 421

RESULT 8
US-10-219-069-71
Sequence 71, Application US/10219069
Publication No. US20030187206A1
GENERAL INFORMATION:

```


APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530P1C40
CURRENT APPLICATION NUMBER: US/10/219,065
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 71
LENGTH: 521
TYPE: DNA
ORGANISM: Homo Sapien
US-10-219-069-71

Alignment Scores:
Pred. No.: 1,98e-83 Length: 521
Score: 600.00 Matches: 111
Percent Similarity: 93.75% Conservative: 9
Best Local Similarity: 86.72% Mismatches: 8
Query Match: 88.76% Indels: 0
Gaps: 0
DB: 13
US-10-019-455a-47 (1-128) x US-10-219-069-71 (1-521)

QY 1 MetAlaArgIleLeuIleLeuLeuGlyGlyLeuValAlaLeuCysAlaGlyHISgly 20
DB 38 ATGGCAAGATATATTGTTACTTTCTCCCGGCTTGTGCTGATGTCGTGATGCA 97
QY 21 MetPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysValIleThr 40
DB 98 ATATTATTTGAGCCCTCTAGCTCCAGAAAGCTCTGTGCAATATGATGATGTCCTACT 157
QY 41 IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
DB 158 ATTTCCTGCTGCTAGTCTCCAGAAAGATTTAATGCCGCACTGTAGATTCAATTACGTT 217
QY 61 LysLysGlyGlnGlnIleIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyAla 80
DB 218 AAAAAGGCGAGCATCTATGTCTACTCAAGCTGTGTAAGAAATGAGCTGGAGMA 277
QY 81 PheThrAlaGlySerValIleTyrGlyAspHisGlnAspLysMetGlyIleValGlyTyrPhe 100
DB 278 TTTTGGCTGGCACTGTTTATGTGATGGCCAGAGCATGGAGATGGAGTCGGGTTATTTC 337

QY 101 ProSerAsnLeuValArgGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120
DB 338 CCCAGAACTTGCTGTAAAGAACGGCTGTGTACCAAGAGAGCTACCAAGAGTTCCACC 397
QY 121 ThrAspIleAspPhePheCysGly 128
DB 398 ACGATATTGACTTCTCTCGCAG 421

RESULT 9
US-10-219-073-71
Sequence 71, Application US/10219073
Publication No. US20030187207A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530P1C52
CURRENT APPLICATION NUMBER: US/10/219,073
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 71
LENGTH: 521
TYPE: DNA
ORGANISM: Homo Sapien
US-10-219-073-71

Alignment Scores:
Pred. No.: 1,98e-83 Length: 521
Score: 600.00 Matches: 111
Percent Similarity: 93.75% Conservative: 9
Best Local Similarity: 86.72% Mismatches: 8
Query Match: 88.76% Indels: 0
Gaps: 0
DB: 13
US-10-019-455a-47 (1-128) x US-10-219-073-71 (1-521)

QY 1 MetAlaArgIleLeuIleLeuLeuGlyGlyLeuValAlaLeuCysAlaGlyHISgly 20
DB 38 ATGGCAAGATATATTGTTACTTTCTCCCGGCTTGTGCTGATGTCGTGATGCA 97
QY 21 MetPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysValIleThr 40

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Db 98 ATATTATGACCGCTCTAGCTCCAGAGAGCTGTGTGACAGTATGATGCTGTACTACT 157
Qy 41 ILeSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysAlaPheIleAsnVal 60
Db 158 ATTTCTGTGGCTAGTGGCTCAAGAGATTATATGCCCCGGAGCTGTAGATTCAATTAACGTT 217
Qy 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyAla 80
Db 218 AAAAAGGCGACGAGATTATGTACTCAAGAGCTGTGTAAGAAAGAAATGAGCTGGAGAA 277
Qy 81 PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
Db 278 TTTTGGCTGGCAGTGTATTATGTGATGCGCCAGACAGATGGAGAGTCTGTGTTATTC 337
Qy 101 ProSerAsnLeuValArgAlaGlnGluArgValTyrGlnGluAlaThrLysGluIleProThr 120
Db 338 CCCAGGAAGCTGTGTCAAGAAACAGCGTGTATCCAGAGAGCTACCAAGAAAGTTCCACACC 397
Qy 121 ThrAspIleAspPhePheCysGlu 128
Db 398 ACGGATATTGACTTCTTCTGCGAG 421

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RESULT 10

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US-10-219-475-71
; Sequence 71, Application US/10219475
; Publication No. US20030187208A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C49
; CURRENT APPLICATION NUMBER: US/10/219,475
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-475-71

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Alignment Scores:

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Pred. No.: 1,98e-83
Score: 600.00
Percent Similarity: 93.75%
Best Local Similarity: 86.72%
Query Match: 88.76%
DB: 13
Gaps: 0

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US-10-019-455a-47 (1-128) x US-10-219-475-71 (1-521)

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Qy 1 MetAlaArgIleLeuIleLeuLeuGlyGlyLeuValAlaLeuCysAlaGlyHisGly 20
Db 38 ATGGCAAGATATGTACTTTCTCCCGGCTTTGGCTGTATGCTGTGATGCA 97
Qy 21 MetPheMetAspLysLeuSerLysLysLeuCysAlaAspGluGlyCysValTyrThr 40
Db 98 ATATTATGACCGCTCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTATACT 157
Qy 41 ILeSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysAlaPheIleAsnVal 60
Db 158 ATTTCTGTGGCTAGTGGCTCAAGAGATTATATGCCCCGGAGCTGTAGATTCAATTAACGTT 217
Qy 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyAla 80
Db 218 AAAAAGGCGACGAGATTATGTACTCAAGAGCTGTGTAAGAAAGAAATGAGCTGGAGAA 277
Qy 81 PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
Db 278 TTTTGGCTGGCAGTGTATTATGTGATGCGCCAGACAGATGGAGAGTCTGTGTTATTC 337
Qy 101 ProSerAsnLeuValArgAlaGlnGluArgValTyrGlnGluAlaThrLysGluIleProThr 120
Db 338 CCCAGGAAGCTGTGTCAAGAAACAGCGTGTATCCAGAGAGCTACCAAGAAAGTTCCACACC 397
Qy 121 ThrAspIleAspPhePheCysGlu 128
Db 398 ACGGATATTGACTTCTTCTGCGAG 421

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RESULT 11

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US-10-219-480-71
; Sequence 71, Application US/10219480
; Publication No. US20030187209A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C38
; CURRENT APPLICATION NUMBER: US/10/219,480
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294

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; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-219-480-71

Alignment Scores:
Pred. No.: 1,98e-83 Length: 521
Score: 600.00 Matches: 111
Percent Similarity: 93.75% Conservative: 9
Best Local Similarity: 86.72% Mismatches: 8
Query Match: 88.76% Indels: 0
DB: Gaps: 13

US-10-019-455a-47 (1-128) x US-10-219-480-71 (1-521)
QY 1 MetAlaArgIleLeuIleLeuLeuGlyGlyLeuValAlaLeuCysAlaGlyHisGly 20
DB 38 ATGGCAAGATATTGTTACTTTCTCCCGGCTTGTGCTGTATGCTGTGCATGCA 97
QY 21 MetPheMetAspIleuSerSerIleuValLeuValAlaAspGluCysValTyrThr 40
DB 98 ATATTATGACCGCTTACCTCCAGAACCTCTGTGCATATATGATGTGCTTACT 157
QY 41 ILeSerIleuAlaArgAlaGlnIleuAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
DB 158 ATTCTCTGGCTAGCTGCTCAGAAAGATTATATGCCCGGACCTGATTCATTACGTT 217
QY 61 LysIleGlyGlnGlnIleTyrValTyrSerIleuValThrGluAsnGlyAlaGlyAla 80
DB 218 AAAAAGGCGACGACATCTATGTCTACTCAAGCTGTAAAGAAATGAGCTGAGAA 277
QY 81 PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
DB 278 TTTGGGCTGGCAGTGTATTATGTGGATGGCCAGACAGATGGAGCTGTGCTTATTTTC 337
QY 101 ProSerIleuValArgGlnIleuArgValTyrGlnGlnAlaThrIleuGlnIleProThr 120
DB 338 CCCAGAACTTGTCAAGGAACACCGCTGTATCCAGAAAGCTTACCAAGAAAGTTCCACC 397
QY 121 ThrAspIleAspPhePheCysGlu 128
DB 398 ACGGATATTGACTTCTTCTGCGAG 421

RESULT 12
US-10-219-483-71
; Sequence 71, Application US/10219483
; Publication No. US20030187210A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Goddard, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gutney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C43
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/10/219,483
; PRIOR APPLICATION NUMBER: 10/119,480

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; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-219-483-71

Alignment Scores:
Pred. No.: 1,98e-83 Length: 521
Score: 600.00 Matches: 111
Percent Similarity: 93.75% Conservative: 9
Best Local Similarity: 86.72% Mismatches: 8
Query Match: 88.76% Indels: 0
DB: Gaps: 13

US-10-019-455a-47 (1-128) x US-10-219-483-71 (1-521)
QY 1 MetAlaArgIleLeuIleLeuLeuGlyGlyLeuValAlaLeuCysAlaGlyHisGly 20
DB 38 ATGGCAAGATATTGTTACTTTCTCCCGGCTTGTGCTGTATGCTGTGCATGCA 97
QY 21 MetPheMetAspIleuSerSerIleuValLeuValAlaAspGluCysValTyrThr 40
DB 98 ATATTATGACCGCTTACCTCCAGAACCTCTGTGCATATATGATGTGCTTACT 157
QY 41 ILeSerIleuAlaArgAlaGlnIleuAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
DB 158 ATTCTCTGGCTAGCTGCTCAGAAAGATTATATGCCCGGACCTGATTCATTACGTT 217
QY 61 LysIleGlyGlnGlnIleTyrValTyrSerIleuValThrGluAsnGlyAlaGlyAla 80
DB 218 AAAAAGGCGACGACATCTATGTCTACTCAAGCTGTAAAGAAATGAGCTGAGAA 277
QY 81 PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
DB 278 TTTGGGCTGGCAGTGTATTATGTGGATGGCCAGACAGATGGAGCTGTGCTTATTTTC 337
QY 101 ProSerIleuValArgGlnIleuArgValTyrGlnGlnAlaThrIleuGlnIleProThr 120
DB 338 CCCAGAACTTGTCAAGGAACACCGCTGTATCCAGAAAGCTTACCAAGAAAGTTCCACC 397
QY 121 ThrAspIleAspPhePheCysGlu 128
DB 398 ACGGATATTGACTTCTTCTGCGAG 421

RESULT 13
US-10-219-525-71
; Sequence 71, Application US/10219525
; Publication No. US20030187211A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary

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Qy 41 lIeSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
Db 158 ATTTCTCTGGCTGACTGCTCAAGAGATTATATGCCCCGAGCTGATTCATTAAAGCTT 217
Qy 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyAla 80
Db 218 AAAAAGGCGCAGATCTATGCTGACTCAAGAGCTGTAAAGAAATGAGAGCTGGAGAA 277
Qy 81 PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
Db 278 TTTTGGCTGGCAGATGTTTATGAGATGGCCAGACGATGCGATGCGGTATTTC 337
Qy 101 ProSerAsnLeuValArgGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120
Db 338 CCCAGAACTTGCTCAAGAGACAGCGTGTACCAAGAGAGCTCAAGAAAGTTCCACACC 397
Qy 121 ThrAspIleAspPhePheCysGlu 128
Db 398 ACCGATTATGACTTCTTCCGAG 421

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RESULT 15

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US-10-219-530-71
; Sequence 71, Application US/10219530
; Publication No. US20030187213A1

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GENERAL INFORMATION:

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; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C54
; CURRENT APPLICATION NUMBER: US/10/219,530
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-530-71

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Alignment Scores:

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Pred. No.: 1,98e-83
Score: 600.00
Percent Similarity: 93.75%

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Length: 521
Matches: 111
Conservative: 9

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Best Local Similarity: 86.72%
Query Match: 88.76%
DB: 13
Gaps: 0

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US-10-019-455a-47 (1-128) x US-10-219-530-71 (1-521)

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Qy 1 MetAlaArgIleLeuIleLeuLeuGlyIleValAlaLeuCysAlaGlyIleVal 20
Db 38 ATGGCAAGATATGTTACTTTCTCCCGGATCTTGCGCTGATGCTGATGATGA 97
Qy 21 MetPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGlnCysValIleThr 40
Db 98 ATATTATGACCGCTTACTTCCCAAGAGCTCTGTGCAAGATGATGATGATGATGAT 157
Qy 41 lIeSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
Db 158 ATTTCTCTGGCTGACTGCTCAAGAGATTATATGCCCCGAGCTGATTCATTAAAGCTT 217
Qy 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyAla 80
Db 218 AAAAAGGCGCAGATCTATGCTGACTCAAGAGCTGTAAAGAAATGAGAGCTGGAGAA 277
Qy 81 PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
Db 278 TTTTGGCTGGCAGATGTTTATGAGATGGCCAGACGATGCGGTATTTC 337
Qy 101 ProSerAsnLeuValArgGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120
Db 338 CCCAGAACTTGCTCAAGAGACAGCGTGTACCAAGAGAGCTCAAGAAAGTTCCACACC 397
Qy 121 ThrAspIleAspPhePheCysGlu 128
Db 398 ACCGATTATGACTTCTTCCGAG 421

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Job time: 289.193 secs

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Tue Dec 30 10:20:49 2003

us-10-019-455a-47.rn1

Page 1

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 29, 2003, 16:24:24 ; Search time 40.6947 Seconds
(without alignments)
1388.315 Million cell updates/sec

Title: US-10-019-455A-47
Perfect score: 676
Sequence: 1 MARILLILGLVALCAGHG.....RVYQEAATKEIPTIDIFPCE 128

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 569978 segs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:
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-Q=/cg2_1/USPTO.spool/US10019455/runat_29122003.160348.277/app.query.fasta_1.1770
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=ini -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=BITS -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10019455 -CGN_1_1_142 -runat_29122003.160348.277 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOC
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database:

Issued Patents NA:
1: /cg2_6/prodata/2/ina/5A.COMB.seq:*
2: /cg2_6/prodata/2/ina/5B.COMB.seq:*
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6: /cg2_6/prodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 275.5 | 40.8 | 459 | 1 | US-08-578-649-1 |
| 2 | 264.5 | 39.1 | 330 | 1 | US-08-578-649-18 |
| 3 | 247 | 36.5 | 581 | 1 | US-08-578-649-4 |
| 4 | 222.5 | 32.9 | 305 | 1 | US-08-578-649-8 |
| 5 | 208 | 30.8 | 596 | 1 | US-08-578-649-24 |
| 6 | 171.5 | 25.4 | 3565 | 1 | US-08-578-649-3 |
| 7 | 93.5 | 13.8 | 2793 | 1 | US-07-646-5378-1 |
| 8 | 91.5 | 13.5 | 2757 | 1 | US-08-306-6918-48 |
| 9 | 91.5 | 13.5 | 2757 | 5 | PCT-US93-06251-79 |
| 10 | 85 | 12.6 | 467 | 4 | US-09-300-958A-30 |
| 11 | 85 | 12.6 | 467 | 4 | US-09-300-958A-28 |
| 12 | 82.5 | 12.2 | 5398 | 3 | US-09-356-952-11 |

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| 13 | 74 | 10.9 | 2085 | 1 | US-08-164-839-3 | Sequence 3, Appl1 |
| 14 | 74 | 10.9 | 2085 | 1 | US-08-583-799-3 | Sequence 3, Appl1 |
| 15 | 74 | 10.9 | 2520 | 1 | US-08-164-839-5 | Sequence 5, Appl1 |
| 16 | 74 | 10.9 | 2520 | 1 | US-08-583-799-5 | Sequence 5, Appl1 |
| 17 | 72 | 10.7 | 1664976 | 4 | US-08-916-4218-1 | Sequence 1, Appl1 |
| 18 | 71 | 10.5 | 2873 | 4 | US-08-630-915A-193 | Sequence 193, Appl1 |
| 19 | 69.5 | 10.3 | 1457 | 3 | US-09-444-053-3 | Sequence 3, Appl1 |
| 20 | 69 | 10.2 | 971 | 4 | US-08-630-915A-197 | Sequence 197, Appl1 |
| 21 | 69 | 10.2 | 1826 | 3 | US-09-286-691-11 | Sequence 11, Appl1 |
| 22 | 69 | 10.2 | 1826 | 3 | US-09-687-147-11 | Sequence 11, Appl1 |
| 23 | 67.5 | 10.0 | 3981 | 4 | US-09-328-352-760 | Sequence 760, Appl1 |
| 24 | 67.5 | 10.0 | 42931 | 4 | US-08-311-731A-129 | Sequence 129, Appl1 |
| 25 | 67 | 9.9 | 1664976 | 4 | US-08-916-4218-1 | Sequence 1, Appl1 |
| 26 | 66.5 | 9.8 | 2064 | 1 | US-08-164-839-30 | Sequence 30, Appl1 |
| 27 | 66.5 | 9.8 | 2064 | 1 | US-08-164-839-32 | Sequence 32, Appl1 |
| 28 | 66.5 | 9.8 | 2064 | 1 | US-08-583-799-32 | Sequence 32, Appl1 |
| 29 | 66.5 | 9.8 | 2064 | 1 | US-08-583-799-32 | Sequence 32, Appl1 |
| 30 | 66.5 | 9.8 | 2148 | 1 | US-08-164-839-69 | Sequence 69, Appl1 |
| 31 | 66.5 | 9.8 | 2148 | 1 | US-08-164-839-71 | Sequence 71, Appl1 |
| 32 | 66.5 | 9.8 | 2148 | 1 | US-08-583-799-69 | Sequence 69, Appl1 |
| 33 | 66.5 | 9.8 | 2148 | 1 | US-08-583-799-71 | Sequence 71, Appl1 |
| 34 | 66 | 9.8 | 840 | 1 | US-08-434-255-7 | Sequence 7, Appl1 |
| 35 | 66 | 9.8 | 840 | 1 | US-08-459-967-7 | Sequence 7, Appl1 |
| 36 | 66 | 9.8 | 840 | 1 | US-08-460-327-7 | Sequence 7, Appl1 |
| 37 | 66 | 9.8 | 840 | 1 | US-08-459-967-7 | Sequence 7, Appl1 |
| 38 | 66 | 9.8 | 840 | 3 | US-09-024-532-1 | Sequence 1, Appl1 |
| 39 | 66 | 9.8 | 840 | 4 | US-09-104-623A-1 | Sequence 1, Appl1 |
| 40 | 66 | 9.8 | 840 | 4 | US-09-019-532-1 | Sequence 1, Appl1 |
| 41 | 66 | 9.8 | 840 | 4 | US-09-417-359A-1 | Sequence 1, Appl1 |
| 42 | 66 | 9.8 | 1110 | 1 | US-08-434-255-5 | Sequence 5, Appl1 |
| 43 | 66 | 9.8 | 1110 | 1 | US-08-459-967-5 | Sequence 5, Appl1 |
| 44 | 66 | 9.8 | 1110 | 1 | US-08-460-327-5 | Sequence 5, Appl1 |
| 45 | 66 | 9.8 | 1110 | 1 | US-08-459-871-5 | Sequence 5, Appl1 |

ALIGNMENTS

RESULT 1
US-08-578-649-1
Sequence 1, Application US/08578649
Patent No. 5770366
GENERAL INFORMATION:
APPLICANT: Ulrich Bogdan
APPLICANT: Reinhard Buttner
APPLICANT: Brigitte Kaluza
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Felle & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578.649
CLASSIFICATION: 435
FILING DATE: 29-July-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-July-1993
ATTORNEY/AGENT INFORMATION:
NAME: Andrew L. Tiajolo
REGISTRATION NUMBER: 31,575
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3864


```

GENERAL INFORMATION:
APPLICANT: Ulrich Bogdan
APPLICANT: Reinhard Butner
APPLICANT: Brigitte Kaluza
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESS: Felle & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 MB storage diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-July-1993
ATTORNEY/AGENT INFORMATION:
NAME: Andrew L. Tiajoleff
REGISTRATION NUMBER: 31,575
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 581 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 110..499
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 110..178
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 179..499
US-08-578-649-4

Alignment Scores:
Pred. No.: 1,22e-25 Length: 581
Score: 247.00 Matches: 55
Percent Similarity: 60.16% Conservative: 22
Best Local Similarity: 42.97% Mismatches: 41
Query Match: 36.54% Indels: 10
DB: 1 Gaps: 4

US-10-019-455a-47 (1-128) x US-08-578-649-4 (1-581)
QY 8 LeuLeuGlyGlyLeuValAlaLeuCysAlaGlyHisGly-----MetPhe 22
DB 125 GTGCTCTGTCGATGCTGCTGCTGCTTTTTCAGGGCCTACAGGCTGATCGAGCT 184
QY 23 MetAspLysLeuSerSerLysLysLeuCysAlaAspGluGlyCysValTyrThrIleSer 42
DB 185 ATGCCCAAGCTGGCTGACTGGAAGCTGTGTGCGACGAGAAATCGACGACCTATCTCC 244
QY 43 LeuAlaAspAlaGlnGlnAspTyrAsnAlaProAspCysAspPheIleAsnValLysLys 62
DB 245 ATGGCTGTGGCCCTCCAGACTACGTGGCCCTGATTGCGCTTCTGACTATATATAGG 304
QY 63 GlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGly---AlaPhe 81

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DB 305 GGGCAAGTGTGATGCTCTCTCCAACTTG-----AAGGCGCGTGGCGCTTTTC 355
QY 82 TrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyLe-----ValGlyTyrPhe 100
DB 356 TGGGAGGCGAGTGTTCAGGAGGTTACTATAGAGACTGGGACGCCCGCTGGCTATTTC 415
QY 101 ProSerAsnLeuValArgGluGlnArgValTyrGlnGlnAlaThrLysGluIleProThr 120
DB 416 CCAGTAGCATTTGTCGGAGAGGACTTCAACTCGAAACCTGGCAAAATGATATAGAACCC 475
QY 121 ThrAspIleAspPhePheCysGlu 128
DB 476 GATCAATGGATTTCTACTGCCAG 499

RESULT 4
US-08-578-649-8
Sequence 8, Application US/08578649
Patent No. 5770366
GENERAL INFORMATION:
APPLICANT: Ulrich Bogdan
APPLICANT: Reinhard Butner
APPLICANT: Brigitte Kaluza
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESS: Felle & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 MB storage diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-July-1993
ATTORNEY/AGENT INFORMATION:
NAME: Andrew L. Tiajoleff
REGISTRATION NUMBER: 31,575
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 305 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: misc_RNA
LOCATION: join(1..29, 277..305)
OTHER INFORMATION: /function="Primer"
US-08-578-649-8

Alignment Scores:
Pred. No.: 1,37e-22 Length: 305
Score: 222.50 Matches: 45
Percent Similarity: 64.65% Conservative: 19
Best Local Similarity: 45.45% Mismatches: 30
Query Match: 32.91% Indels: 5
DB: 1 Gaps: 3

US-10-019-455a-47 (1-128) x US-08-578-649-8 (1-305)

```


QY 30 LysLeuGlyAlaAspGluGluCysValTyrThrIleSerLeuAlaArgAlaGluGluAsp 49
 DB 7 AAGTTTCGGCGGATCAGAGTGCAGCCCTATCTCCAGGCTGTGGCTTCAGGAC 66
 QY 50 TyrAsnAlaProAspCysArgPheIleAsnValLysGlyGlnGlnIleTyrValTyr 69
 DB 67 TACATGGCCCCGACTGCGATCTCTGACCAATCAGCGGCGCAAGTGTATGCTTC 126
 QY 70 SerLysLeuValThrGluAsnGlyAlaGly--AlaPheTPAlaGlySerValTyrGly 88
 DB 127 TCCAGGCTG-----AAGGCGCTGGCGGCGCTCTCTGGAGAGCAGCGTTCAAGGA 177
 QY 89 AspHisGln--AspGluMetGlyIleValGlyTyrPheProSerAsnLeuValArgGlu 107
 DB 178 GATTACTATGAGATCGTGTGCTGCTGCGCTATTTCCCGAGTACGATTGTCCGAGAG 237
 QY 108 GlnArgValTyrGlnGluAlaThrLysGluIleProThrAspIleAspPhe 126
 DB 238 GACCAAGCCCTGAAACCTGGCAAGTCATGTAAGACAGATAAATGGATTCTAC 294
 RESULT 5
 US-08-578-649-24
 ; Sequence 24, Application US/08578649
 ; Patent No. 5770366
 ; GENERAL INFORMATION:
 ; APPLICANT: Ulrich Bogdan
 ; APPLICANT: Reinhard Butner
 ; APPLICANT: Brigitte Kaluza
 ; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Felfe & Lynch
 ; STREET: 805 Third Avenue
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10022
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch 1.44 MB storage diskette
 ; COMPUTER: IBM PS/2
 ; OPERATING SYSTEM: PC-DOS
 ; SOFTWARE: WordPerfect
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/578,649
 ; FILING DATE: 29-July-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: DE P 43 24 247.2
 ; FILING DATE: 20-July-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Andrew L. Tiaoloff
 ; REGISTRATION NUMBER: 31,575
 ; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 688-9200
 ; TELEFAX: (212) 638-3884
 ; INFORMATION FOR SEQ ID NO: 24:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 596 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: join(40..111, 40..166, 214..347, 393..503, 549
 ; LOCATION: ..569)
 ; NAME/KEY: sig_peptide
 ; LOCATION: 40..111
 ; FEATURE:
 ; NAME/KEY: exon

; LOCATION: 40..166
 ; FEATURE:
 ; NAME/KEY: exon
 ; LOCATION: 214..347
 ; FEATURE:
 ; NAME/KEY: exon
 ; LOCATION: 393..503
 ; FEATURE:
 ; NAME/KEY: exon
 ; LOCATION: 549..569
 ; NAME/KEY: one-of(194, 369, 527)
 ; LOCATION: /note="N in positions 194, 369
 ; OTHER INFORMATION: and 527 denotes an indefinite number and sequence
 ; OTHER INFORMATION: of nucleotides "
 US-08-578-649-24
 Alignment Scores:
 Pred. No.: 3,94e-20 Length: 596
 Score: 208.00 Matches: 61
 Percent Similarity: 48.35% Conservative: 27
 Best Local Similarity: 33.52% Mismatches: 35
 Query Match: 30.77% Indels: 60
 DB: 1 Gaps: 10
 US-10-019-455a-47 (1-128) x US-08-578-649-24 (1-596)
 QY 1 MetAlaArgIleLeuIleLeuLeuGlyGlyLeuValAlaLeuCysAla-----Gly 18
 DB 40 ATGGCCCGGTCCTCGTG--TGCCTTGTCATCACTTCTGCTCTGCTTCCTCCGA 96
 QY 19 HisGlyMetPhe-----MetAspLysLeuSerSerLysLysLeuCysAlaAspGlu 35
 DB 97 CTTGGTTCAGAGGGGTGTCTCTATGCCAAGCTGCTACCGGAAGCTGTGCGACACAG 156
 QY 36 GluCysValTyr----- 39
 DB 157 GAGTGCAGCGG-TAAGATGGGAGGAGTAGAATTGGNCCCTTCTATCTCCCTAGAC 215
 QY 40 ThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsn 59
 DB 216 CCTATCTCAGTGGCTGTGGCCCTTCAGAGACTACATGCCCCCGACTGCGATTCCTGAC 275
 QY 60 ValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGly 79
 DB 276 ATTACCGGGGCGCAAGTGTGTATGTCTTCCAAAGCTG-----AAGGCGCGTGGG 326
 QY 80 --AlaPheTPAlaGlySer----- 85
 DB 327 CGGCTCTTCTGGGAGGAGCGCGTGGCTTGGAGAGTAAGAAAGCTTTAACTCTCTT 386
 QY 86 -----ValTyrGlyAspHisGlnAspGluMetGlyIle--ValGlyTyrPheProSer 102
 DB 389 CCCAGGTTCAAGGAGGATTAATGAGATGCTGCTCCCTGGGCTATTTCCCACT 446
 QY 103 AsnLeuValArgGluGlnAlaArgValTyrGlnGluAlaThrLysGluIleProThrAsp 122
 DB 447 AGCATTTCTCGAGAGACCAAGCCTGAAACCTGGCAAAAGTCGATGTG--AAGACGAC 503
 QY 123 Ile-----AspPhe 126
 DB 504 GTGAGTGTATGAGGGGCTGGCANTTCCCTTTCTTTTTCAGAAATGGGATTCTAC 563
 QY 127 CysGlu 128
 DB 564 TGCCAG 569
 RESULT 6
 US-08-578-649-3
 ; Sequence 3, Application US/08578649
 ; Patent No. 5770366
 ; GENERAL INFORMATION:

```

APPLICANT: Ulrich Bogdan
APPLICANT: Reinhard Buttner
APPLICANT: Brigitte Kaluza
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-July-1993
ATTORNEY/AGENT INFORMATION:
NAME: Andrew L. Tisjoleff
REGISTRATION NUMBER: 31,575
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3565 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: sig peptide
LOCATION: 1378..1449
FEATURE:
NAME/KEY: exon
LOCATION: 1378..1504
FEATURE:
NAME/KEY: exon
LOCATION: 1586..1719
FEATURE:
NAME/KEY: exon
LOCATION: 2804..2914
FEATURE:
NAME/KEY: exon
LOCATION: 3232..3252
OTHER INFORMATION: /note= "N in position 2216
denotes an indefinite number ans sequence of
nucleotides"
US-08-578-649-3

Alignment Scores:
Score: No.: 7,05e-14 Length: 3565
Pident: 171.50 Matches: 46
Percent Similarity: 51.26% Conservative: 15
Best Local Similarity: 38.66% Mismatches: 21
Query Match: 25.37% Indels: 37
DB: 1 Gaps: 6

US-10-019-455A-47 (1-128) x US-08-578-649-3 (1-3565)

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Db      1378 ATGACCCTGCCTCCTGTG---TGCCTTGGTGTATCATCTTCGCTGTGCCCTTCCGGA   1434
QY      19 HisGLyMetChe-----MetAspLysLeuSerSerLysLysLeuCySAIAspGlu   35
          |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      1435 CCGTGTCTCAAGGGGTGTCTCTATTGCCAAGACTGGCTACCCGAAAGCTGTGGCGCACAG   1494
QY      36 GLucS-----ValThrTrlLeSerLeuAlArGAlagInglu   48
          |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      1495 GAGTGCAGCCGTMAGAATGGGAGGGGTAGATTGGCTTGGTGTAGCCTGTGTGAT   1554
QY      38 -----ValThrTrlLeSerLeuAlArGAlagInglu   48
          ::|||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      1555 GTGCTGATTCCTCCCTTATCTTCCTTCCCTACACCTATCTTCATGAGCTGTGGCCTTCAG   1614
QY      49 AspPyrAsnAlAProAspCYSAISPhelIeasnValLysGIgIngluIleTyreVal   68
          |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      1615 GACTACATATGGCCCCGACTGCCGATCTCTGACCATTACCGGGGCGCAAGTGTGTATCTC   1674
QY      69 TyrSerLysLeuValThnGluAsnGIyAlaGly--AlaPheTPAlaGlySerVal   86
          ::|||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      1675 TTCCTCAAGCTG-----AAGGGCCGTGGGGCGGCTTCTGGGGAGCGACGCTG   1722

RESULT 7
US-07-646-537B-1
; Sequence 1, Application US/07646537B
; Patent No. 5348664
; GENERAL INFORMATION:
; APPLICANT: Barbacid, Mariano
; TITLE OF INVENTION: Vav Proto-Oncogene Protein
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESS: Bristol-Myers Squibb Company
; STREET: P.O. Box 4000
; CITY: Princeton
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 08543-4000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/646,537B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaul, Timothy J.
; REGISTRATION NUMBER: 33,111
; REFERENCE/DOCKET NUMBER: DC10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 921-5901
; TELEFAX: (609) 921-4526
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2793 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 14..2545
; US-07-646-537B-1

Alignment Scores:
Pred. No.:           0.00481
Score:               93.50
Percent Similarity:  52.86%
Best Local Similarity: 32.86%
Query Match:        13.83%
DB:                  1
Gaps:                3
Length:              2793
Matches:             23
Conservative:       14
Mismatch:            20
Indels:              13

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Db      2285 GACATCATC-----AGATCCTTACACAGAGGACAGACAGAGGCTGTGCGCA 2432
Qy      84 GlyservalTYrGlyaspHisgInaspGluMetGlyIleValGlyTYrPheProserAsn 103
Db      2433 GGGAGATCTATGTGCGCG-----GTGGCTGTGTTCCCTGCCCAAC 2471
Qy      104 LeuValArgGluGlnArgValTYrGlnGlu 113
Db      2472 TACGTGAGAGAGAT-----TATTCGAA 2495

RESULT 10
US-09-300-958A-30
; Sequence 30, Application US/09300958A
; Patent No. 6495319
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Trengle, Thomas
; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
; FILE REFERENCE: P-PH 3457
; CURRENT APPLICATION NUMBER: US/09/300,958A
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/083,331
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/098,070
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/118,624
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 4762
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-300-958A-30

Alignment Scores:
Pred. No.: 0.0197 Length: 4762
Score: 91.50 Matches: 22
Percent Similarity: 52.24% Conservative: 13
Best Local Similarity: 32.84% Mismatches: 21
Query Match: 13.54% Indels: 11
Gaps: 2

US-10-019-455A-47 (1-128) x US-09-300-958A-30 (1-4762)
Qy      41 IleserLeuAlaArgAlaGlnGluAspTYrAsnAlaProaspCyserGlyPheIleAsnVal 60
Db      2405 CTGGCGATTCCTGCTGCTGATGATCTTCTGCAAGAGATATGAGAGTGTGCTTG 2464
Qy      61 LysLysGlyGlnGlnIleTYrSerLysLeuValThrGluAsnGlyAlaGlyAla 80
Db      2465 TTGAAAGAGAGATGTGTGAAGATTACACAAAGATG-----AGTCAATATGCGC 2512
Qy      81 PheTIPAlaGlySerValTYrGlyaspHisgInaspGluMetGlyIleValGlyTYrPhe 100
Db      2513 TGGTGGAGAGAGAAAGTAATGCGAGG-----GTGGCTGTGTTT 2551
Qy      101 ProserAsnLeuValArgGlu 107
Db      2552 CCATCCACATATGTGGAAGAG 2572

RESULT 11
US-09-300-958A-28
; Sequence 28, Application US/09300958A
; Patent No. 6495319
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Trengle, Thomas
; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of

```

```

; FILE REFERENCE: P-PH 3457
; CURRENT APPLICATION NUMBER: US/09/300,958A
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/083,331
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/098,070
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/118,624
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 467
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (428)
; NAME/KEY: unsure
; LOCATION: (462)
US-09-300-958A-28

Alignment Scores:
Pred. No.: 0.00585 Length: 467
Score: 85.00 Matches: 24
Percent Similarity: 51.28% Conservative: 16
Best Local Similarity: 30.77% Mismatches: 26
Query Match: 12.57% Indels: 12
Gaps: 3

US-10-019-455A-47 (1-128) x US-09-300-958A-28 (1-467)
Qy      46 AlaGlnGluAspTYrAsnAlaProaspCyserGlyPheIleAsnValLysLysGlyGln 65
Db      152 GCTCGATGACCTTCTGTGCAAGAGATATGAGAGTGTGCTTGTGAAGAGATGTG 211
Qy      66 IleTYrValTYrSerLysLeuValThrGluAsnGlyAlaGlyAlaPheTIPAlaGlySer 85
Db      212 GTGAAGATTACACAAAGATG-----AGTCAATATGCTGTGAGAGAGAGAA 259
Qy      86 ValTYrGlyaspHisgInaspGluMetGlyIleValGlyTYrPheProserAsnLeuVal 105
Db      260 GTAATGCGAGG-----GTGGCTGTGTTCCATCAATATGTG 258
Qy      106 ArgGluGlnArgValTYrGlnGluAlaThrLysGluIleProThrThraPile 123
Db      299 ---GAAAGAGAGATGAATTAATCAAAATCCCGTTGCCACCCGACCAAAATT 349

RESULT 12
US-09-356-952-11
; Sequence 11, Application US/09356952
; Patent No. 611763
; GENERAL INFORMATION:
; APPLICANT: Borjack-Sjodin, Ann
; APPLICANT: Margalit, S. M.
; APPLICANT: Bor-Sogli, Dafna
; APPLICANT: Cole, Philip
; APPLICANT: Kurlyan, John
; TITLE OF INVENTION: A CRYSTAL OF A PAS-SOS COMPLEX AND METHODS OF USE
; FILE REFERENCE: THEREOF
; FILE REFERENCE: 600-1-228N
; CURRENT APPLICATION NUMBER: US/09/356,952
; PRIOR FILING DATE: 1998-07-19
; EARLIER APPLICATION NUMBER: 60/093,631
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 5398
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-356-952-11

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Alignment Scores:

Pred. No.: 0.438 Length: 5398
 Score: 82.50 Matches: 25
 Percent Similarity: 48.31% Conservative: 18
 Best Local Similarity: 28.09% Mismatches: 35
 Query Match: 12.20% Indels: 11
 Gaps: 4

US-10-019-455A-47 (1-128) x US-09-356-352-11 (1-5398)

QY 26 LeuSerSerLysLysLeuCysAlaAspGluGluGlyValThrIleSerLeuAlaArg 45
 DB 445 CTTCTCTTCCCTCCGACAGGTGACAGCAGATTGCGCATTCGATTAAGTATGAC 504
 QY 46 AlaGlnGluAspThrAsnAlaPro-----AspCysArgPheIleAsnVal 60
 DB 505 GCTGCTTATGACTTATTAATTCATCCATTAAAGACAGTCTTCGCACTTTGCTCTGA 564
 QY 61 LysLysGlyGlnGlnIleThrValThrSerLysLeuValThrGluAsnGlyAla 80
 DB 565 CAACAAGGGAACACATTATATACCTTAACAA-----AATCATCTGGG--- 609
 QY 81 PheThrAlaGlySerValThrGlyAspHisGlnAspGluMetGlyIleValGlyThrPhe 100
 DB 610 TGGTGGGATGAGATTAGTTATTGACGACAGTAATGGGAAGTTAAC--AGAGGCTGTTT 666
 QY 101 ProSerAsnLeuValArgGluGlnArg 109
 DB 667 CCTCAAACTCGGTAGACCTTAAGA 693

RESULT 13
 US-08-164-839-3
 ; Sequence 3, Application US/08164839

GENERAL INFORMATION:
 APPLICANT: YASUEDA, HISASHI
 APPLICANT: NAKANISHI, KAZUO
 APPLICANT: MOTOKI, MASAO
 APPLICANT: NAGASE, KAZUO
 APPLICANT: MATSUI, HIROSHI
 TITLE OF INVENTION: GENE ENCODING TRANSGUTAMINASE DERIVED
 TITLE OF INVENTION: FROM FISH
 NUMBER OF SEQUENCES: 72
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
 STREET: 1755 Jefferson Davis Highway, Fourth Floor
 CITY: Arlington
 STATE: Virginia
 COUNTRY: U.S.A.
 ZIP: 22202

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/164,839
 FILING DATE:
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/004,729
 FILING DATE: 14-JAN-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Oblon, No. 5514573man F.
 REGISTRATION NUMBER: 24,618
 REFERENCE/DOCKET NUMBER: 10-599-0
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703)412-3000
 TELEFAX: (703)413-2220
 TELEX: 248855 OPAT UR
 INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 2085 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 ORIGINAL SOURCE:
 ORGANISM: Pagrus major
 TISSUE TYPE: liver

FEATURE:

NAME/KEY: CDS
 LOCATION: 1..2082

US-08-164-839-3

Alignment Scores:
 Pred. No.: 1.76 Length: 2085
 Score: 74.00 Matches: 21
 Percent Similarity: 52.50% Conservative: 21
 Best Local Similarity: 26.25% Mismatches: 28
 Query Match: 10.95% Indels: 10
 Gaps: 3

US-10-019-455A-47 (1-128) x US-08-164-839-3 (1-2085)

QY 49 AspThrAsnAlaProAspCysArgPheIleAsnValLysGlyGlnGlnIleThrVal 68
 DB 1174 GAGGTGAACGCTGACACCATCTACTGATCTCTCCAAAAGATGGCCAAACGA----- 1224
 QY 69 ThrSerLysLeuValThrGluAsnGlyAla-----PheThrAlaGlySer 85
 DB 1225 -----CGAAGATCAGACAGACCATCTAGTGGGGAACATCAGCAAAAGGC 1278
 QY 86 ValThrGlyAspHisGlnAspGluMetGlyIleValGlyThrProSerAsnLeuVal 105
 DB 1279 GTTACGGCAACACAGAGAGATGTCACTCTGCACTCAATAATCTCGAAGCTCCAG 1338
 QY 106 ArgGluGlnArgValThrGlnGluAlaThrLysGluIle-----ProThrAspIle 123
 DB 1339 AAGGAGAGGGAAGGTGACAAAGAGCGGAGCGCGGTACAGAGCATCCAAAGAGATC 1398

RESULT 14
 US-08-583-799-3
 ; Sequence 3, Application US/08583799

GENERAL INFORMATION:
 APPLICANT: YASUEDA, HISASHI
 APPLICANT: NAKANISHI, KAZUO
 APPLICANT: MOTOKI, MASAO
 APPLICANT: NAGASE, KAZUO
 APPLICANT: MATSUI, HIROSHI
 TITLE OF INVENTION: GENE ENCODING TRANSGUTAMINASE DERIVED
 TITLE OF INVENTION: FROM FISH
 NUMBER OF SEQUENCES: 72
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
 STREET: 1755 Jefferson Davis Highway, Fourth Floor
 CITY: Arlington
 STATE: Virginia
 COUNTRY: U.S.A.
 ZIP: 22202

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/583,799
 FILING DATE:
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/004,729
 FILING DATE: 14-JAN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Obion, No. 5607849man F.
 REGISTRATION NUMBER: 24,618
 REFERENCE/DOCKET NUMBER: 10-599-0
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703)412-3000
 TELEFAX: (703)413-2220

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
 LENGTH: 2085 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 ORIGINAL SOURCE:
 ORGANISM: Pagrus major
 TISSUE TYPE: liver

FEATURE:

NAME/KEY: CDS
 LOCATION: 1..2082
 US-08-583-799-3

Alignment Scores:

| Pred. No.: | Length: | Matches: | Conservative: | Mismatches: | Indels: | Gaps: |
|------------------------|---------|----------|---------------|-------------|---------|-------|
| Score: | 1.76 | 2085 | 21 | 28 | 10 | 3 |
| Percent Similarity: | 74.00 | | | | | |
| Best Local Similarity: | 52.50% | | | | | |
| Query Match: | 10.95% | | | | | |

US-10-019-455a-47 (1-128) x US-08-583-799-3 (1-2085)

QY 49 AspTYrAsnAlaProAspCysArgPheIleAsnValIysLysGlyGlnGlnIleTyVal 68
 DB 1174 GAGGTGAACGCTGACACCATCTGATCGTCCAAAAGATGCCAACA----- 1224
 QY 69 TyrSerLysLeuValThrGluAsnGlyAlaGlyAla-----PheTrpAlaGlySer 85
 DB 1225 -----CGGAAGATCACAGAGACCATGCTAGTGTGGGAGAGACATCAGCAAAAAGC 1278
 QY 86 ValTYrGlyAspHisGlnAspGluMetGlyIleValGlyTyrrPheProSerAsnLeuVal 105
 DB 1279 GTTACGGCAACCAACAGAGATGCTACTGCTGCACTCAAAATATCTGAGGCTCCAG 1338
 QY 106 ArgGluGlnArgValTYrGlnGlnIleAlaThrLysGlnIle-----ProThrThrAspIle 123
 DB 1339 AAGGAGAGGAAGTGTACAGAAGAGCGGAGCGCGGTCTACAGAGCCATCCAAAGAGATC 1398

RESULT 15
 US-08-164-839-5
 Sequence 5, Application US/08164839

Patent No. 5514573
 GENERAL INFORMATION:
 APPLICANT: YASUEDA, HISASHI
 APPLICANT: YAMAMOTO, KAZUO
 APPLICANT: MOTOKI, MASAO
 APPLICANT: NAGASE, KAZUO
 APPLICANT: MATSUI, HIROSHI
 TITLE OF INVENTION: GENE ENCODING TRANSGUTAMINASE DERIVED FROM FISH
 NUMBER OF SEQUENCES: 72
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
 ADDRESSEE: P.C.
 STREET: 1755 Jefferson Davis Highway, Fourth Floor
 CITY: Arlington
 STATE: Virginia
 COUNTRY: U.S.A.
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/164,839

FILING DATE:

CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/004,729

FILING DATE:

ATTORNEY/AGENT INFORMATION:
 NAME: Obion, No. 5514573man F.
 REGISTRATION NUMBER: 24,618
 REFERENCE/DOCKET NUMBER: 10-599-0
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703)412-3000
 TELEFAX: (703)413-2220

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
 LENGTH: 2520 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 ORIGINAL SOURCE:
 ORGANISM: Pagrus major
 TISSUE TYPE: liver

FEATURE:

NAME/KEY: CDS
 LOCATION: 34..2121
 US-08-164-839-5

Alignment Scores:

| Pred. No.: | Length: | Matches: | Conservative: | Mismatches: | Indels: | Gaps: |
|------------------------|---------|----------|---------------|-------------|---------|-------|
| Score: | 2.31 | 2520 | 21 | 28 | 10 | 3 |
| Percent Similarity: | 74.00 | | | | | |
| Best Local Similarity: | 52.50% | | | | | |
| Query Match: | 26.25% | | | | | |

US-10-019-455a-47 (1-128) x US-08-164-839-5 (1-2520)

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 DB 1210 GAGGTGAACGCTGACACCATCTGATCGTCCAAAAGATGCCAACA----- 1260
 QY 69 TyrSerLysLeuValThrGluAsnGlyAlaGlyAla-----PheTrpAlaGlySer 85
 DB 1261 -----CGGAAGATCACAGAGACCATGCTAGTGTGGGAGAGACATCAGCAAAAAGC 1314
 QY 86 ValTYrGlyAspHisGlnAspGluMetGlyIleValGlyTyrrPheProSerAsnLeuVal 105
 DB 1315 GTTACGGCAACCAACAGAGATGCTACTGCTGCACTCAAAATATCTGAGGCTCCAG 1374
 QY 106 ArgGluGlnArgValTYrGlnGlnIleAlaThrLysGlnIle-----ProThrThrAspIle 123
 DB 1375 AAGGAGAGGAAGTGTACAGAAGAGCGGAGCGCGGTCTACAGAGCCATCCAAAGAGATC 1434

Search completed: December 29, 2003, 22:08:14
 Job time: 46.6947 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 22:08:26, Search time 1045 Seconds
(without alignments) 12918.830 Million cell updates/sec

Title: US-10-019-455A-48

Sequence: 1 catggcagcttcatgataa.....atattgactctctctgtgaa 330

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: GenEmbl:*

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- 3: gb_in:*
- 4: gb_om:*
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- 41: em_hcgo_oth:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 330 | 100.0 | 330 | 6 | BD010836 Novel pol |
| 2 | 330 | 100.0 | 330 | 6 | BD093137 Novel pol |
| 3 | 330 | 100.0 | 384 | 6 | BD010835 Novel pol |
| 4 | 330 | 100.0 | 384 | 6 | BD093136 Novel pol |
| 5 | 294.8 | 89.3 | 330 | 6 | BD010817 Novel pol |
| 6 | 294.8 | 89.3 | 330 | 6 | BD093118 Novel pol |
| 7 | 294.8 | 89.3 | 384 | 6 | BD010805 Novel pol |
| 8 | 294.8 | 89.3 | 384 | 6 | BD093106 Novel pol |
| 9 | 294.8 | 89.3 | 929 | 10 | AF243504 Mus muscu |
| 10 | 294.8 | 89.3 | 947 | 6 | BD093122 Novel pol |
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| 17 | 261 | 79.1 | 261 | 6 | BD093130 Novel pol |
| 18 | 249 | 75.5 | 330 | 6 | BD010816 Novel pol |
| 19 | 249 | 75.5 | 330 | 6 | BD093117 Novel pol |
| 20 | 249 | 75.5 | 384 | 6 | BD010802 Novel pol |
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| 23 | 249 | 75.5 | 521 | 6 | AX362311 Sequence |
| 24 | 249 | 75.5 | 521 | 6 | AX454774 Sequence |
| 25 | 249 | 75.5 | 521 | 6 | AX491252 Sequence |
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| 27 | 249 | 75.5 | 865 | 9 | AF243505 Homo sapi |
| 28 | 249 | 75.5 | 923 | 6 | BD010820 Novel pol |
| 29 | 249 | 75.5 | 923 | 6 | BD093121 Novel pol |
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| 31 | 181.2 | 54.9 | 484 | 5 | AF233518 Gallus ga |
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| 33 | 130.8 | 39.6 | 466 | 5 | AF233519 Rana cete |
| 34 | 126.4 | 38.3 | 144765 | 2 | BX510362 Mus muscu |
| 35 | 111.6 | 33.8 | 232 | 9 | HS242525 Homo sapi |
| 36 | 111.6 | 33.8 | 121151 | 9 | HS705016 Human DNA |
| 37 | 80.2 | 24.3 | 259 | 9 | HS252326 Homo sapi |
| 38 | 71.8 | 21.8 | 545 | 10 | RNU67884 Rattus norv |
| 39 | 64 | 19.4 | 580 | 10 | MMU1A Mus muscu |
| 40 | 64 | 19.4 | 581 | 6 | A42945 Sequence 4 |
| 41 | 63.4 | 19.2 | 581 | 6 | AX016788 Sequence |
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| 44 | 63.4 | 19.2 | 433 | 6 | AX253435 Sequence |
| 45 | 63.4 | 19.2 | 459 | 6 | A42942 Sequence 1 |

ALIGNMENTS

RESULT 1
BD010836 330 bp DNA linear PAT 31-JAN-2002
LOCUS Novel polypeptide and DNA thereof.
DEFINITION
ACCESSION BD010836
VERSION BD010836.1 GI:18639209
KEYWORDS JP 2001069994-A/37.
SOURCE
ORGANISM Rattus sp.
Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
1 (bases 1 to 330)
Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
Yoshimura, K. and Tanaka, H.

TITLE Novel polypeptide and DNA thereof
JOURNAL Patent: JP 2001069994-A 37 21-MAR-2001;
TAKEDA CHEMICAL INDUSTRIES LTD
OS Rattus sp. (rat)
COMMENT PN UP 2001069994-A/37
PD 21-MAR-2001
PF 29-JUN-2000 JP 2000195911
PR YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI
SHINICHI MOGI,
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC
A61P19/08,
PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC
G01N33/53//
PC C12P21/08, C12N15/00, A61K37/02, C12N5/00

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/organism="Rattus sp."
/mol_type="genomic DNA"
/db_xref="taxon:10118"
Location/Qualifiers
FH source 1. .330
FT /organism="Rattus sp. (rat)"
Location/Qualifiers

BASE COUNT 91 a 62 c 91 g 86 t

Query Match 100.0%; Score 330; DB 6; Length 330;
Best Local Similarity 100.0%; Pred. No. 2,4e-94;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATGGCATGTTTATGATTAACCTTCTCTAAGAGTTGTGTGCAGATGAGAGTGTTC 60
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QY 61 TATACCATTTCTCTGGCAAGACACAGAGAGACTACATGCCCCGGAGCTGTGATTC 120
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QY 301 CCAACCAAGGATATTGACTTCTTCTGTGAA 330
DB 301 CCAACCAAGGATATTGACTTCTTCTGTGAA 330

RESULT 2
BD093137 330 bp DNA linear PAT 27-AUG-2002
LOCUS Novel polypeptide and its DNA.
DEFINITION BD093137
ACCESSION BD093137.1 GI:22638725
VERSION WO 0102564-A/37.
KEYWORDS Rattus sp.
SOURCE Rattus sp.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 330)
REFERENCE Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
Yoshimura, K. and Tanaka, H.
TITLE Novel polypeptide and DNA thereof
JOURNAL Patent: JP 2001069994-A 36 21-MAR-2001;

JOURNAL Patent: WO 0102564-A 37 11-JAN-2001;
TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO
OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,
HIDEYUKI TANAKA
COMMENT OS Rattus sp. (rat)
PN WO 0102564-A/37
PD 11-JAN-2001
PF 29-JUN-2000 WO 2000JP004278
PR 30-JUN-1999 JP 99P 186718
PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI
MOGI,
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/12, C12N5/10, C12P21/02, C07K14/47, C07K16/18, A61K45/00, PC
A61K38/17,
PC A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/7088// (C12P21/
PC 02, C12R1:19)

FEATURES
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/organism="Rattus sp."
/mol_type="genomic DNA"
/db_xref="taxon:10118"
Location/Qualifiers
FH key Location/Qualifiers

BASE COUNT 91 a 62 c 91 g 86 t

Query Match 100.0%; Score 330; DB 6; Length 330;
Best Local Similarity 100.0%; Pred. No. 2,4e-94;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATGGCATGTTTATGATTAACCTTCTCTAAGAGTTGTGTGCAGATGAGAGTGTTC 60
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QY 61 TATACCATTTCTCTGGCAAGACACAGAGAGACTACATGCCCCGGAGCTGTGATTC 120
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DB 301 CCAACCAAGGATATTGACTTCTTCTGTGAA 330

RESULT 3
BD010835 384 bp DNA linear PAT 31-JAN-2002
LOCUS Novel polypeptide and DNA thereof.
DEFINITION BD010835
ACCESSION BD010835.1 GI:18639208
VERSION UP 2001069994-A/36.
KEYWORDS Rattus sp.
SOURCE Rattus sp.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 384)
REFERENCE Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
Yoshimura, K. and Tanaka, H.
TITLE Novel polypeptide and DNA thereof
JOURNAL Patent: JP 2001069994-A 36 21-MAR-2001;

COMMENT
TAKEDA CHEMICAL INDUSTRIES LTD
OS Rattus sp. (rat)
PN JP 2001069994-A/36
PD 21-MAR-2001
PF 29-JUN-2000 JP 2000195911
PR YASUOKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI

SHINICHI MOGI,
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC
A61P19/08,
PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC
G01N33/53//
PC C12P21/08, C12N15/00, A61K37/02, C12N5/00
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FH Key Location/Qualifiers
FT source 1..384
/organism="Rattus sp. (rat)"
Location/Qualifiers

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ORIGIN

Query Match 100.0%; Score 330; DB 6; Length 384;
Best Local Similarity 100.0%; Pred. No. 2.5e-94;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 355 CCAACCGAGATATTGACTTTCTGTGAA 384

RESULT 4
BD093136 384 bp DNA linear PAT 27-AUG-2002

LOCUS BD093136
DEFINITION Novel polypeptide and its DNA.
ACCESSION BD093136.1 GI:22638724
VERSION BD093136.1
KEYWORDS WO 0102564-A/36.
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE
AUTHORS Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
Yoshimura, K. and Tanaka, H.
TITLE Novel polypeptide and its DNA
JOURNAL Patent: JP 2001069994-A 36 11-JAN-2001;
TAKEDA CHEMICAL INDUSTRIES LTD, YASUOKI ITO, KAZUNORI NISHI, KAZUHIRO

COMMENT
OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,
HIDEYUKI TANAKA
OS Rattus sp. (rat)
PN WO 0102564-A/36
PD 11-JAN-2001
PF 29-JUN-2000 WO 2000JP004278
PR 30-JUN-1999 JP 99P 186718
PI YASUOKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI

MOGI,
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/12, C12N5/10, C12P21/02, C07K14/47, C07K16/18, A61K45/00, PC
A61K38/17,
PC A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/7088// (C12P21/
PC 02, C12R1:19)
CC
FH Key Location/Qualifiers
FT source 1..384
/organism="Rattus sp."
/mol_type="genomic DNA"
/db_xref="taxon:10118"

BASE COUNT 98 a 72 c 109 g 105 t
ORIGIN

Query Match 100.0%; Score 330; DB 6; Length 384;
Best Local Similarity 100.0%; Pred. No. 2.5e-94;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATGGCATGTTTATGATTAACCTTTCTTTAAGAACTTGTGTGACATGAGAGAGTGTGTC 60
DB 55 CATGGCATGTTTATGATTAACCTTTCTTTAAGAACTTGTGTGACATGAGAGAGTGTGTC 114
QY 61 TATACCATTTCTGTGCAAGAGACAGAAAGACTAATGCCCCGAGTGTAGTTCATC 120
DB 115 TATACCATTTCTGTGCAAGAGACAGAAAGACTAATGCCCCGAGTGTAGTTCATC 174
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DB 355 CCAACCGAGATATTGACTTTCTGTGAA 384

RESULT 5
BD010817 330 bp DNA linear PAT 31-JAN-2002

LOCUS BD010817
DEFINITION Novel polypeptide and DNA thereof.
ACCESSION BD010817
VERSION BD010817.1 GI:18639190
KEYWORDS JP 2001069994-A/18.
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
Yoshimura, K. and Tanaka, H.
TITLE Novel polypeptide and DNA thereof
JOURNAL Patent: JP 2001069994-A 18 21-MAR-2001;
TAKEDA CHEMICAL INDUSTRIES LTD
OS Mus sp. (mouse)
PN JP 2001069994-A/18

PD 21-MAR-2001
 PF 29-JUN-2000 JP 2000195911
 PR YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI
 SHINICHI MOGI,
 YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
 PI C12N15/09, A61K38/00, A61K45/00, A61P9/00, A61P19/02, PC
 A61P19/08
 PC C07K16/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC
 G01N33/53//
 PC C12P21/08, C12N15/00, A61K31/02, C12N5/00
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 FH Key Location/Qualifiers
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 FT /organism="Mus sp. (mouse)"
 FT Location/Qualifiers
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 /db_xref="taxon:10095"

BASE COUNT 91 a 60 c 92 g 87 t
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 Query Match 89.3%; Score 294.8; DB 6; Length 330;
 Best Local Similarity 93.3%; Pred. No. 4.6e-83;
 Matches 308; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

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 QY 181 GGGGCAATTCGGGCTGGCAGTGTGTTATGTTGACCCACAGATGATGATGATGATGATG 240
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 DB 301 CCAACCAAGATATTGACTTCTTCTGTGAA 330

RESULT 6
 BD093118 330 bp DNA linear PAT 27-AUG-2002
 LOCUS
 DEFINITION Novel polypeptide and its DNA.
 ACCESSION BD093118
 VERSION BD093118.1 GI:22638706
 KEYWORDS WO 0102564-A/18.
 SOURCE Mus sp.
 ORGANISM Mus sp.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
 Yoshimura, K. and Tanaka, H.
 TITLE Novel polypeptide and its DNA
 JOURNAL Patent: WO 0102564-A 18 11-JAN-2001;
 TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO
 OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,
 HIDEYUKI TANAKA
 COMMENT OS Mus sp. (mouse)
 PN WO 0102564-A/18

PD 11-JAN-2001
 PF 29-JUN-2000 WO 2000P004278
 PR 30-JUN-1999 JP 99P 186718
 PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI
 MOGI,
 YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
 PI C12N15/12, C12N15/10, C12P21/02, C07K16/47, C07K16/18, A61K45/00, PC
 A61K38/17,
 PC A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/70808// (C12P21/
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 Best Local Similarity 93.3%; Pred. No. 4.6e-83;
 Matches 308; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

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 DB 121 GATGTCAGAAAGGCGACAGATCTATGTTTATTCAGAGCTGTGTAAACAGAAATGAGACT 180
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 DB 241 TATTTCCCGAGCAACTTGTGTGAAGGACGCGTGTATACCGAGAGGCCACCAAGAGATC 300
 QY 301 CCAACCAAGATATTGACTTCTTCTGTGAA 330
 DB 301 CCAACCAAGATATTGACTTCTTCTGTGAA 330

RESULT 7
 BD010805 384 bp DNA linear PAT 31-JAN-2002
 LOCUS
 DEFINITION Novel polypeptide and DNA thereof.
 ACCESSION BD010805
 VERSION BD010805.1 GI:18639178
 KEYWORDS JP 2001069994-A/6.
 SOURCE Mus sp.
 ORGANISM Mus sp.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
 Yoshimura, K. and Tanaka, H.
 TITLE Novel polypeptide and DNA thereof
 JOURNAL Patent: JP 2001069994-A 6 21-MAR-2001;
 TAKEDA CHEMICAL INDUSTRIES LTD
 COMMENT OS Mus sp. (mouse)
 PN JP 2001069994-A/6
 PD 21-MAR-2001
 PF 29-JUN-2000 JP 2000195911
 PR YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI

SHINICHI MOGI,
 PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
 PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P19/00, A61P19/02, PC
 A61P19/08,
 PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC
 G01N33/53//
 PC C12P21/08, C12N15/00, A61K37/02, C12N5/00
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 FT source 1..384
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 Matches 308; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

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 DB 115 TATACATTTCTCTGGCAAGACAGAGATTAACATGCCCCGAGATGAGTGTGTC 174
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 QY 301 CCAACCAAGGATATGATCTTCTGTGAA 330
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 DB 355 CCAACCAAGGATATGATCTTCTGTGAA 384
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RESULT 8
 LOCUS BD093106 384 bp DNA linear PAT 27-AUG-2002
 DEFINITION Novel polypeptide and its DNA.
 ACCESSION BD093106
 VERSION BD093106.1 GI:22638694
 KEYWORDS WO 0102564-A/6.
 SOURCE Mus sp.
 ORGANISM Mus sp.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 384)
 Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
 Yoshimura, K. and Tanaka, H.
 Novel polypeptide and its DNA
 Patent: WO 0102564-A 6 11-JAN-2001;
 TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO
 OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,
 HIDEYUKI TANAKA
 COMMENT
 OS Mus sp. (mouse)
 PN WO 0102564-A/6
 PD 11-JAN-2001
 PF 29-JUN-2000 WO 2000JP004278
 PR 30-JUN-1999 JP 99P 186718
 PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI

PI MOGI,
 PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
 PC C12N15/12, C12N15/10, C12P21/02, C07K14/47, C07K16/18, A61K45/00, PC
 A61K38/17,
 PC A61K39/139, A61K49/16, A61P19/02, A61P19/08, A61K31/0088// (C12P21/
 02, C12N1.19)
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BASE COUNT 98 a 68 c 111 g 107 t
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Query Match 89.3%; Score 294.8; DB 6; Length 384;
 Best Local Similarity 93.3%; Pred. No. 4,7e-83;
 Matches 308; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 CATGGCATGTTATGATTAACCTTCTCTAAGAGTTGTGTGCAGATGAGAGTGTGTC 60
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 QY 61 TATACATTTCTCTGGCAAGACAGAGATTAACATGCCCCGAGATGAGTGTGTC 120
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 QY 241 TATTTCCCGAGCACTTGTGTTAGAGCAACAGATGAGATGAGATGAGTGTGCT 300
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 QY 301 CCAACCAAGGATATGATCTTCTGTGAA 330
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 LO 355 CCAACCAAGGATATGATCTTCTGTGAA 384
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RESULT 9
 LOCUS AF243504 929 bp mRNA linear ROD 26-DEC-2000
 DEFINITION Mus musculus fibrocyte-derived protein (Fdp) mRNA, complete cds.
 ACCESSION AF243504
 VERSION AF243504.1 GI:11991841
 KEYWORDS
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 929)
 Cohen-Salmon, M., Frenz, D., Liu, W., Verpy, E., Voegelting, S. and
 Petit, C.
 Fdp, a new fibrocyte-derived protein related to MIA/CD-RAP, has an
 in vitro effect on the early differentiation of the inner ear
 mesenchyme

JOURNAL J. Biol. Chem. 275 (51), 40036-40041 (2000)

MEELINE 20568254
 PUBMED 10998416

2 (bases 1 to 929)
 Cohen-Salmon, M., Frenz, D., Verpy, E., Voegelting, S. and Petit, C.

Direct Submission
 Submitted (09-MAR-2000) Biotechnologies, Institut Pasteur, 25 rue

JOURNAL

du Dr. Roux, Paris 75015, France

FEATURES
 source location/Qualifiers
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NLVEORVYOEAETKEIPTDIDFCE"
BASE COUNT      260 a      156 c      220 g      293 t
ORIGIN
Query Match      89.3%; Score 294.8; DB 10; Length 929;
Best Local Similarity 93.3%; Pred. No. 4.8e-83;
Matches 308; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 CATGGCATGTTTATGATTAACCTTCTCTAAGAAGTTGTGCGAGTGAAGAGTGTGTC 60
DB 63 CATGGTATTTATGATTAACCTTCTCTAAGAAGTTGTGCGAGTGAAGAGTGTGTC 122
QY 61 TATACCATTTCTCTGCAAGAGCAGACAGAGTCAATGCCCCGAGCTGAGTTTATC 120
DB 123 TATACTATTTCTCTGCAAGAGCAGACAGAGTCAATGCCCCGAGCTGAGTTTATC 182
QY 121 AATGTCAAGAAAGGAGCAGATCTATGTTTATTCCAAAGCTGTGTAAAGAAATGAGACT 180
DB 183 GATGTCAAGAAAGGAGCAGATCTATGTTTATTCCAAAGCTGTGTAAAGAAATGAGACT 242
QY 181 GGGGCAATTTGGGCTGGAGTGTGTTATGTTAGTGCACCAAGATGAGATGGGAATTGTGGGT 240
DB 243 GGAGAGTTTGGGCTGGAGTGTGTTATGTTAGTGCACCAAGATGAGATGGGAATTGTGGGT 302
QY 241 TATTTCCCGAGCAACTTGTGTTAGAGCAGACAGTGTATCCAGAGGCCACCAAGAGATT 300
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QY 301 CCAACCAAGATATTGACTTCTTGTGAA 330
DB 363 CCAACCAAGATATTGACTTCTTGTGAA 392

RESULT 10
BD010821      947 bp      DNA      linear      PAT 31-JUN-2002
LOCUS
DEFINITION
Novel polypeptide and DNA thereof.
ACCESSION
BD010821.1 GI:18639194
VERSION
JP 2001069994-A/22.
KEYWORDS
Mus sp.
SOURCE
Mus sp.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 947)
Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
Yoshimura, K. and Tanaka, H.
Novel polypeptide and DNA thereof
Patent: JP 2001069994-A 22 21-MAR-2001;
TAKEDA CHEMICAL INDUSTRIES LTD
COMMENT
OS Mus sp. (mouse)
PN JP 2001069994-A/22
PD 21-MAR-2001
PE 29-JUN-2000 JP 2000195911
PR YASUOKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI
SHINICHI MOGI,
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA

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PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC
A61P19/08
PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC
G01N33/53//
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Location/Qualifiers
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BASE COUNT      279 a      158 c      221 g      289 t
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Query Match      89.3%; Score 294.8; DB 6; Length 947;
Best Local Similarity 93.3%; Pred. No. 4.8e-83;
Matches 308; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 CATGGCATGTTTATGATTAACCTTCTCTAAGAAGTTGTGCGAGTGAAGAGTGTGTC 60
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DB 183 GATGTCAAGAAAGGAGCAGATCTATGTTTATTCCAAAGCTGTGTAAAGAAATGAGACT 244
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DB 305 TATTTCCCGAGCAACTTGTGTTAGAGCAGACAGTGTATCCAGAGGCCACCAAGAGATT 364
QY 301 CCAACCAAGATATTGACTTCTTGTGAA 330
DB 365 CCAACCAAGATATTGACTTCTTGTGAA 394

RESULT 11
BD093122      947 bp      DNA      linear      PAT 27-AUG-2002
LOCUS
DEFINITION
Novel polypeptide and its DNA.
ACCESSION
BD093122.1 GI:22638710
VERSION
WO 0102564-A/22.
KEYWORDS
Mus sp.
SOURCE
Mus sp.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 947)
Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
Yoshimura, K. and Tanaka, H.
Novel polypeptide and its DNA
Patent: WO 0102564-A 22 11-JAN-2001;
TAKEDA CHEMICAL INDUSTRIES LTD, YASUOKI ITO, KAZUNORI NISHI, KAZUHIRO
OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,
HIDEYUKI TANAKA
COMMENT
OS Mus sp. (mouse)
PN WO 0102564-A/22
PD 11-JAN-2001
PE 30-JUN-2000 WO 2000JP004278
PR 30-JUN-1999 JP 99P 186718
PI YASUOKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI
MOGI,
PI MOGI,

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PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/12, C12N5/10, C12P21/02, C07K14/47, C07K16/19, A61K45/00, PC
A61K38/17
PC A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/7088//C12P21/
PC 02, C12R1:19)
CC
PC
FH Key Location/Qualifiers.

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BASE COUNT 279 a 158 c 221 g 289 t

ORIGIN

Query Match 89.3%; Score 294.8; DB 6; Length 947;
Best Local Similarity 93.3%; Pred. No. 4.8e-93; Indels 0; Gaps 0;
Matches 308; Conservative 0; Mismatches 22;

QY 1 CATGGCATGTTATGATTAACCTTCTCTAGAGAGTGTGTGAGATGAGAGTGTGTC 60
DB 65 CATGGTATTTATGATTAACCTTCTCTAGAGAGTGTGTGAGATGAGAGTGTGTC 124
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DB 125 TATACCATTTCTGCGAAGACACAGAGAGATCAATGCCCCGACTGTAGTTCATC 184
QY 121 AATGTCAAGAAAGGCGACAGATCTATGTTTATTCAGAGCTGTGTACAGAAATGAGACT 180
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QY 301 CCAACCCAGGATATTGACTTCTTCTGTGAA 330
DB 365 CCAACCCAGGATATTGACTTCTTCTGTGAA 394

RESULT 12
MM1243939 958 bp mRNA linear ROD 29-JAN-2001
LOCUS Mus musculus mRNA for melanoma inhibitory activity-like protein
DEFINITION (M1al gene).
ACCESSION AJ243939
VERSION AJ243939.1 GI:12619174
KEYWORDS melanoma inhibitory activity-like protein; M1al gene.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 Rendtorff, N.D., Frodin, M., Attie-Bitach, T., Vekemans, M. and
Timmerup, N.
Identification and characterization of an inner ear-expressed human
melanoma inhibitory activity (M1A)-like gene (M1AL) with a frequent
polymorphism that abolishes translation
Genomics 71 (1), 40-52 (2001)

JOURNAL
MEDLINE 21100875
PUBMED 11161796
REFERENCE 2 (bases 1 to 958)
AUTHORS Rendtorff, N.D.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-1999) Rendtorff N.D., Department of Medical
Genetics, Institute of Medical Biochemistry and Genetics,
Blegdamsvej 3, 2200 Copenhagen N, DENMARK
COMMENT Related sequence: AJ243952
FEATURES Location/Qualifiers

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BASE COUNT 273 a 161 c 225 g 299 t

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Query Match 89.3%; Score 294.8; DB 10; Length 958;
Best Local Similarity 93.3%; Pred. No. 4.8e-93; Indels 0; Gaps 0;
Matches 308; Conservative 0; Mismatches 22;

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QY 61 TATACCATTTCTGCGAAGACACAGAGAGATCAATGCCCCGACTGTAGTTCATC 120
DB 138 TATACCATTTCTGCGAAGACACAGAGAGATCAATGCCCCGACTGTAGTTCATC 197
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DB 198 GATGTCAAGAAAGGCGACAGATCTATGTTTATTCAGAGCTGTGTACAGAAATGAGACT 257
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DB 258 GGAGAGTTTGGGCTGCGAGCTTATGATGACACAGAGATGAGATGAGATGAGTGTGCT 317
QY 241 TATTTCCCGACCACTTGTGTAGAGACAGAGATGATCCAGAGAGCCACAGAGAGATT 300
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QY 301 CCAACCCAGGATATTGACTTCTTCTGTGAA 330
DB 378 CCAACCCAGGATATTGACTTCTTCTGTGAA 407

RESULT 13
AF233333 1054 bp mRNA linear ROD 06-JUL-2000
LOCUS Mus musculus otocaplin mRNA, complete cds.
DEFINITION AF233333
ACCESSION AF233333
VERSION AF233333.1 GI:8927429
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 1054)
AUTHORS Robertson, N.G., Heller, S., Lin, J.S., Resendes, B.L., Wernowicz, S.,
Dennis, C.S., Bell, A.M., Hudepeth, A.J. and Morton, C.C.
A novel conserved cochlear gene, OTON: identification, expression
analysis, and chromosomal mapping

TITLE

| JOURNAL | Genomics 66 (3), 242-248 (2000) |
|---------------------------|--|
| MEDLINE | 20334619 |
| PUBMED | 10873378 |
| REFERENCE | 2 (bases 1 to 1054) |
| AUTHORS | Robertson N.G., Haller, S., Lin, J.S., Resendes, B.L., Weremowicz, S., Denis, C.S., Bell, A.M., Hudspeeth, A.J. and Morton, C.C. |
| TITLE | Direct Submission |
| JOURNAL | Submitted (10-FEB-2000) Pathology, Brigham and Women's Hospital, 75 Francis Street, Boston, MA 02115, USA |
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| Query Match | 89.3%; Score 294.8; DB: 10; Length 1054; |
| Best Local Similarity | 93.3%; Pred. No. 4,8e-83; |
| Matches 308; Conservative | 0; Mismatches 22; Indels 0; Gaps 0; |
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| DB | 72 CATGCGTATTATGATTAACCTTCCTCTAGAAGTTGTGTGCAGATGAGAGTGTGTC 131 |
| QY | 61 TATACCATTTCTCTGSCAAGACACAGAGAAGTCAATATGCCCGACTGATGTTTATC 120 |
| DB | 132 TATACCATTTCTCTGSCAAGACACAGAGAAGTCAATATGCCCGACTGATGTTTATC 191 |
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| DB | 192 GATGTCAGAAAGGCGACAGATCTATGTTTATTCACAGCTGGTGAACAGAAATGAGACT 251 |
| QY | 181 GGGGCAATCTGGGCTGGCACTGTTATGTTGACCAACAGATGAGATGGATTTGGGCT 240 |
| DB | 252 GGAAGATTTGGGCTGGCACTGTTATGTTGACCAACAGATGAGATGGATTTGGGCT 311 |
| QY | 241 TATTTCCCGACGAACCTGTTAGAGACACAGAGTGATACAGAGAGCCACCAAGAGATT 300 |
| DB | 312 TATTTCCCGACGAACCTGTTAGAGAGACAGAGTGATACAGAGAGCCACCAAGAGATC 371 |
| QY | 301 CCAACCAAGATATTGACTTCTCTGTGAA 330 |
| DB | 372 CCAACCAAGATATTGACTTCTCTGTGAA 401 |
| RESULT 14 | |
| BD010830 | 307 bp DNA linear PAT 31-JAN-2002 |
| LOCUS | |
| DEFINITION | Novel polypeptide and DNA thereof. |
| ACCESSION | BD010830 |
| VERSION | BD010830.1 GI:18639203 |
| KEYWORDS | JP 2001069994-N/31. |
| SOURCE | Rattus sp. |
| ORGANISM | Rattus sp. |
| REFERENCE | 1 (bases 1 to 307) |
| AUTHORS | Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y., Yoshimura, K. and Tanaka, H. |
| TITLE | Novel polypeptide and DNA thereof |
| JOURNAL | Patent: JP 2001069994-A 31 21-MAR-2001; |
| | TAKEEDA CHEMICAL INDUSTRIES LTD |

| COMMENT | OS | Rattus sp. (rac) |
|-----------------------|-------------------|--|
| | PN | JP 2001069994-A/31 |
| | PD | 21-MAR-2001 |
| | PF | 29-JUN-2000 JP 2000195911 |
| | PR | |
| | PI | YASUOKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI |
| | PC | SHINICHI MOGI. |
| | PI | YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA |
| | PC | C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC |
| | PC | A61P9/08, |
| | PC | C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC |
| | PC | G01N33/53// |
| | PC | C12P21/08, C12N15/00, A61K37/02, C12N5/00 |
| FEATURES | CC | Location/Qualifiers |
| source | EH | Key |
| | FT | source |
| | FT | /organism='Rattus sp. (rac)' |
| | | Location/Qualifiers |
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| BASE COUNT | 84 a | 56 c 90 g 77 t |
| ORIGIN | | |
| Query Match | 85.3% | Score 281.6; DB 6; Length 307; |
| Best Local Similarity | 98.3% | Pred. No. 7.9e-79; |
| Matches | 295; Conservative | 0; Mismatches 4; Indels 1; Gaps 1; |
| Qy | 1 | CATGCATGTTTATGATTAACCTTCTCTAGAGAGTTGTGTGCAGATGAGAGTGTCTC 60 |
| Db | 7 | CATGCTGATTTATGATTAACCTTCTCTCTAGAGAGTTGTGTGCAGATGAGAGTGTCTC 66 |
| Qy | 61 | TATACCATTTCTCTGGCAGACAGACAGAGACTCAATGCCCCGAGCTGATGCTATC 120 |
| Db | 67 | TATACCATTTCTCTGGCAGACAGACAGAGAACTCAATGCCCCGAGCTGATGCTATC 126 |
| Qy | 121 | AATGCAAGAAAGGCGACAGATCTATGTTTATTCAGAGCTGGTGAAGAAATGGAGCT 180 |
| Db | 127 | AATGCAAGAAAGGCGACAGATCTATGTTTATTCAGAGCTGGTGAAGAAATGGAGCT 186 |
| Qy | 181 | GGGGCATTCTGGGCTGGCAGTGTATGTTGATACCCAGCAGATGGGAATTGTGGT 240 |
| Db | 187 | GGGGCATTCTGGGCTGGCAGTGTATGTTGATACCCAGCAGATGGGAATTGTGGT 246 |
| Qy | 241 | TATTTCCCGACGAATTGGTTAGAGAGCAACGATGTATCCAGGA-GGCCACCAAGAGAT 299 |
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| RESULT 15 | | |
| BD093131 | BD093131 | 307 bp DNA linear PAT 27-AUG-2002 |
| LOCUS | | Novel polypeptide and its DNA. |
| DEFINITION | | Novel polypeptide and its DNA |
| ACCESSION | | BD093131 |
| VERSION | | BD093131.1 GI:22638719 |
| KEYWORDS | | WO 0102564-A/31. |
| SOURCE | | Rattus sp. |
| ORGANISM | | Rattus sp. |
| | | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| | | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; |
| | | Rattus. |
| REFERENCE | | 1 (bases 1 to 307) |
| AUTHORS | | Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y., |
| TITLE | | Yoshimura, K. and Tanaka, H. |
| JOURNAL | | Novel polypeptide and its DNA |
| | | Patent: WO 0102564-A 31 11-JAN-2001; |
| | | TAKEDA CHEMICAL INDUSTRIES LTD YASUOKI ITO, KAZUNORI NISHI, KAZUHIRO |
| | | OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA, |
| | | HIDEYUKI TANAKA |
| COMMENT | | OS Rattus sp. (rac) |
| | | PN WO 0102564-A/31 |
| | | PD 11-JAN-2001 |

Tue Dec 30 10:20:50 2003

us-10-019-455a-48.rge

PF 29-JUN-2000 WO 2000JP004278
PR 30-JUN-1999 JP 99P 186718
PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI

PI MOGI,
PI YUKO, NOGUCHI KOJI, YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/12, C12N15/10, C12P21/02, C07K14/47, C07K16/18, A61K45/00, PC
A61K38/17,
PC A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/7088//C12P21/
02, C12R1.19)
CC
FH Key Location/Qualifiers Location/Qualifiers

FEATURES
source 1..307
/organism="Rattus sp."
/mol_type="genomic DNA"
/db_xref="taxon:10118"

BASE COUNT 84 a 56 c 90 g 77 t
ORIGIN

Query Match 85.3%; Score 281.6; DB 6; Length 307;
Best Local Similarity 98.3%; Pred. No. 7.8e-79;
Matches 295; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 CATGSCATGTTTATGATTAACCTTTCTTTAGAGAGTTCTGTGSCAGATGAGAGTGTGTC 60
DB 7 CATGGTGTATTATGATTAACCTTTCTTTAGAGAGTTGTGSCAGATGAGAGTGTGTC 66
QY 61 TATACCATTTCTCTGGCAGAGCAGAGAGACTACAAATGCCCGGACTGTAGTTTCATC 120
DB 67 TATACCATTTCTCTGGCAGAGCAGAGAGACTACAAATGCCCGGACTGTAGTTTCATC 126
QY 121 AATGTCAAGAAAGGCGACAGATCTATGTTTATTCAGAGCTGTACAGAAAATGAGCT 180
DB 127 AATGTCAAGAAAGGCGACAGATCTATGTTTATTCAGAGCTGTACAGAAAATGAGCT 186
QY 181 GGGGCAATCTGGGCTGGCAGTGTATTATGTTGACCAACAGATGAGATGGGAATTGTGGT 240
DB 187 GGGGCAATCTGGGCTGGCAGTGTATTATGTTGACCAACAGATGAGATGGGAATTGTGGT 246
QY 241 TATTTCCCAAGCACTGTGTAGAGAGCAAGAGTGTACCAAGGA-GGCCACCAAGAGAT 299
DB 247 TATTTCCCAAGCACTGTGTAGAGAGCAAGAGTGTACCAAGGAAGGCCACCAAGAGAT 306

Search completed: December 30, 2003, 04:08:00
Job time : 1045 secs

GenCore version 5.1.6
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CM nucleic - nucleic search, using sw model

Run on: December 30, 2003, 01:02:37 ; Search time 1098.31 Seconds
(without alignments)
7302.593 Million cell updates/sec

Title: US-10-019-455A-48
Perfect score: 330
Sequence: 1 catgcatgttatgataa.....atattgactctctctgtgaa 330

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues
45562784

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST: *
1: em_estdb: *
2: em_esthm: *
3: em_estnu: *
4: em_estov: *
5: em_estpl: *
6: em_estro: *
7: em_hrc: *
8: gb_est1: *
9: gb_est2: *
10: gb_est3: *
11: gb_est4: *
12: gb_est5: *
13: gb_est6: *
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17: em_gss_hum: *
18: em_gss_inv: *
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23: em_gss_mus: *
24: em_gss_pro: *
25: em_gss_rtd: *
26: em_gss_phg: *
27: em_gss_vrt: *
28: gb_gss1: *
29: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 294.8 | 89.3 | 398 | 13 | B0570035 g1143b10. |
| 2 | 294.8 | 89.3 | 488 | 13 | B0564607 g119h02.Y |
| 3 | 294.8 | 89.3 | 514 | 13 | B0568498 g1109c02. |
| 4 | 294.8 | 89.3 | 534 | 13 | B0564134 g111d01.Y |

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| 7 | 294.8 | 89.3 | 630 | 13 | B0568471 g1108b04. |
| 8 | 294.8 | 89.3 | 684 | 13 | B0563768 g106c09.Y |
| 9 | 294.8 | 89.3 | 686 | 10 | B05611549 BB611549 |
| 10 | 293.2 | 88.8 | 474 | 13 | B0565637 g142g03.Y |
| 11 | 293.2 | 88.8 | 409 | 13 | B0566932 g173g09.Y |
| 12 | 280.2 | 84.9 | 490 | 13 | B0565411 g137b12.Y |
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| 14 | 269.6 | 81.7 | 365 | 13 | B0565411 g137b12.Y |
| 15 | 252.8 | 76.6 | 355 | 13 | B0565411 g137b12.Y |
| 16 | 216.8 | 65.7 | 795 | 13 | B0568785 BU748241 |
| 17 | 183.6 | 55.6 | 280 | 13 | B0566776 BE236443 |
| 18 | 181.6 | 55.0 | 527 | 10 | B0563227 AK047965 |
| 19 | 160.6 | 48.7 | 677 | 13 | B0563227 AK047965 |
| 20 | 126.4 | 38.3 | 3240 | 11 | AA222797 mv77b12.Y |
| 21 | 126.4 | 37.6 | 492 | 9 | AA222797 mv77b12.Y |
| 22 | 124.2 | 37.2 | 533 | 9 | AA222797 mv77b12.Y |
| 23 | 122.8 | 37.2 | 678 | 10 | BB647928 BB647928 |
| 24 | 121.6 | 36.8 | 349 | 9 | AM021345 AM021345 |
| 25 | 121.2 | 36.7 | 338 | 9 | AM021345 AM021345 |
| 26 | 100.2 | 30.4 | 1201 | 13 | BX448440 BX448440 |
| 27 | 97.2 | 29.6 | 978 | 13 | BX448440 BX448440 |
| 28 | 94.2 | 28.5 | 646 | 13 | B0563767 B0563767 |
| 29 | 92.8 | 28.1 | 170 | 13 | B0569268 B0569268 |
| 30 | 92.8 | 27.5 | 186 | 13 | B0564457 B0564457 |
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| 33 | 80.2 | 24.3 | 593 | 9 | AL717905 AL717905 |
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| 35 | 80.2 | 24.3 | 544 | 13 | B0208982 B0208982 |
| 36 | 71.8 | 21.8 | 594 | 14 | CA370333 CA370333 |
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| 38 | 70.8 | 21.5 | 424 | 14 | CB796570 CB796570 |
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| 41 | 63.4 | 19.2 | 473 | 14 | CA433401 CA433401 |
| 42 | 63.4 | 19.2 | 480 | 14 | BM715936 BM715936 |
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| 44 | 63.4 | 19.2 | 515 | 13 | B0892734 B0892734 |
| 45 | 63.4 | 19.2 | 515 | 13 | B0892734 B0892734 |

ALIGNMENTS

RESULT 1
B0570035 398 bp mRNA linear EST 19-JUN-2002
g1143b10.Y1 Mouse Organ of Corti cDNA bluecscript Mus musculus cDNA
clone g1143b10 5', mRNA sequence.

ACCESSION B0570035
VERSION B0570035.1
KEYWORDS GI:21473352
SOURCE EST.
ORGANISM Mus musculus (house mouse)

REFERENCE 1 (bases 1 to 398)
AUTHORS Kachar,B.
TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing

JOURNAL Unpublished
COMMENT Contact: Kachar B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: kachar@nidcd.nih.gov
Plate: 143 row: D column: 10
Seq primer: M13R1 reverse primer (ABI).
Location/Qualifiers

FEATURES

source

1. 398
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 /mol_type="mRNA"
 /strain="BALB/c"
 /db_xref="taxon:10090"
 /clone="g143b10"
 /sex="male and female"
 /dev_stage="post natal day 5 to 13"
 /clone_idb="Mouse Organ of Corti, Vector: pBluescript; The
 /note="Organ: Organ of Corti, Vector: pBluescript; The
 organ of Corti (OC) was fine dissected from a total of 386
 OC as follows: 102 samples from post-natal (p) day 5; 72
 from p6; 60 from p7; 46 from p8; 18 from p9; 20 from p10;
 14 from p12 and 24 from p13. After killing animals by
 cervical dislocation followed by decapitation, the bulla
 was removed and opened in Leibowitz medium. The bony
 capsule of the cochlea was chipped away, stria vascularis
 and spiral ligament were removed and the sensory
 epithelium was carefully dissected out of the modiolus.
 Total RNA was extracted using the micro Fasttrack kit
 (catalog # K1593-02; Invitrogen, Carlsbad, CA), according
 to manufacturer's instructions. Reverse transcription and
 library construction were carried out with the Uni-Zap XR
 vector kit (catalog # 237211, Stratagene) and Uni-Zap XR
 Gigapack III Gold Cloning kit (catalog # 237612), both
 from Stratagene (La Jolla, CA, USA), according to
 manufacturer's instructions. Briefly: 1.5 ug mRNA was
 reverse transcribed using a hybrid oligo(dT) linker-primer
 that contains an Xho I site. First strand synthesis was
 primed with the linker-primer and transcribed using
 Moloney murine leukemia virus reverse transcriptase
 (MMLV-RT) and 5-methyl dCTP. The second strand was
 synthesized with DNA polymerase and RNase H. Complementary
 DNA was blunt ended with pfu DNA polymerase, ligated with
 EcoR I adapters in the presence of ligase and digested
 with Xho I. The cDNA was sequentially size fractionated
 over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden)
 and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA)
 columns to enrich for cDNAs greater than 400bp and 1000 bp
 , respectively. The cDNA was then directionally ligated to
 the Uni-Zap XR vector, which had been pre-digested with
 EcoR I and Xho I. The phagemid was packaged with Gigapack
 III Gold and, upon titration on XLI Blue MRF⁺ cells, the
 yield of the phage library was estimated to be 11,100,000
 recombinants. Stratagene's ExAssist Interference
 resistance helper phage (catalogue # 211203) was adopted
 to rescue plasmid DNA from the phages. Upon plating of the
 rescued library, individual cDNA clones were selected and
 grown in 96-well, 2 ml growth plate. Plasmid DNA was
 purified from 200 ul of saturated culture with the
 Concert36(TM) plasmid purification kit (Invitrogen,
 Carlsbad, CA) as instructed by the manufacturer. ESTs from
 the 5' end of the cDNA clones were generated with the
 universal M13 reverse primer (CAGGAACAGCTATGACC) and 25¢
 BioSystems, Foster City, CA). Sequencing reactions were
 performed on MJ Tetrad thermal cyclers (MJ Research,
 Waltham, MA), and analyzed on 3700 automated capillary
 sequencers using POPs polymer (Applied Biosystems, Foster
 City, CA). The frequency distribution of the library is
 as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10;
 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of
 genes are present in GenBank and have known function; 23%
 have hits in GenBank, but do not have assigned function;
 12% are uncharacterized ESTs and 20% are unidentified."

| Db | QY | Db | QY | Db | QY | Db | QY | Db | QY | | |
|-----|--|-----|-----|--|-----|-----|--|-----|-----|--|-----|
| 67 | CATGCTGATTTATGATTAACCTTCTTAAAGAACTTGTGCGATAGAGCTGTC | 126 | 301 | CCACCCGAGATTTGACTTCTTCTGTGA | 330 | 307 | TATTTCCCGAGAACTTGTGTAGAGAGCGAGTATACAGAGCCACAGAGATC | 366 | 367 | CCACCCGAGATTTGACTTCTTCTGTGA | 396 |
| 61 | TATACATTTCTCTGCGAAGAGACAGAAAGATTAACATCCCACTAGTTCATC | 186 | 127 | TATACATTTCTCTGCGAAGAGACAGAAAGATTAACATCCCACTAGTTCATC | 186 | 121 | AATGTCAAGAAAGGCGAGAGATCTATGTTTATTCAGAGCTGTGTACAGAAATGAGCT | 246 | 187 | GATGTCAAGAAAGGCGAGAGATCTATGTTTATTCAGAGCTGTGTACAGAAATGAGCT | 246 |
| 127 | TATACATTTCTCTGCGAAGAGACAGAAAGATTAACATCCCACTAGTTCATC | 186 | 247 | GGAGGATTTGCGCTGCGAGAGTGTATGATGATCCACAGAGTGTGAGTGGAAATGTAGT | 306 | 247 | GGAGGATTTGCGCTGCGAGAGTGTATGATGATCCACAGAGTGTGAGTGGAAATGTAGT | 306 | 247 | GGAGGATTTGCGCTGCGAGAGTGTATGATGATCCACAGAGTGTGAGTGGAAATGTAGT | 306 |
| 121 | AATGTCAAGAAAGGCGAGAGATCTATGTTTATTCAGAGCTGTGTACAGAAATGAGCT | 246 | 247 | GGAGGATTTGCGCTGCGAGAGTGTATGATGATCCACAGAGTGTGAGTGGAAATGTAGT | 306 | 247 | GGAGGATTTGCGCTGCGAGAGTGTATGATGATCCACAGAGTGTGAGTGGAAATGTAGT | 306 | 247 | GGAGGATTTGCGCTGCGAGAGTGTATGATGATCCACAGAGTGTGAGTGGAAATGTAGT | 306 |
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| 181 | GGGCGATTTGCGCTGCGAGAGTGTATGATGATCCACAGAGTGTGAGTGGAAATGTAGT | 306 | 247 | GGAGGATTTGCGCTGCGAGAGTGTATGATGATCCACAGAGTGTGAGTGGAAATGTAGT | 306 | 247 | GGAGGATTTGCGCTGCGAGAGTGTATGATGATCCACAGAGTGTGAGTGGAAATGTAGT | 306 | 247 | GGAGGATTTGCGCTGCGAGAGTGTATGATGATCCACAGAGTGTGAGTGGAAATGTAGT | 306 |
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| 241 | TATTTCCCGAGAACTTGTGTAGAGAGCGAGTATACAGAGCCACAGAGATC | 366 | 307 | TATTTCCCGAGAACTTGTGTAGAGAGCGAGTATACAGAGCCACAGAGATC | 366 | 307 | TATTTCCCGAGAACTTGTGTAGAGAGCGAGTATACAGAGCCACAGAGATC | 366 | 307 | TATTTCCCGAGAACTTGTGTAGAGAGCGAGTATACAGAGCCACAGAGATC | 366 |
| 307 | TATTTCCCGAGAACTTGTGTAGAGAGCGAGTATACAGAGCCACAGAGATC | 366 | 307 | TATTTCCCGAGAACTTGTGTAGAGAGCGAGTATACAGAGCCACAGAGATC | 366 | 307 | TATTTCCCGAGAACTTGTGTAGAGAGCGAGTATACAGAGCCACAGAGATC | 366 | 307 | TATTTCCCGAGAACTTGTGTAGAGAGCGAGTATACAGAGCCACAGAGATC | 366 |
| 301 | CCACCCGAGATTTGACTTCTTCTGTGA | 330 | 307 | TATTTCCCGAGAACTTGTGTAGAGAGCGAGTATACAGAGCCACAGAGATC | 366 | 307 | TATTTCCCGAGAACTTGTGTAGAGAGCGAGTATACAGAGCCACAGAGATC | 366 | 307 | TATTTCCCGAGAACTTGTGTAGAGAGCGAGTATACAGAGCCACAGAGATC | 366 |
| 367 | CCACCCGAGATTTGACTTCTTCTGTGA | 396 | 307 | TATTTCCCGAGAACTTGTGTAGAGAGCGAGTATACAGAGCCACAGAGATC | 366 | 307 | TATTTCCCGAGAACTTGTGTAGAGAGCGAGTATACAGAGCCACAGAGATC | 366 | 307 | TATTTCCCGAGAACTTGTGTAGAGAGCGAGTATACAGAGCCACAGAGATC | 366 |

RESULT 2

LOCUS

B0564607

488 bp

mRNA

linear

EST 19-JUN-2002

DEFINITION

g119h02.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA

ACCESSION

B0564607

B0564607.1

GI:21467924

VERSION

B0564607.1

GI:21467924

KEYWORDS

EST.

Mus musculus (house mouse)

SOURCE

Mus musculus

(house mouse)

ORGANISM

Mus musculus

(house mouse)

REFERENCE

1

(bases 1 to 488)

AUTHORS

Kachar, B.

Kachar, B.

TITLE

EST analysis of gene expression in the mouse Organ of Corti at the

JOURNAL

Unpublished

COMMENT

Contact: Kachar, B.

National Institute of Deafness and other Communication Disorders

FEATURES

source

1. 488

FEATURES

source

1. 488

FEATURES

source

1. 488

FEATURES

source

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FEATURES

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source

1. 488

FEATURES

source

1. 488

library construction were carried out with the Uni-Zap XR vector kit (catalog # 23721, Stratagene) and Uni-Zap XR GigaPack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with GigaPack III Gold and, upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's Exsist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAAACAGCTAGGACC) and 254 strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 143 a 83 c 135 g 127 t
ORIGIN

Query Match 89.3%; Score 294.8; DB 13; Length 488;
Best Local Similarity 93.3%; Pred. No. 2,4e-81;
Matches 308; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

1 CATGCATGTTTATGATTAACCTTTCTTAAGAGTTGTGTGAGATGAGAGTGTCTC 60
61 CATGGTATTTATGATTAACCTTTCTTAAGAGTTGTGTGAGATGAGAGTGTCTC 120
61 TATACATTTCTTGGCAAGACACAGAAACTACATATGCCCGGACTGTAGTTTATC 120
121 TATATATTTCTTGGCAAGACACAGAAACTACATATGCCCGGACTGTAGTTTATC 180
121 AATGTCAGAAAGGGCAGACAGATCATGTTTATTCAGAGTGTGTACAGAAATGAGCT 180
181 GATGTCAGAAAGGGCAGACAGATCATGTTTATTCAGAGTGTGTACAGAAATGAGCT 240
181 GGGGATTTCTGGGCTGGCAGTGTATGATGTCACACAGATGATGAGATTTGTGGCT 240
241 GGAGAGTTTGGCTGGCAGTGTATGATGTCACACAGATGATGAGATTTGTGGCT 300
241 TATTTCCCGACACTTGTGTTAGAGACAAAGAGTTCACAGAGGCCACCAAGAGATT 300
301 TATTTCCCGACACTTGTGTTAGAGACAAAGAGTTCACAGAGGCCACCAAGAGATT 360
301 CCACACAGATGATGACTTCTTCTGTGAA 330
361 CCACACAGATGATGACTTCTTCTGTGAA 390

RESULT 3
LOCUS B0568498 514 bp mRNA linear EST 19-JUN-2002
DEFINITION g1109c02.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA
clone g1109c02 5', mRNA sequence.
ACCESSION B0568498
VERSION B0568498.1 GI:21471815
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE Kacher,B. 1 (bases 1 to 514)
EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
TITLE Unpublished
JOURNAL Contact: Kacher,B.
COMMENT Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: Kacher@nidcd.nih.gov
Plate: 109 row: c column: 02
Seq primer: M13RP1 reverse primer (AB1).
Location/Qualifiers
1. 514
/organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
/db_xref="taxon:10090"
/clone="g1109c02"
/sex="male and female"
/dev_stage="Post natal day 5 to 13"
/clone_11b="Mouse Organ of Corti cDNA pBluescript"
/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (p) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 23721, Stratagene) and Uni-Zap XR GigaPack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with GigaPack III Gold and, upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000

recombinants. StrataGene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 µl of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAAACAGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in Genbank and have known function; 23% have hits in Genbank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 147 a 85 c 143 g 139 t

ORIGIN
Query Match 89.3%; Score 294.8; DB 13; Length 514;
Best Local Similarity 93.3%; Pred. No. 2.4e-81;
Matches 308; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

1 CATGGCATGTTTATGATTAACCTTTCTTACAGAGTTGTGACAGATGAGCTGTC 60
59 CATGGTATTTATGATTAACCTTTCTTACAGAGTTGTGACAGATGAGCTGTC 118
61 TATACATTTCTCTGCAAGACAGCAAGCACTACCAATGCCCGAGCTAGCTCAGC 120
119 TATACATTTCTCTGCAAGACAGCAAGCACTACCAATGCCCGAGCTAGCTCAGC 178
121 AATGTCAAGAAAGGCGACAGATGATTTATTCAGAGCTGGTAAAGAAATGAGCT 180
179 GATGTCAAGAAAGGCGACAGATGATTTATTCAGAGCTGGTAAAGAAATGAGCT 238
181 GGGGCATTTGGGCTGACAGTGTATGATGACCAAGAGATGAGTGGAAATTTGGGT 240
239 GGAAGATTTGGGCTGACAGTGTATGATGACCAAGAGATGAGTGGAAATTTGGGT 298
241 TATTTCCCAAGCACTGTTAGAGCAAGCACTGTTAGAGCAAGCACTGTTAGAGCA 300
299 TATTTCCCAAGCACTGTTAGAGCAAGCACTGTTAGAGCAAGCACTGTTAGAGCA 358
301 CCAACCAAGCACTGTTAGAGCAAGCACTGTTAGAGCAAGCACTGTTAGAGCA 330
359 CCAACCAAGCACTGTTAGAGCAAGCACTGTTAGAGCAAGCACTGTTAGAGCA 388

RESULT 4 B0564134 534 bp mRNA linear EST 19-JUN-2002
B0564134 LOCUS B0564134 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA
DEFINITION clone g11d01 5', mRNA sequence.

ACCESSION B0564134
VERSION B0564134
KEYWORDS B0564134.1 GI:21467451
SOURCE EST.
ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 (bases 1 to 534)
AUTHORS Kachar, B.
TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
JOURNAL Unpublished
COMMENT Contact: Kachar, B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders

FEATURES

SOURCE

50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: kachar@nidcd.nih.gov
Plate: 11 row: d column: 01
Seq primer: M13Rpl reverse primer (ABI).
Location/Qualifiers

1. 534
/organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
/db_xref="taxon:10090"
/clone="g11d01"
/sex="male and female"
/dev_stage="Post natal day 5 to 13"
/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigaapak III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 µg mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigaapak III Gold and, upon titration on XL1 Blue MRF⁺ cells, the yield of the phage library was estimated to be 11,100,000 recombinants. StrataGene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 µl of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAAACAGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in Genbank and have known function; 23% have hits in Genbank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT

155 a 87 c 148 g 144 t

QY 241 TATTTCCCGACCACTTGTTAGAGACGACGATGTACCGAGGCCACCAAGAGATT 300
 Db 300 TATTTCCCGACCACTTGTTAGAGAGCGCGGTGTATACGAGGCCACCAAGAGATC 359
 QY 301 CCACCCAGGATATTGACTTCTTCTGTGAA 330
 Db 360 CCACCCAGGATATTGACTTCTTCTGTGAA 389
 RESULT 6
 B0564944 608 bp mRNA linear EST 19-JUN-2002
 LOCUS g127909.y1 Mouse Organ of Corti cDNA plibuescript Mus musculus CDNA
 DEFINITION clone g127909 5', mRNA sequence.
 ACCESSION B0564944
 VERSION B0564944.1 GI:21468261
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 608)
 AUTHORS Kachar, B.
 TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
 JOURNAL Unpublished
 COMMENT Contact: Kachar, B.
 Structural Cell Biology
 National Institute of Deafness and other Communication Disorders
 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
 Tel: 301-402-1599
 Fax: 301-402-1765
 Email: kacharbenid@nih.gov
 Plate: 27 row: 9 column: 09
 Seq primer: M13RP1 reverse primer (AB1).
 Location/Qualifiers
 1..608
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="BALB/c"
 /db_xref="taxon:10090"
 /clone="g127909"
 /sex="male and female"
 /dev_stage="Post natal day 5 to 13"
 /note="Organ: Organ of Corti. Vector: plibuescript. The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR Vector kit (catalog # 237211, Stratagene) and Uni-Zap XR GigaPack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Upstala, Sweden)

BASE COUNT 169 a 107 c 166 g 166 t
 ORIGIN
 Query Match 89.3%; Score 294.8; DB 13; Length 608;
 Best Local Similarity 93.3%; Pred. No. 2,7e-81;
 Matches 308; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
 QY 1 CATGCGATGTTTATGATTAACCTTCTTCTTAAAGTTGTGTGACATGAGATGTC 60
 Db 67 CATGCGATGTTTATGATTAACCTTCTTCTTAAAGTTGTGTGACATGAGATGTC 126
 QY 61 TATACCATTTCTGTGCAAGACACAGAAAGCTTCAATGCCCGCATGTAGTTCATC 120
 Db 127 TATACCATTTCTGTGCAAGACACAGAAAGCTTCAATGCCCGCATGTAGTTCATC 186
 QY 121 AATGTCAGAAAGGCGACAGATCTATGTTTATTCAGAGTGTGACAGAAATGAGCT 180
 Db 187 GATGTCAGAAAGGCGACAGATCTATGTTTATTCAGAGTGTGACAGAAATGAGCT 246
 QY 181 GGGGATCTGTGGGCTGGAGTGTATGTGACCCAGATGAGATGGATGTGGT 240
 Db 247 GGAGGTTTGGGCTGGAGTGTATGTGACCCAGATGAGATGGATGTGGT 306
 QY 241 TATTTCCCGACCACTTGTTAGAGACGATGTACCGAGGCCACCAAGAGATT 300
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 QY 301 CCACCCAGGATATTGACTTCTTCTGTGAA 330
 Db 367 CCACCCAGGATATTGACTTCTTCTGTGAA 396
 RESULT 7
 B0568471 630 bp mRNA linear EST 19-JUN-2002
 LOCUS g108904.y1 Mouse Organ of Corti cDNA plibuescript Mus musculus CDNA
 DEFINITION clone g108904 5', mRNA sequence.
 ACCESSION B0568471
 VERSION B0568471.1 GI:21471788
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 630)

and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with GigaPack II Gold and, upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(RTM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. The 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACGCTATGAC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

AUTHORS Kachar, B.
TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
JOURNAL Unpublished
COMMENT Contact: Kachar, B.
 Structural Cell Biology
 National Institute of Deafness and other Communication Disorders
 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
 Tel: 301-402-1599
 Fax: 301-402-1765
 Email: kachar@nidcd.nih.gov
 Plate: 108 row: 9 column: 04
 Seq primer: M13RPI reverse primer (ABI).

FEATURES

source
 1. .630
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="BALB/c"
 /db_xref="taxon:10090"
 /clone="g108g04"
 /sex="male and female"
 /dev_stage="Post natal day 5 to 13"
 /clone_lib="Mouse Organ of Corti cDNA pluescript"
 /note="Organ: Organ of Corti, Vector: pluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 23721, Stratagene) and Uni-Zap XR GigaPack III Gold Cloning Kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 100 bp, respectively. The cDNA was then directionally ligated to the uni-zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with GigaPack III Gold and, upon titration on Xba Blue MRF⁺ cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExaScript interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAAACAGCTAGAC) and 25x strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster

BASE COUNT

178 a 111 c 167 g 174 t
 City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in Genbank and have known function; 23% have hits in Genbank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

Query Match 89.3%; Score 294.8; DB 13; Length 630;
 Best Local Similarity 93.3%; Pred. No. 2.7e-81;
 Matches 308; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

| | | | |
|----|-----|---|-----|
| Qy | 1 | CATGGCAGTGTATGATGAATCTTCTTGAAGAGTGTGACAGATGAGAGTGTGTC | 60 |
| Db | 67 | CATGGTGAATTTATGATGAATCTTCTTGAAGAGTGTGACAGATGAGAGTGTGTC | 126 |
| Qy | 61 | TATACATTTCTGTGCAAGAGACAGAGAACTACATATGCCCCGAGCTGTAGTTATC | 120 |
| Db | 127 | TATACATTTCTGTGCAAGAGACAGAGAACTACATATGCCCCGAGCTGTAGTTATC | 186 |
| Qy | 121 | AATGCAAGAAAGGAGAGAGATCTATGTTTCCAGCTGTGAAGAAATGAGGT | 180 |
| Db | 187 | GATGTCAAGAAAGGAGAGATCTATGTTTCCAGCTGTGAAGAAATGAGGT | 246 |
| Qy | 181 | GGGCAATTCGTGGCTGAGTGTATGAGTGAACCAAGATGAGTGGAAATGTGAGT | 240 |
| Db | 247 | GGAGATTTTGGCTGAGTGTATGAGTGAACCAAGATGAGTGGAAATGTGAGT | 306 |
| Qy | 241 | TATTTCCAGCAACTGTGTTAAGAGCAAGAGTGTACAGAGCCACCAAGAGATT | 300 |
| Db | 307 | TATTTCCAGCAACTGTGTTAAGAGCAAGAGTGTACAGAGCCACCAAGAGATT | 366 |
| Qy | 301 | CCAGCAGAGATTTGACTCTTTCTGTGA | 330 |
| Db | 367 | CCAGCAGAGATTTGACTCTTTCTGTGA | 396 |

RESULT 8

B0563768 684 bp mRNA linear EST 19-JUN-2002
 LOCUS g106c09.y1 Mouse Organ of Corti cDNA pluescript Mus musculus cDNA
 DEFINITION g106c09 5', mRNA sequence.

ACCESSION B0563768
 VERSION B0563768.1 GI:21466749
 KEYWORDS EST.

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 684)

AUTHORS Kachar, B.
TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
JOURNAL Unpublished
COMMENT Contact: Kachar, B.
 Structural Cell Biology
 National Institute of Deafness and other Communication Disorders
 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
 Tel: 301-402-1599
 Fax: 301-402-1765
 Email: kachar@nidcd.nih.gov
 Plate: 06 row: c column: 09
 Seq primer: M13RPI reverse primer (ABI).

FEATURES

source
 1. .684
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="BALB/c"
 /db_xref="taxon:10090"
 /clone="g106c09"
 /sex="male and female"
 /dev_stage="Post natal day 5 to 13"

/clone.lib="Mouse Organ of Corti cDNA plibuescript"
 /note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 366 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus.

Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 23721, Stratagene) and Uni-Zap XR GigaPack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sephadex (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with GigaPack III Gold and upon titration on XL Blue MRF⁺ cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExaScript interference resistance helper phage (catalog # 21103) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96 (TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAAACACCTTAAC) and 25x strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Thermal thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in Genbank and have known function; 23% have hits in Genbank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 194 a 120 c 178 g 192 t
 ORIGIN

Query Match 89.3%; Score 294.8; DB 13; Length 684;
 Best Local Similarity 93.3%; Pred. No. 2.9e-81;
 Matches 308; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

1 CATGCGATGTTTATGATTAATCTTCTCTTAAGAGTTGTGCGATGAGCGATGTCTC 60
 DB 67 CATGGTATTTATGATTAATCTTCTCTTAAGAGTTGTGCGATGAGCGATGTCTC 126
 QY 61 TATACCATTTCTCGCAAGAGCAAGAGCTACATGCCCGGATGATGATTCATC 120
 DB 127 TATACCATTTCTCGCAAGAGCAAGAGCTACATGCCCGGATGATGATTCATC 186
 QY 121 AATGCAAGAAAGGCGAGAGATCTATGTTTATTCAGAGCTGTAAAGAAATGAGACT 180

DB 187 GATGTCAGAAAGGCGAGAGATCTATGTTTATTCAGAGCTGTAAAGAAATGAGACT 246
 QY 181 GGGCGATTTCTGGCTGCGACATGTTTATGTTGACACACAGATGAGATGGAAATTGGGT 240
 DB 247 GAGAGTTTGGGCTGCGACATGTTTATGTTGACACACAGATGAGATGGAAATTGGGT 306
 QY 241 TATTTCCCGCAACATTGTTAGAGCAAGAGCTGTACAGAGGCCACCAAGAGATT 300
 DB 307 TATTTCCCGCAACATTGTTAGAGCAAGAGCTGTATACAGAGGCCACCAAGAGATT 366
 QY 301 CCAACCAAGATATGATCTTCTCTGTA 330
 DB 367 CCAACCAAGATATGATCTTCTCTGTA 396

RESULT 9
 BB611549
 LOCUS

DEFINITION
 BB611549 RIKEN full-length enriched, 13 days embryo head Mus

ACCESSION
 BB611549

VERSION
 BB611549.1 GI:15393547

KEYWORDS
 EST.

SOURCE
 Mus musculus (house mouse)

ORGANISM
 Mus musculus

REFERENCE
 ARAKAWA, T., CARNINCI, P., FUKUDA, S., FURUNO, M., HANAGAKI, T., HARA, A., HIRAMOTO, K., HORII, F., ISHII, Y., ITO, M., KAWAI, J., KONNO, H., KOWA, M., KOYA, S., MATSUYAMA, T., MIYAZAKI, A., NOMURA, J., OHNO, M., OKAZAKI, Y., OKIDO, T., SAITO, R., SAKAI, C., SAKAI, K., SANO, H., SASAKI, P., SHIBATA, K., SHINGAWA, A., SHIRAKI, T., SOGABE, Y., SUZUKI, H., TAGAMI, M., TAGAWA, A., TAKAHASHI, F., TAKEDA, Y., TANAKA, T., TOYA, T., MURAMATSU, M. and HAYASHIZAKI, Y.

TITLE
 RIKEN Mouse ESTs (Arakawa, T., et al. 2001)

JOURNAL
 Unpublished

COMMENT
 Contact: Yoshinori Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Saito-cho, Tsukuba, Ibaraki, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@sc.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matsuhiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a non-redundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Yamanaka, I., Kiyosawa, H., Kondo, S., Saito, T., Shingawa, A., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., Arakawa, T., Ishii, Y. and Hayashizaki, Y.

Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct. Funct. Genomics 2 pre, L72-L86 (2001)

Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

e mouse tissues.

Location/Qualifiers

FEATURES

SOURCE

1. 696
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="3110083012"
 /tissue_type="head"
 /dev_stage="13 days embryo"
 /lab_host="SOLR"
 /clone_lib="RIKEN full-length enriched, 13 days embryo head"
 /note="Site 1: XhoI; Site 2: SctI. cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5']
 GAGGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTT 3', cDNA was prepared by using trihalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 50.0. Second strand cDNA was prepared with the primer adapter of sequence [5']
 GAGGAGAGATTCGAGCTTATTATTAATTCCTCCCTCCCTCCCT 3'. cDNA was cleaved with XhoI and SctI."

BASE COUNT

204 a 122 c 176 g 194 t

ORIGIN

Query Match 69.3%; Score 294.8; DB 10; Length 696;
 Best Local Similarity 93.3%; Fred. No. 2.9e-81;
 Matches 308; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 CATGGCATGTTATGATTAACCTTCTCTAGAGAGTGTGCGAGATGAGAGTGTGC 60
 DB 78 CATGGTATTATGATTAACCTTCTCTAGAGAGTGTGCGAGATGAGAGTGTGC 137
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 DB 138 TATACATTTCTGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 197
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 QY 181 GGGGATCTGCGAG 240
 DB 258 GAGAGATTTTGGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 317
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 DB 318 TATTTCCTCCAGCACTTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 377
 QY 301 CCAACCAAGGATATTGACTTTCTTGGA 330
 DB 378 CCAACCAAGGATATTGACTTTCTTGGA 407

RESULT 10

BO565637 474 bp mRNA linear EST 19-JUN-2002
 LOCUS 474 bp mRNA linear EST 19-JUN-2002
 DEFINITION clone g142g03.5, mRNA sequence.

ACCESSION

BO565637
 BO565637.1 GI:21468954

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Kachar, B.

REFERENCE

1 (bases 1 to 474)
 EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing

JOURNAL

Unpublished
 Contact: Kachar, B.

COMMENT

Structural Cell Biology
 National Institute of Deafness and other Communication Disorders
 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA

Tel: 301-402-1599
 Fax: 301-402-1765
 Email: Kachar@nidcd.nih.gov

Plate: 42 row: 9 column: 03
 Seq primer: M13Rpl reverse primer (AB1).

FEATURES

source

1. 474

/organism="Mus musculus"

/mol_type="mRNA"

/strain="BALB/c"

/db_xref="taxon:10090"

/clone="g142g03"

/sex="male and female"

/dev_stage="post natal day 5 to 13"

/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was clipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA) according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR GigaPack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMuV-Rt) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been pre-digested with EcoR I and Xho I. The phagemid was packaged with GigaPack III Gold and, upon titration on X1 Blue MRF⁺ cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96 (TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (GAGGAAACGATGAC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on 96 well thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of

Genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified.

BASE COUNT 145 a 78 c 131 g 120 t

Query Match 88.8%; Score 293.2; DB 13; Length 474;
Best Local Similarity 93.0%; Pred. No. 7.4e-61;
Matches 307; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 CATGGCAGTTTATGATTAACCTTTCTTAAGAGTTGTGACAGATGAGAGTGTCTC 60
DB 68 CATGGTATTTATGATTAACCTTTCTTAAGAGTTGTGACAGATGAGAGTGTCTC 127
QY 61 TATACATTTCTTCTGGCAAGACACAGAGACTAATGCCCGAGCTTGAAGTTCATC 120
DB 128 TATACATTTCTTCTGGCAAGACACAGAGACTAATGCCCGAGCTTGAAGTTCATC 187
QY 121 AATGTCAAGAAAGGAGACAGATCTATGTTTATTCAGAGCTGTAAACAGAAATGAGACT 180
DB 188 GATGTCAAGAAAGGAGACAGATCTATGTTTATTCAGAGCTGTAAACAGAAATGAGACT 247
QY 181 GAGGCAATTCGCTGGCAGAGTGTATGCTGACACAGAGATGAGATGGGAAATTGTGGGT 240
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QY 241 TATTTCCCAAGCACTGTGTAGAGACAGAGATGACAGAGAGCCACCAAGAGATT 300
DB 308 TATTTCCCAAGCACTGTGTAGAGAGGAGCGCTGTATACAGAGAGCCACCAAGAGATT 367
QY 301 CCACACGAGATATTGACTTCTTCTGTGA 330
DB 368 CCACACGAGATATTGACTTCTTCTGTGA 397

RESULT 11 409 bp mRNA linear EST 19-JUN-2002
LOCUS B0566932
DEFINITION g173g09.y1 Mouse Organ of Corti cDNA Bluescript Mus musculus cDNA
ACCESSION B0566932
VERSION B0566932.1 GI:21470249
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 409)
Kachar, B.
EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
Unpublished
JOURNAL Contact: Kachar, B.
COMMENT Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: kacharbenidc@nih.gov
Plate: 73 row: 9 column: 09
Seq primer: M3RP1 reverse primer (AB1).
Location/Qualifiers
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/mol_type="mRNA"
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/clone="g173g09"
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/dev_stage="Post natal day 5 to 13"
/clone_1ib="Mouse Organ of Corti cDNA Bluescript"
/note="Organ of Corti; Vector: cDNA; Vector: Bluescript; The organ of Corti (OC) was fine dissected from a total of 386

OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was clipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 23721, Stratagene) and Uni-Zap XR GigaPack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly, 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been pre-digested with EcoR I and Xho I. The phagemid was packaged with GigaPack III Gold and, upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAAACAGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified.

BASE COUNT 102 a 75 c 121 g 111 t

Query Match 84.9%; Score 280.2; DB 13; Length 409;
Best Local Similarity 92.7%; Pred. No. 8.1e-77;
Matches 305; Conservative 0; Mismatches 23; Indels 1; Gaps 1;

QY 1 CATGGCAGTTTATGATTAACCTTTCTTAAGAGTTGTGCA-CATGAGAGTGTGT 59
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DB 141 CTATACATTTCTTCTGGCAAGACACAGAGACTAATGCCCGAGCTTGAAGTTCAT 200
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QY 180 TGGGCGATCTTGGGCTGGCAGTGTATTGCTGACCAACAGATGAGATGGGATTTGGG 239
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 RESULT 12 490 bp mRNA linear EST 19-JUN-2002
 LOCUS B0565411
 DEFINITION g137b12.y1 Mouse Organ of Corti cDNA Bluescript Mus musculus cDNA
 ACCESSION B0565411
 VERSION B0565411.1 GI:21468728
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 490)
 AUTHORS Kachar, B.
 TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
 JOURNAL Unpublished
 COMMENT Contact: Kachar, B.
 Structural Cell Biology
 National Institute of Deafness and other Communication Disorders
 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
 Tel: 301-402-1599
 Fax: 301-402-1765
 Email: kachar@nidcd.nih.gov
 Plate: 37 row: b column: 12
 Seq primer: M13RP1 reverse primer (ABT).
 FEATURES
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 /clone_lib="Mouse Organ of Corti cDNA Bluescript"
 /organ_of_corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR GigaPack III Gold Cloning Kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary

DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with GigaPack III Gold and upon titration on XL1 Blue MRF⁺ cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExSist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAAACGCTAAGC) and 25x strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 191 a 77 c 109 g 112 t 1 others
 ORIGIN
 Query Match 83.0%; Score 274; DB 13; Length 490;
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 DB 141 CATGGGATTTATGATTAACCTTTCTTGAAGTTGTGCAGATGAGAGTGTGC 200
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 DB 201 TATACCATTTCTCTGGGAAGACACAGAGAAATTTACATGCCCAACTAGTTATC 260
 QY 121 AATGTCAGAAAGGGCGACGATCTATTGTTTCCAGCTGGTAACAGAAATGAGCT 180
 DB 261 GATGTCAGAAAGGGCGACGAAATCTATTGTTTCTCAGCTGGTAACAGAAATGAGCT 320
 QY 181 GGGGCAATCTGGGCTGGCAGTGTATTGCTGACCAACAGATGAGATGGGATTTGGG 240
 DB 321 GGAAGTTTGGGCTGGCAGTGTATTGCTGACCAACAGATGAGATGGGATTTGGG 380
 QY 241 TATTTCCCGACCACTTGTAGAGAGCAAGAGTGTACCGAGGCGCCACCAAGAGAT 300
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 LOCUS B0567343
 DEFINITION g188d08.y1 Mouse Organ of Corti cDNA Bluescript Mus musculus cDNA
 ACCESSION B0567343
 VERSION B0567343.1 GI:21470660
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)

Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

JOURNAL MEDLINE PUBMED
22354683
12466851

CONTACT: Yoshinobu Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watanabe, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Kirk W. Beisel (Boys Town National Research Hospital 555 North 30th Street Omaha, NE 68131 USA) whose assistance we gratefully acknowledge. Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES

Location/Qualifiers

source
1..365
/organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="F930026020"
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BASE COUNT 97 a 60 c 110 g 98 t
ORIGIN

Query Match 76.6%; Score 252.8; DB 13; Length 365;
Best Local Similarity 92.4%; Pred. No. 3e-68; 22; Indels 0; Gaps 0;
Matches 266; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

1 CATGCAGTTTATGATTAATTTCTTTCTTAAGAGTTGTGTCAGATGAGAGTGTGTC 60
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3 TATACATTTCTCTGCAAGAGCAGAGAGCTACATGCCCGAGTGTAGTGTATC 120
4 TATATCTATTTCTCTGCAAGAGCAGAGAGTTTCAATGCCCGAGTGTAGTGTATC 197
5 AATGTCAGAAAGGCGCAGATCTATGTTTATTCAGCTGTGTACAGAAATGAGACT 180
6 GATGTCAGAAAGGCGCAGATCTATGTTTATTCAGCTGTGTACAGAAATGAGACT 257

181 GGGGCAATTCGGGCTGGCAGTGTGTTATGTCACACAGAGTGAATGGCAATTGGCGT 240
258 GCAGAGTTTGGGCTGGCAGTGTGTTATGTCACACAGAGTGAATGGCAATTGGCGT 317
241 TATTTCCCGCAACTGGTTAGAGCAGCAGGTGTACAGAGGCC 288
318 TATTTCCCGCAACTGGTTAGAGCAGCAGGTGTATACAGAGGCC 365

RESULT 15

BO565179 485 bp mRNA linear EST 19-JUN-2002
LOCUS g132a07.y1 Mouse Organ of Corti cDNA Bluescript Mus musculus cDNA
DEFINITION clone g132a07 5', mRNA sequence.
ACCESSION BO565179
VERSION BO565179.1 GI:21468496
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Mammalia: Eutheria: Rodentia: Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 485)

REFERENCE
AUTHORS Kachar, B.
TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
JOURNAL Unpublished
COMMENT Contact: Kachar, B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: kachar@nidcd.nih.gov
Plate: 32 row: a column: 07
Seq primer: M13RPI reverse primer (ABI).
Location/Qualifiers

FEATURES

source

1..485
/organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
/db_xref="taxon:10090"
/clone="g132a07"
/sex="male and female"
/dev_stage="Postnatal day 5 to 13"
/clone_lib="Mouse Organ of Corti cDNA Bluescript"
/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was clipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro FastTrack Kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR GigaPack III Gold Cloning Kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug RNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden)

and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack II Gold and, upon titration on XL1 Blue MRF⁺ cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 µl of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAAACGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 146 a 92 c 122 g 125 t
ORIGIN

Query Match 65.7%; Score 216.8; DB 13; Length 485;
Best Local Similarity 93.0%; Pred. No. 7.1e-57;
Matches 227; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

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| Db | 1 | GGAAGATTACATGCCCCAGACTGTAGTTCATCATGTCAGAGAGGCGAGCATCTA | 60 |
| QY | 147 | TGTTTATTCAGAGCTGTAAACAGAAAATGAGCTGGGGCACTTCTGGGCTGGCACTTTTA | 206 |
| Db | 61 | TGTTTATTCAGAGCTGTAAACAGAAAATGAGCTGGGGCACTTCTGGGCTGGCACTTTTA | 120 |
| QY | 207 | TGGTGACCAACAGATAGATGGGAATTTGGGTTATTTCCAGCAACTGGTTAGAGA | 266 |
| Db | 121 | TGGTGACCAACAGATAGATGGGAATTTGGGTTATTTCCAGCAACTGGTTAGAGA | 180 |
| QY | 267 | GCAACGAGTGTACAGAGAGGCCACCAAGAGATTCCACCGGATATTGACTTCTTCTG | 326 |
| Db | 181 | GCAACGAGTGTATACAGAGAGGCCACCAAGAGATTCCACCGGATATTGACTTCTTCTG | 240 |
| QY | 327 | TGAA 330 | |
| Db | 241 | TGAA 244 | |

Search completed: December 30, 2003, 06:07:18
Job time : 1099.64 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 22:01:01 ; Search time 109.538 Seconds
(without alignments)
8132.484 Million cell updates/sec

Title: US-10-019-455A-48

Perfect score: 330
Sequence: 1 catggcatgttcatggataa.....atattgactctctctgtgaa 330

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: N.Geneseq_19Jun03.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | ID | Description |
|------------|-------|--------------------|-----|-------------|
| 1 | 330 | 100.0 | 330 | 22 AAFS9099 |
| 2 | 330 | 100.0 | 330 | 22 AAFS9098 |
| 3 | 294.8 | 89.3 | 330 | 22 AAFS9080 |
| 4 | 294.8 | 89.3 | 384 | 22 AAFS9088 |
| 5 | 294.8 | 89.3 | 947 | 22 AAFS9084 |
| 6 | 281.6 | 85.3 | 307 | 22 AAFS9093 |
| 7 | 261 | 79.1 | 261 | 22 AAFS9092 |
| 8 | 249 | 75.5 | 330 | 22 AAFS9079 |

| | | | | | |
|----|------|------|------|--------------|--------------------|
| 9 | 249 | 75.5 | 384 | 22 AAFS9065 | Human MLP nucleoti |
| 10 | 249 | 75.5 | 387 | 24 AAS17583 | DNA encoding novel |
| 11 | 249 | 75.5 | 426 | 22 AAB26341 | Human growth regul |
| 12 | 249 | 75.5 | 521 | 24 ABL95740 | Human angiogenesis |
| 13 | 249 | 75.5 | 521 | 24 ABL88251 | Human PRO8873 CDNA |
| 14 | 249 | 75.5 | 521 | 24 ABRK3571 | CDNA encoding huma |
| 15 | 249 | 75.5 | 891 | 22 AAH98228 | Human EST-derived |
| 16 | 249 | 75.5 | 891 | 22 AAH26342 | Human growth regul |
| 17 | 249 | 75.5 | 923 | 22 AAFS9083 | Human MLP nucleoti |
| 18 | 249 | 75.5 | 1201 | 22 AAH26343 | Human growth regul |
| 19 | 64 | 19.4 | 581 | 16 AAQ84052 | Sequence encoding |
| 20 | 63.4 | 19.2 | 433 | 22 AAH47783 | Recombinant human |
| 21 | 63.4 | 19.2 | 459 | 16 AAQ84050 | Sequence encoding |
| 22 | 63.4 | 19.2 | 459 | 22 AAH70083 | Melanoma inhibitor |
| 23 | 63.4 | 19.2 | 459 | 22 AAD18732 | Human antisense ol |
| 24 | 63.4 | 19.2 | 555 | 23 AAVS9229 | Human prostate exp |
| 25 | 62.4 | 18.9 | 330 | 16 AAQ84061 | Sequence encoding |
| 26 | 61.8 | 18.7 | 442 | 24 ABL63602 | Breast cancer rela |
| 27 | 61.8 | 18.7 | 442 | 24 ABL64012 | Breast cancer rela |
| 28 | 57.4 | 17.4 | 305 | 16 AAQ84055 | Amplified fragment |
| 29 | 47.2 | 14.3 | 1060 | 22 AAF92140 | Human PRO19670 CDN |
| 30 | 47.2 | 14.3 | 1060 | 24 AAB574460 | Human CDNA encodin |
| 31 | 47.2 | 14.3 | 1060 | 24 ABL95738 | Human angiogenesis |
| 32 | 47.2 | 14.3 | 1060 | 24 ABL88249 | Human PRO19670 CDN |
| 33 | 47.2 | 14.3 | 1060 | 25 ACAS7963 | Human PRO19670 CDN |
| 34 | 47.2 | 14.3 | 1060 | 25 ACAS8892 | CDNA encoding huma |
| 35 | 47.2 | 14.3 | 1060 | 25 ACAG6045 | Novel human secret |
| 36 | 47.2 | 14.3 | 1060 | 25 ACAG6345 | CDNA encoding huma |
| 37 | 47.2 | 14.3 | 1060 | 25 ABR98433 | Human CDNA encodin |
| 38 | 47.2 | 14.3 | 1060 | 25 ABR98935 | Novel human secret |
| 39 | 47.2 | 14.3 | 1060 | 25 ACAG5980 | Human secreted/tra |
| 40 | 47.2 | 14.3 | 1060 | 25 ABR98024 | Human PRO polynuc |
| 41 | 47.2 | 14.3 | 1060 | 25 ABR78808 | Human PRO polynuc |
| 42 | 47.2 | 14.3 | 1060 | 25 ABR75821 | Human CDNA encodin |
| 43 | 47.2 | 14.3 | 1060 | 25 ABR77026 | Human PRO polynuc |
| 44 | 47.2 | 14.3 | 1060 | 25 ABR16866 | Human CDNA encodin |
| 45 | 47.2 | 14.3 | 1061 | 22 AAG46205 | Human DNA encoding |

ALIGNMENTS

| | | |
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| RESULT 1 | AAFS9099 | standard; DNA; 330 BP. |
| ID | AAFS9099 | |
| AC | AAFS9099; | |
| XX | | |
| DT | 23-Apr-2001 | (first entry) |
| XX | | |
| DE | Rat MLP nucleotide sequence SEQ ID NO:48. | |
| XX | | |
| KW | MIP; MIA; melanoma inhibitory activity; cancer; bone disease; | |
| KW | joint disease; pathologic angiogenesis; diagnosis; antiinflammatory; | |
| KW | cardiac; gene therapy; secretory cell function regulator; promoter; | |
| KW | inhibitor; ds. | |
| XX | | |
| OS | Rattus sp. | |
| XX | | |
| PN | W0200102564-A1. | |
| XX | | |
| PD | 11-JAN-2001. | |
| XX | | |
| PF | 29-JUN-2000; 2000WO-JP04278. | |
| XX | | |
| PR | 30-JUN-1999; 99JP-0186718. | |
| XX | | |
| PA | (TAKE) TAKEDA CHEM IND LTD. | |
| XX | | |
| PI | Itoh Y, Nishi K, Ogi K, Okubo S, Mogi S, Noguchi Y, Yoshimura K; | |
| XX | Tanaka H; | |
| DR | WPI, 2001-159271/16. | |

DR P-PSDB; AAB69131.
 XX Safe, low-toxicity secretory cell function-regulatory protein and
 PT encoded DNA, applicable as drugs, in diagnosis and development of
 PT promoters and inhibitors for preventing or treating e.g. bone and joint
 diseases -
 XX
 XX
 PS Claim 12; Page 107; 111pp; Japanese.
 CC The present invention describes novel MLP proteins and their encoding
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
 CC activities, and can be used in gene therapy and as secretory cell
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in
 CC the diagnosis and development of promoters and inhibitors for preventing
 CC or treating bone and joint diseases as well as pathologic angiogenesis.
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
 CC in the exemplification of the present invention.
 XX
 SQ Sequence 330 BP; 91 A; 62 C; 91 G; 86 T; 0 other;
 Query Match 100.0%; Score 330; DB 22; Length 330;
 Best Local Similarity 100.0%; Pred. No. 4,4e-100; Indels 0; Gaps 0;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CATGGCATGTTTATGATAAATCTTCTCTTAAAGAGTTGTGACAGATGAGAGTGTGTC 60
 Db 1 CATGGCATGTTTATGATAAATCTTCTCTTAAAGAGTTGTGACAGATGAGAGTGTGTC 60
 QY 61 TATACCATTTCTCTGGCAAGAGCAGAGAAAGACTACATGCCCCGAGCTGTAGTTTCATC 120
 Db 61 TATACCATTTCTCTGGCAAGAGCAGAGAAAGACTACATGCCCCGAGCTGTAGTTTCATC 120
 QY 121 AATGTCAGAAAGGCGACAGATCTATGTTTATCCAACTGTGTAAACAAAATGAGACT 180
 Db 121 AATGTCAGAAAGGCGACAGATCTATGTTTATCCAACTGTGTAAACAAAATGAGACT 180
 QY 181 GGGGCAATTCGGGCTGGCACTGTTTATGTCACCAAGAGTGAATGGAATTTGGGCT 240
 Db 181 GGGGCAATTCGGGCTGGCACTGTTTATGTCACCAAGAGTGAATGGAATTTGGGCT 240
 QY 241 TATTTCCCGCAGCACTTGTTAGAGCAACGAGTGTACAGAGGCCCAAGAGAGATT 300
 Db 241 TATTTCCCGCAGCACTTGTTAGAGCAACGAGTGTACAGAGGCCCAAGAGAGATT 300
 QY 301 CCAACCAAGGATTTGACTTCTTCTGTGAA 330
 Db 301 CCAACCAAGGATTTGACTTCTTCTGTGAA 330
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 AAF59098
 ID AAF59098 standard; DNA; 384 BP.
 XX
 AC AAF59098;
 XX
 XX
 DT 23-APR-2001 (first entry)
 DE Rat MLP nucleotide sequence SEQ ID NO:46.
 XX
 XX MIP; MIA; melanoma inhibitory activity; cancer; bone disease;
 KM joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
 KM cardiant; gene therapy; secretory cell function regulator; promoter;
 XX inhibitor; ds.
 XX
 OS Rattus sp.
 XX
 PN WO200102564-A1.
 XX
 PD 11-JAN-2001.
 XX
 PF 29-JUN-2000; 2000WO-JP04278.
 XX
 PR 30-JUN-1999; 99JP-0186718.

XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Itoh Y, Nishi K, Ogi K, Okubo S, Mogi S, Noguchi Y, Yoshimura K;
 PI Tanaka H;
 XX
 DR WPI; 2001-159271/16.
 DR P-PSDB; AAB69130.
 XX
 XX Safe, low-toxicity secretory cell function-regulatory protein and
 PT encoded DNA, applicable as drugs, in diagnosis and development of
 PT promoters and inhibitors for preventing or treating e.g. bone and joint
 diseases -
 XX
 PS Claim 13; Page 105-106; 111pp; Japanese.
 CC The present invention describes novel MLP proteins and their encoding
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
 CC activities, and can be used in gene therapy and as secretory cell
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in
 CC the diagnosis and development of promoters and inhibitors for preventing
 CC or treating bone and joint diseases as well as pathologic angiogenesis.
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
 CC in the exemplification of the present invention.
 XX
 SQ Sequence 384 BP; 98 A; 72 C; 109 G; 105 T; 0 other;
 Query Match 100.0%; Score 330; DB 22; Length 384;
 Best Local Similarity 100.0%; Pred. No. 4,8e-100; Indels 0; Gaps 0;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CATGGCATGTTTATGATAAATCTTCTCTTAAAGAGTTGTGACAGATGAGAGTGTGTC 60
 Db 55 CATGGCATGTTTATGATAAATCTTCTCTTAAAGAGTTGTGACAGATGAGAGTGTGTC 114
 QY 61 TATACCATTTCTCTGGCAAGAGCAGAGAAAGACTACATGCCCCGAGCTGTAGTTTCATC 120
 Db 115 TATACCATTTCTCTGGCAAGAGCAGAGAAAGACTACATGCCCCGAGCTGTAGTTTCATC 174
 QY 121 AATGTCAGAAAGGCGACAGATCTATGTTTATCCAACTGTGTAAACAAAATGAGACT 180
 Db 175 AATGTCAGAAAGGCGACAGATCTATGTTTATCCAACTGTGTAAACAAAATGAGACT 234
 QY 181 GGGGCAATTCGGGCTGGCACTGTTTATGTCACCAAGAGTGAATGGAATTTGGGCT 240
 Db 235 GGGGCAATTCGGGCTGGCACTGTTTATGTCACCAAGAGTGAATGGAATTTGGGCT 294
 QY 241 TATTTCCCGCAGCACTTGTTAGAGCAACGAGTGTACAGAGGCCCAAGAGAGATT 300
 Db 295 TATTTCCCGCAGCACTTGTTAGAGCAACGAGTGTACAGAGGCCCAAGAGAGATT 354
 QY 301 CCAACCAAGGATTTGACTTCTTCTGTGAA 330
 Db 355 CCAACCAAGGATTTGACTTCTTCTGTGAA 384
 RESULT 3
 AAF59080
 ID AAF59080 standard; DNA; 330 BP.
 XX
 AC AAF59080;
 XX
 XX
 DT 23-APR-2001 (first entry)
 DE Mouse MLP nucleotide sequence SEQ ID NO:25.
 XX
 XX MIP; MIA; melanoma inhibitory activity; cancer; bone disease;
 KM joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
 KM cardiant; gene therapy; secretory cell function regulator; promoter;
 XX inhibitor; ds.
 XX
 OS Mus musculus.

PN WO200102564-A1.
 XX 11-JUN-2001.
 PD
 XX 29-JUN-2000; 2000WO-JP04278.
 PF
 XX 30-JUN-1999; 99JP-0186718.
 PR
 XX (TAKE) TAKEDA CHEM IND LTD.
 PA
 XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
 PI Tanaka H;
 P1
 DR WPI; 2001-159271/16.
 DR P-PSDB; AAB69127.
 XX
 XX Safe, low-toxicity secretory cell function-regulatory protein and
 PT encoded DNA, applicable as drugs, in diagnosis and development of
 PT promoters and inhibitors for preventing e.g. bone and joint
 PT diseases -
 PS Claim 10; Page 98; 111pp; Japanese.
 XX
 CC The present invention describes novel MLP proteins and their encoding
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
 CC activities, and can be used in gene therapy and as secretory cell
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in
 CC the diagnosis and development of promoters and inhibitors for preventing
 CC or treating bone and joint diseases as well as pathologic angiogenesis.
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
 CC in the exemplification of the present invention.
 CC
 SQ Sequence 330 BP; 91 A; 60 C; 92 G; 87 T; 0 other;
 Query Match 89.3%; Score 294.8; DB 22; Length 330;
 Best Local Similarity 93.3%; Pred. No. 2.7e-88;
 Matches 308; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
 QY 1 CATGCACTTTATGATGAATACTTTCTTAAGAAGTTGTGAGATGAGAGTGTGC 60
 DB 1 CATGGTATTTATGATGAATACTTTCTTAAGAAGTTGTGAGATGAGAGTGTGC 60
 QY 61 TATACATTTCTCTGCGAAGACAGAGACTACATATGCCCGGACTGAGTTGATC 120
 DB 61 TATATATTTCTCTGCGAAGACAGAGACTACATATGCCCGGACTGAGTTGATC 120
 QY 121 AATGCAAGAAAGGCGACAGATCTATGTTTATTCAGAGCTGTGTACAGAAATGAGCT 180
 DB 121 GATGCAAGAAAGGCGACAGATCTATGTTTATTCAGAGCTGTGTACAGAAATGAGCT 180
 QY 181 GGGGCAATCTGGGCTGCGAGTGTATGTGACACCAAGATGAGATGAGATGAGCT 240
 DB 181 GGAGAGTTTGGGCTGCGAGTGTATGTGACACCAAGATGAGATGAGATGAGCT 240
 QY 241 TATTTCCCGACCACTTGTTAGAGAGCAAGAGTGTATCCAGAGGCGCCAAAGAGAT 300
 DB 241 TATTTCCCGACCACTTGTTAGAGAGCAAGAGTGTATCCAGAGGCGCCAAAGAGAT 300
 QY 301 CCAACCAAGATATGACTTCTTCTGTGAA 330
 DB 301 CCAACCAAGATATGACTTCTTCTGTGAA 330
 RESULT 4
 AAF59068
 ID AAF59068 standard; DNA; 384 BP.
 AC AAF59068;
 XX
 DT 23-APR-2001 (first entry)
 XX
 DE Mouse MLP nucleotide sequence SEQ ID NO:10.
 XX

KM MLP, MIA, melanoma inhibitory activity; cancer; bone disease;
 KM joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
 KM cardiant; gene therapy; secretory cell function regulator; promoter;
 KM inhibitor; ds.
 OS
 XX Mus musculus.
 XX
 XX WO200102564-A1.
 PN
 XX 11-JUN-2001.
 PD
 XX 29-JUN-2000; 2000WO-JP04278.
 PF
 XX 30-JUN-1999; 99JP-0186718.
 PR
 XX (TAKE) TAKEDA CHEM IND LTD.
 PA
 XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
 PI Tanaka H;
 P1
 DR WPI; 2001-159271/16.
 DR P-PSDB; AAB69125.
 XX
 XX Safe, low-toxicity secretory cell function-regulatory protein and
 PT encoded DNA, applicable as drugs, in diagnosis and development of
 PT promoters and inhibitors for preventing e.g. bone and joint
 PT diseases -
 PS Claim 11; Page 93; 111pp; Japanese.
 XX
 CC The present invention describes novel MLP proteins and their encoding
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
 CC activities, and can be used in gene therapy and as secretory cell
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in
 CC the diagnosis and development of promoters and inhibitors for preventing
 CC or treating bone and joint diseases as well as pathologic angiogenesis.
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
 CC in the exemplification of the present invention.
 CC
 SQ Sequence 384 BP; 98 A; 68 C; 111 G; 107 T; 0 other;
 Query Match 89.3%; Score 294.8; DB 22; Length 384;
 Best Local Similarity 93.3%; Pred. No. 2.9e-88;
 Matches 308; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
 QY 1 CATGCACTTTATGATGAATACTTTCTTAAGAAGTTGTGAGATGAGAGTGTGC 60
 DB 55 CATGGTATTTATGATGAATACTTTCTTAAGAAGTTGTGAGATGAGAGTGTGC 114
 QY 61 TATACATTTCTCTGCGAAGACAGAGACTACATATGCCCGGACTGAGTTGATC 120
 DB 115 TATATATTTCTCTGCGAAGACAGAGACTACATATGCCCGGACTGAGTTGATC 174
 QY 121 AATGCAAGAAAGGCGACAGATCTATGTTTATTCAGAGCTGTGTACAGAAATGAGCT 180
 DB 175 GATGCAAGAAAGGCGACAGATCTATGTTTATTCAGAGCTGTGTACAGAAATGAGCT 234
 QY 181 GGGGCAATCTGGGCTGCGAGTGTATGTGACACCAAGATGAGATGAGATGAGCT 240
 DB 235 GGAGAGTTTGGGCTGCGAGTGTATGTGACACCAAGATGAGATGAGATGAGCT 294
 QY 241 TATTTCCCGACCACTTGTTAGAGAGCAAGAGTGTATCCAGAGGCGCCAAAGAGAT 300
 DB 295 TATTTCCCGACCACTTGTTAGAGAGCAAGAGTGTATCCAGAGGCGCCAAAGAGAT 354
 QY 301 CCAACCAAGATATGACTTCTTCTGTGAA 330
 DB 355 CCAACCAAGATATGACTTCTTCTGTGAA 384
 RESULT 5
 AAF59084
 ID AAF59084 standard; DNA; 947 BP.
 XX


```

XX AAF59084;
AC
XX 23-APR-2001 (first entry)
DT
XX
XX
XX
DE Mouse MLP nucleotide sequence SEQ ID NO:30.
XX
XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
XX joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
XX cardiant; gene therapy; secretory cell function regulator; promoter;
XX inhibitor; ds.
XX
XX Mus musculus.
XX
XX WO200102564-A1.
XX
XX 11-JAN-2001.
XX
XX 29-JUN-2000; 2000WO-JP04278.
XX
XX 30-JUN-1999; 99JP-0186718.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K,
XX Tanaka H;
XX
XX MPI; 2001-159271/16.
XX
XX Safe, low-toxicity secretory cell function-regulatory protein and
XX encoded DNA, applicable as drugs, in diagnosis and development of
XX promoters and inhibitors for preventing or treating e.g. bone and joint
XX diseases -
XX
XX Example 2; Page 100-101; 11pp; Japanese.
XX
XX The present invention describes novel MLP proteins and their encoding
XX DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
XX activities, and can be used in gene therapy and as secretory cell
XX function regulators. The MLP proteins and DNAs can be used in drugs, in
XX the diagnosis and development of promoters and inhibitors for preventing
XX or treating bone and joint diseases as well as pathologic angiogenesis.
XX AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
XX in the exemplification of the present invention.
XX
XX Sequence 947 BP; 279 A; 158 C; 221 G; 289 T; 0 other;
SQ
Query Match 89.3%; Score 294.8; DB 22; Length 947;
Best Local Similarity 93.3%; Pred. No. 4.3e-88;
Matches 308; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 1 CATGCATGTTATGATTAACCTTCTTAAAGAGTGTGTCAGATGAGAGTGTGTC 60
DB 65 CATGCTGATTTATGATTAACCTTCTTAAAGAGTGTGTCAGATGAGAGTGTGTC 124
QY 61 TATTCATTTCTCTGGCAAGACACAGAGACTACATGCCCGGACTGTAGTTCATC 120
DB 125 TATCTATTTCTCTGGCAAGACACAGAGACTACATGCCCGGACTGTAGTTCATC 184
QY 121 AATGTCAAGAAAGGCGACAGATCTATGTTTATTCAGAGCTGTAAACAGAAAATGAGCT 180
DB 185 GATGTCAAGAAAGGCGACAGATCTATGTTTATTCAGAGCTGTAAACAGAAAATGAGCT 244
QY 181 GGGGCATTTCTGGGCTGGCAGTGTATTATGTCACCAAGATGAGATGGGAATTTGGGT 240
DB 245 GGAAGATTTCTGGGCTGGCAGTGTATTATGTCACCAAGATGAGATGGGAATTTGGGT 304
QY 241 TATTTCCCGACACTGTTGTTAGAGACCAAGAGTACAGAGGCGCACCAAGAGGAT 300
DB 305 TATTTCCCGACACTGTTGTTAGAGACCAAGAGTACAGAGGCGCACCAAGAGGAT 364
QY 301 CCAACCAAGGATTTGATCTTCTCTGTGAA 330

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DB 365 CCAACCAAGGATTTGATCTTCTCTGTGAA 394
RESULT 6
AAF59093
ID AAF59093 standard; DNA; 307 BP.
XX
XX AAF59093;
AC
XX 23-APR-2001 (first entry)
DT
XX
XX Rat MLP nucleotide sequence SEQ ID NO:41.
XX
XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
XX joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
XX cardiant; gene therapy; secretory cell function regulator; promoter;
XX inhibitor; ds.
XX
XX Rattus sp.
XX
XX WO200102564-A1.
XX
XX 11-JAN-2001.
XX
XX 29-JUN-2000; 2000WO-JP04278.
XX
XX 30-JUN-1999; 99JP-0186718.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K,
XX Tanaka H;
XX
XX MPI; 2001-159271/16.
XX
XX Safe, low-toxicity secretory cell function-regulatory protein and
XX encoded DNA, applicable as drugs, in diagnosis and development of
XX promoters and inhibitors for preventing or treating e.g. bone and joint
XX diseases -
XX
XX Example 9; Page 104; 11pp; Japanese.
XX
XX The present invention describes novel MLP proteins and their encoding
XX DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
XX activities, and can be used in gene therapy and as secretory cell
XX function regulators. The MLP proteins and DNAs can be used in drugs, in
XX the diagnosis and development of promoters and inhibitors for preventing
XX or treating bone and joint diseases as well as pathologic angiogenesis.
XX AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
XX in the exemplification of the present invention.
XX
XX Sequence 307 BP; 84 A; 56 C; 90 G; 77 T; 0 other;
SQ
Query Match 85.3%; Score 281.6; DB 22; Length 307;
Best Local Similarity 98.3%; Pred. No. 6.7e-84;
Matches 295; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY 1 CATGCATGTTATGATTAACCTTCTTAAAGAGTGTGTCAGATGAGAGTGTGTC 60
DB 7 CATGCTGATTTATGATTAACCTTCTTAAAGAGTGTGTCAGATGAGAGTGTGTC 66
QY 61 TATTCATTTCTCTGGCAAGACACAGAGACTACATGCCCGGACTGTAGTTCATC 120
DB 67 TATTCATTTCTCTGGCAAGACACAGAGACTACATGCCCGGACTGTAGTTCATC 126
QY 121 AATGTCAAGAAAGGCGACAGATCTATGTTTATTCAGAGCTGTAAACAGAAAATGAGCT 180
DB 127 AATGTCAAGAAAGGCGACAGATCTATGTTTATTCAGAGCTGTAAACAGAAAATGAGCT 186
QY 181 GGGGCATTTCTGGGCTGGCAGTGTATTATGTCACCAAGATGAGATGGGAATTTGGGT 240
DB 187 GGGGCATTTCTGGGCTGGCAGTGTATTATGTCACCAAGATGAGATGGGAATTTGGGT 246

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QY 241 TATTTCCCACTTGTAGAGACAGAGTGTACAGCA-GGCCACCAAGAGAT 299
DB 247 TATTTCCCACTTGTAGAGACAGAGTGTACAGCAAGAGAT 306

RESULT 7
AAFS9092 standard; DNA; 261 BP.

AAFS9092;

23-APR-2001 (first entry)

Rat MLP nucleotide sequence SEQ ID NO:40.

MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
cardiant; gene therapy; secretory cell function regulator; promoter;
inhibitor; ds.

Rattus sp.

WO200102564-A1.

11-JAN-2001.

29-JUN-2000; 2000WO-JP04278.

30-JUN-1999; 99JP-0186718.

(TAKE) TAKEDA CHEM IND LTD.

Itch Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;

Tanaka H;

WPI; 2001-159271/16.

Safe, low-toxicity secretory cell function-regulatory protein and
PT encoded DNA, applicable as drugs, in diagnosis and development of
PT promoters and inhibitors for preventing or treating e.g. bone and joint
PT diseases -

Example 9; Page 104; 111pp; Japanese.

CC The present invention describes novel MLP proteins and their encoding
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
CC activities, and can be used in gene therapy and as secretory cell
CC function regulators. The MLP proteins and DNAs can be used in drugs, in
CC the diagnosis and development of promoters and inhibitors for preventing
CC or treating bone and joint diseases as well as pathologic angiogenesis.
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
CC in the exemplification of the present invention.

Sequence 261 BP; 72 A; 46 C; 75 G; 68 T; 0 other;

Query Match 79.1%; Score 261; DB 22; Length 261;
Best Local Similarity 100.0%; Pred. No. 4.9e-77;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GGATAACTTTCTTGAAGAGTGTGTGAGATGAGAGTGTCTTATACCATTTCTCT 74
DB 1 GATTAACCTTTCTTGAAGAGTGTGTGAGATGAGAGTGTCTTATACCATTTCTCT 60
QY 75 GGCAAGAGCAGAGAGAGCTACATGATGAGAGTGTGTGAGATGAGAGTGTCTCT 134
DB 61 GGCAAGAGCAGAGAGAGCTACATGATGAGAGTGTGTGAGATGAGAGTGTCTCT 120
QY 135 GCAGAGATCTATGTTTATCCAGAGTGTGTGAGAGTGTGTGAGAGTGTCTCT 194
DB 121 GCAGAGATCTATGTTTATCCAGAGTGTGTGAGAGTGTGTGAGAGTGTCTCT 180
QY 195 TGCGAGTGTATGTTGAGAGCAGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 254

DB 181 TGCGAGTGTATGTTGAGAGCAGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 240
QY 255 CTTGTTAGAGAGCAAGAGT 275
DB 241 CTTGTTAGAGAGCAAGAGT 261

RESULT 8
AAFS9079 standard; DNA; 330 BP.

AAFS9079;

23-APR-2001 (first entry)

Human MLP nucleotide sequence SEQ ID NO:23.

MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
cardiant; gene therapy; secretory cell function regulator; promoter;
inhibitor; ds.

Homo sapiens.

WO200102564-A1.

11-JAN-2001.

29-JUN-2000; 2000WO-JP04278.

30-JUN-1999; 99JP-0186718.

(TAKE) TAKEDA CHEM IND LTD.

Itch Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;

Tanaka H;

WPI; 2001-159271/16.

Safe, low-toxicity secretory cell function-regulatory protein and
PT encoded DNA, applicable as drugs, in diagnosis and development of
PT promoters and inhibitors for preventing or treating e.g. bone and joint
PT diseases -

Example 8; Page 97; 111pp; Japanese.

CC The present invention describes novel MLP proteins and their encoding
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
CC activities, and can be used in gene therapy and as secretory cell
CC function regulators. The MLP proteins and DNAs can be used in drugs, in
CC the diagnosis and development of promoters and inhibitors for preventing
CC or treating bone and joint diseases as well as pathologic angiogenesis.
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
CC in the exemplification of the present invention.

Sequence 330 BP; 91 A; 60 C; 91 G; 88 T; 0 other;

Query Match 75.5%; Score 249; DB 22; Length 330;
Best Local Similarity 84.8%; Pred. No. 5.6e-73;
Matches 279; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1 CATGCAATTTTATGAGATTAATCTTCTTGAAGAGTGTGTGAGATGAGAGTGTCTC 60
DB 1 CATGCAATTTTATGAGATTAATCTTCTTGAAGAGTGTGTGAGATGAGAGTGTCTC 60
QY 61 TATACATTTTCTTGGCAAGAGCAGAGAGTGTGTGAGAGTGTGTGAGAGTGTCTCT 120
DB 61 TATACATTTTCTTGGCAAGAGCAGAGAGTGTGTGAGAGTGTGTGAGAGTGTCTCT 120
QY 121 AATGCAAGAGAGAGCAGAGATTAATCTTCTTGAAGAGTGTGTGAGAGTGTCTCT 180
DB 121 AATGCAAGAGAGAGCAGAGATTAATCTTCTTGAAGAGTGTGTGAGAGTGTCTCT 180

QY 181 GGGGATTTCTGGGCTGCGAGTGTATATGTTGACCAACAGATGAGATGCGAATTGTGGCT 240
 DB 181 GGAGATTTTGGGCTGCGAGTGTATATGTTGACCAACAGATGAGATGCGAATTGTGGCT 240
 QY 241 TATTTCCCGAGCACTTGTGTAGAGCAACAGATGATCCAGAGGCCCAAGAGAT 300
 DB 241 TATTTCCCGAGCACTTGTGTAGAGCAACAGATGATCCAGAGGCCCAAGAGAT 300
 QY 301 CCAACCAAGATTTGACTTCTTCTGTGA 329
 DB 301 CCCACCAAGATTTGACTTCTTCTGTGA 329
 RESULT 9
 AAF59065
 ID AAF59065 standard; DNA; 384 BP.
 AC AAF59065;
 XX
 DT 23-APR-2001 (first entry)
 XX
 DE Human MLP nucleotide sequence SEQ ID NO:4.
 XX
 KM MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
 KM joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
 KM cardiant; gene therapy; secretory cell function regulator; promoter;
 KM inhibitor; ds.
 KM
 XX
 OS Homo sapiens.
 XX
 PN WO200102564-A1.
 XX
 PD 11-JAN-2001.
 XX
 PE 29-JUN-2000; 2000WO-JP042778.
 XX
 PR 30-JUN-1999; 99JP-0186718.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K,
 PI Tanaka H;
 DR WPI; 2001-159271/16.
 DR P-PSDB; AAB69123.
 XX
 XX Safe, low-toxicity secretory cell function-regulatory protein and
 PT encoded DNA, applicable as drugs, in diagnosis and development of
 PT promoters and inhibitors for preventing or treating e.g. bone and joint
 PT diseases -
 XX
 XX Example 1; Page 91; 11pp; Japanese.
 XX
 CC The present invention describes novel MLP proteins and their encoding
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
 CC activities, and can be used in gene therapy and as secretory cell
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in
 CC the diagnosis and development of promoters and inhibitors for preventing
 CC or treating bone and joint diseases as well as pathologic angiogenesis.
 CC AAF59065 to AAF59099 and AAB69122 to AAB69132 represent sequences used
 CC in the exemplification of the present invention.
 CC
 XX
 XX Sequence 384 BP; 99 A; 70 C; 106 G; 109 T; 0 other;
 SQ
 Query Match 75.5%; Score 249; DB 22; Length 384;
 Best Local Similarity 84.8%; Pred. No. 6e-73;
 Matches 279; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
 QY 1 CATGGATGTTTATGATAAATTTCTTCTTACAGAGTTGTGCGACATGAGAGTGTGTC 60
 DB 55 CATGGATATTTATGACCGCTAGCTTCCAGAGAGCTGTGCGACATGATAGTGTGTC 114

QY 61 TATACATTTCTGTGGCAAGACACAGAAAGACTACAAATGCCCCGAGTGTAGTTCATC 120
 DB 115 TATATCTTTCTGTGGTGTAGTGTCTCAAGAAATATATATGCCCCGAGTGTATTCATT 174
 QY 121 AATGTCAAGAAAGGCGACGAGATCTATGTTTATTCAGAGTGTGTAACAGAAATGAGCT 180
 DB 175 AAGCTTAAAAAAGGCGACGAGATCTATGTTTACTCAAGCTGTGTAAGAAATGAGCT 234
 QY 181 GGGGATTTCTGGGCTGCGAGTGTATATGTTGACCAACAGATGAGATGCGAATTGTGGCT 240
 DB 235 GGAGATTTTGGGCTGCGAGTGTATATGTTGACCAACAGATGAGATGCGAATTGTGGCT 294
 QY 241 TATTTCCCGAGCACTTGTGTAGAGCAACAGATGATCCAGAGGCCCAAGAGAT 300
 DB 295 TATTTCCCGAGCACTTGTGTAGAGCAACAGATGATCCAGAGGCCCAAGAGAT 354
 QY 301 CCAACCAAGATTTGACTTCTTCTGTGA 329
 DB 355 CCCACCAAGATTTGACTTCTTCTGTGA 383
 RESULT 10
 AAS17583
 ID AAS17583 standard; cDNA; 387 BP.
 AC AAS17583;
 XX
 DT 26-FEB-2002 (first entry)
 XX
 DE DNA encoding novel secreted protein #12.
 XX
 KM Secreted protein; cytosolic; immunosuppressive; vlnery; vaccine;
 KM antiinflammatory; neuroprotective; nephrotoxic; cardiovascular;
 KM human; cancer; autoimmune disease; wound healing disorder; infection;
 KM haematopoietic disorder; inflammatory disorder; infertility;
 KM neurological disease; psychiatric disease; cardiovascular disease;
 KM respiratory disease; renal; gastrointestinal; ss.
 KM
 XX
 OS Homo sapiens.
 XX
 PN WO200179454-A1.
 XX
 PD 25-OCT-2001.
 XX
 PE 11-APR-2001; 2001WO-US11797.
 XX
 PR 13-APR-2000; 2000US-196603P.
 PR 24-APR-2000; 2000US-199417P.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PI Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;
 DR WPI; 2002-061975/08.
 DR P-PSDB; AAU09871.
 XX
 XX New secreted proteins or polypeptides, useful for treating e.g. cancer,
 PT autoimmune diseases, wound healing disorder, infections, haematopoietic
 PT disorders, inflammatory disorders, infertility, cancer -
 PT
 XX
 XX Claim 2; Page 44; 92pp; English.
 PS
 CC The invention relates to an isolated novel secreted polypeptide (I) and
 CC polynucleotide (II). (I) and (II) are useful for treating cancer,
 CC autoimmune diseases, wound healing disorder, infections, haematopoietic
 CC disorders, inflammatory disorders, infertility, neurological and
 CC psychiatric diseases, cardiovascular diseases, respiratory diseases,

renal diseases, or gastrointestinal diseases. These may also be used to treat diseases, abnormalities and disorders caused by abnormal expression, production, function and/or metabolism of the genes, as vaccines for inducing immunological response in a mammal, and in screening methods for detecting the effect of added compounds on the production of mRNA and polypeptide in cells. The polypeptides can be used as immunogens to produce antibodies immunospecific for the polypeptides, and to identify membrane-bound or soluble receptors. The polynucleotides may be used as diagnostic reagents, in chromosome localisation studies, and in tissue expression studies. The present sequence represents the coding sequence of novel human secreted protein #12.

Sequence 387 BP; 101 A; 70 C; 106 G; 110 T; 0 other;

Query Match 75.5%; Score 249; DB 24; Length 387;
Best Local Similarity 84.8%; Pred. No. 6e-73;
Matches 279; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

1 CATGGCATGTTTATGATTAACCTTCTTCTTAAGAGTTGTGTGCAATGAGAGTGTCTC 60
55 CATGGAATTTTATGAGACCGCTCTAGCTTCCAGAGAGCTCTGTGCAATGAGAGTGTCTC 114
61 TATACATTTCTCTGGCAGAGCAGACAGAGAGACTACATGCCCCGAGCTGAGTTCATC 120
115 TATCTATTTCTCTGGCTAGTGTCTCAAGAAATTAATGCCCCGAGCTGAGTTCATC 174
121 AATGTCAGAAAGGCGACAGATCTATGTTTATTCAGAGTGTGTACAGAAATGAGAGCT 180
175 AACGTTAAAAAGGCGACAGATCTATGTTTATTCAGAGTGTGTACAGAAATGAGAGCT 234
181 GGGGCAATCTGGGCTGCGAGTGTGTTATGTTGTCACACAGATGAGATGGAAATTTGGCT 240
235 GGAGAAATTTGGGCTGCGAGTGTGTTATGTTGTCACAGAGATGAGATGGAGTGTGCT 294
241 TATTTCCCGACAGCTGTTGAGAGAGAGAGTGTACCCGAGAGCCACAGAGAGATT 300
295 TATTTCCCGACAGCTGTTGAGAGAGAGAGTGTACCCGAGAGCCACAGAGAGATT 354
301 CCAACCGAGATTTGACTTCTTCTGTGA 329
355 CCCACCGAGATTTGACTTCTTCTGTGA 383

RESULT 11

AAH26341 standard; cDNA; 426 BP.

AAH26341;

02-OCT-2001 (first entry)

Human growth regulatory-like polypeptide clone 16372272.

Growth regulatory-like polypeptide; human; cartilage; melanoma; neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;

ss.

Homo sapiens.

WO200155332-A2.

02-AUG-2001.

25-JAN-2001; 2001WO-US02455.

25-JAN-2000; 2000US-0491404.

02-MAY-2000; 2000US-0563786.

(HYSE-) HYSEQ INC.

Mize NK, Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C;

Dmanac RT;

XX

DR WPI; 2001-483233/52.

Isolated human growth regulatory-like polypeptide useful for treating e.g. Alzheimer's disease, cancer, autoimmune disorder, hyperproliferative disorders, coagulation disorders, and nervous system disorders -

Example 1; Page 114; 119p; English.

The present sequence is that of Hyseq clone identification number 16372272, which was obtained from a human thymus cDNA library using standard PCR with primers specific for vector sequences flanking the inserts, sequencing by hybridisation sequence signature analysis, and Sanger sequencing techniques. This expressed sequence tag was used in the assembly of a full-length cDNA sequence (see AAH26341) encoding a novel human growth regulatory-like polypeptide (GRP, see AAH2671). The GRP belongs to the same protein family as growth regulatory proteins, growth factors, human melanoma derived growth regulatory protein precursor (64% similarity and 45% identity over 111 amino acids) or melanoma inhibitory activity, cattle cartilage-derived retinoic acid sensitive protein (CD-RAP, 44% identity and 64% similarity over 126 amino acids) and other retinoic acid-sensitive proteins. GRP polypeptides and polynucleotides of the invention can be used in the prophylaxis, treatment (including gene therapy) and diagnosis of disorders and diseases caused by, or involving, cartilage development and maintenance, inhibition of melanoma cell growth and tumours, including neuroectodermal tumours such as gliomas. The polynucleotides can also be used to design probes and primers, for chromosome and gene mapping, in the recombinant production of protein, in the generation of antisense, ribozyme and peptide-nucleic acid molecules, and to produce transgenic animals.

Sequence 426 BP; 119 A; 73 C; 113 G; 120 T; 1 other;

Query Match 75.5%; Score 249; DB 22; Length 426;
Best Local Similarity 84.8%; Pred. No. 6.3e-73;
Matches 279; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

1 CATGGCATGTTTATGATTAACCTTCTTCTTAAGAGTTGTGTGCAATGAGAGTGTCTC 60
73 CATGGAATTTTATGAGACCGCTCTAGCTTCCAGAGAGCTCTGTGCAATGAGAGTGTCTC 132
61 TATACATTTCTCTGGCAGAGCAGACAGAGAGACTACATGCCCCGAGCTGAGTTCATC 120
133 TATCTATTTCTCTGGCTAGTGTCTCAAGAAATTAATGCCCCGAGCTGAGTTCATC 192
121 AATGTCAGAAAGGCGACAGATCTATGTTTATTCAGAGTGTGTACAGAAATGAGAGCT 180
193 AACGTTAAAAAGGCGACAGATCTATGTTTATTCAGAGTGTGTACAGAAATGAGAGCT 252
181 GGGGCAATCTGGGCTGCGAGTGTGTTATGTTGTCACACAGATGAGATGGAAATTTGGCT 240
253 GGAGAAATTTGGGCTGCGAGTGTGTTATGTTGTCACAGAGATGAGATGGAGTGTGCT 312
241 TATTTCCCGACAGCTGTTGAGAGAGAGAGTGTACCCGAGAGCCACAGAGAGATT 300
313 TATTTCCCGACAGCTGTTGAGAGAGAGAGTGTACCCGAGAGCCACAGAGAGATT 372
301 CCAACCGAGATTTGACTTCTTCTGTGA 329
373 CCCACCGAGATTTGACTTCTTCTGTGA 401

RESULT 12

ABL95740 standard; cDNA; 521 BP.

ABL95740;

19-JUL-2002 (first entry)

Human angiogenesis related cDNA PRO9873 SEQ ID NO: 359.

XX

XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
 KM atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
 KM cardiac; cytoskeletal; angiogenic; hypotensive; vlnnerary;
 KW antiarteriosclerotic; gene; ss.
 XX Homo sapiens.
 XX WO200208284-A2.
 XX 31-JAN-2002.
 PD 09-JUL-2001; 2001WO-US21735.
 XX 20-JUL-2000; 2000US-219556P.
 XX 25-JUL-2000; 2000US-220624P.
 XX 25-JUL-2000; 2000US-220624P.
 XX 28-JUL-2000; 2000WO-US20710.
 XX 02-AUG-2000; 2000US-222695P.
 XX 17-AUG-2000; 2000US-0643657.
 XX 23-AUG-2000; 2000WO-US23328.
 XX 24-AUG-2000; 2000WO-US2378P.
 XX 07-SEP-2000; 2000US-230978P.
 XX 15-SEP-2000; 2000US-000000P.
 XX 18-SEP-2000; 2000US-0664610.
 XX 18-SEP-2000; 2000US-0665350.
 XX 24-OCT-2000; 2000US-242922P.
 XX 08-NOV-2000; 2000US-0709238.
 XX 08-NOV-2000; 2000WO-US10952.
 XX 10-NOV-2000; 2000WO-US10873.
 XX 01-DEC-2000; 2000WO-US32678.
 XX 20-DEC-2000; 2000US-0747259.
 XX 20-DEC-2000; 2000WO-US34956.
 XX 22-JAN-2001; 2001US-0796498.
 XX 28-FEB-2001; 2001WO-US06520.
 XX 28-FEB-2001; 2001WO-US06666.
 XX 01-MAR-2001; 2001US-0802706.
 XX 09-MAR-2001; 2001US-0808689.
 XX 14-MAR-2001; 2001US-0816744.
 XX 22-MAR-2001; 2001US-0828366.
 XX 05-APR-2001; 2001US-0854208.
 XX 10-MAY-2001; 2001US-0854208.
 XX 10-MAY-2001; 2001US-0866034.
 XX 25-MAY-2001; 2001US-0866034.
 XX 25-MAY-2001; 2001WO-US17092.
 XX 25-MAY-2001; 2001WO-US17092.
 XX 30-MAY-2001; 2001US-0870574.
 XX 30-MAY-2001; 2001WO-US17443.
 XX 01-JUN-2001; 2001WO-US17800.
 XX 20-JUN-2001; 2001WO-US19692.
 XX 28-JUN-2001; 2001WO-US00000.
 XX (GETH) GENENTECH INC.
 XX (BAKE) BAKER K P.
 XX (FERR) FERRARA N.
 XX (GERB) GERBER H.
 XX (GERR) GERRTSEN M E.
 XX (GODD) GODDARD A.
 XX (GODO) GODOWSKI P J.
 XX (GURN) GURNEY A L.
 XX (HILL) HILLAN K J.
 XX (MARS) MARSTERS S A.
 XX (PANU) PANI J.
 XX (PAON) PAONI N F.
 XX (STEP) STEPHAN J F.
 XX (WATA) WATANABE C K.
 XX (WILL) WILLIAMS P M.
 XX (WOOD) WOOD W I.
 XX Baker KP, Ferrara N, Gerber H, Gerltsen ME, Goddard A, Paoni NF,
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W,

DR WPI: 2002-171999/22.
 DR P-PSDB; ABB95602.
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal -
 XX Claim 1, Fig 359; 567bp; English.
 XX The present invention provides the protein and coding sequences of human
 CC PRO proteins. These are useful for treating or diagnosing a
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac
 CC hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The present sequence is a coding sequence of the invention.
 XX Sequence 521 BP; 167 A; 86 C; 131 G; 137 T; 0 other;
 SQ
 Query Match 75.5%; Score 249; DB 24; Length 521;
 Best Local Similarity 84.8%; Pred. No. 6.9e-73;
 Matches 279; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
 QY 1 CATGCATGTTTATGAGTAACCTTCTTACAGAGTTGTGTGAGATGAGAGCTGTC 60
 DB 92 CATGAAATTTATGAGACCGCTTACCTTCCAGAGAGCTGTGAGATGAGAGTGTGTC 151
 QY 61 TATACCATTTCTGTGACAGACAGAGAGACTCAATGCCCCGAGCTAGAGTTATC 120
 DB 152 TATACTATTTCTGTGAGAGCTGAGAGCTCAAGAAATTAATAGCCCGAGCTAGATTCAT 211
 QY 121 AATGTCAAGAAAGGACAGAGATCTATTTATTTCCAGAGCTGTGTACAGAAATGAGACT 180
 DB 212 AAGCTTAAAGAGGACAGAGATCTATTTATTTCAAGAGCTGTGTAAAGAAATGAGACT 271
 QY 181 GGAGCATTTGGGCTGTGAGAGAGTGTATGAGTGCACACAGATGAGATGAGATTTGTGCT 240
 DB 272 GGAGAAATTTGGGCTGTGAGAGAGTGTATGAGTGTGAGTGCACAGAGATGAGATGAGTGTGCT 331
 QY 241 TATTTCCAGAGAGTGTGAGAGAGAGTGTATGAGTGTGAGTGCACAGAGAGTGTGAGAT 300
 DB 332 TATTTCCAGAGAGTGTGAGAGAGAGTGTATGAGTGTGAGTGCACAGAGAGTGTGAGAT 391
 QY 301 CCAGCAGAGATTTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 329
 DB 392 CCAGCAGAGATTTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 420
 RESULT 13
 ABL88251
 ID ABL88251 standard; cDNA; 521 BP.
 XX ABL88251;
 AC 16-MAY-2002 (first entry)
 DT 16-MAY-2002 (first entry)
 DE Human PRO9873 cDNA sequence SEQ ID NO:359.
 XX Human; angiogenesis; cardiac; cytoskeletal; antiangiogenic; hypotensive;
 KM vlnnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
 KM gene therapy; cardiovascular disorder; endothelial disorder; cancer;
 KM angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
 KM age-related macular degeneration; arterial restenosis; angina;
 KM rheumatoid arthritis; myocardial infarction; thrombophlebitis;
 KM lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
 KM wound healing; chromosome mapping; gene mapping; gene; ss.
 XX Homo sapiens.
 OS WO200200690-A2.
 XX 03-JAN-2002.

XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 CS
 OS Homo sapiens.
 XX WPI; 2002-172001/22.
 DR P-PSDB; AAB83627.

PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful for treating a PRO related disorder and for diagnosing tumours
 PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
 PT tumour or liver tumour -
 PS
 XX Claim 2; Figure 71; 359pp; English.

XX The invention relates to one hundred and twenty two nucleic acids
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
 CC agonists and antagonists are useful for treating a PRO related disorder.
 CC The PRO polypeptides are useful for diagnosing tumours, especially lung
 CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. The PRO polypeptides are useful for stimulating the
 CC proliferation of, or gene expression, in pericyte cells, for stimulating
 CC the proliferation or differentiation of chondrocyte cells, for
 CC stimulating the release of tumour necrosis factor-alpha from human dermal
 CC for stimulating or inhibiting the proliferation of normal human dermal
 CC fibroblast cells. The PRO polypeptide may also be used as molecular
 CC weight markers and for tissue typing. The PRO nucleic acids have
 CC applications in molecular biology, including use as hybridisation probes,
 CC and in chromosome and gene mapping. ABK3536-ABK3567 represent human
 CC PRO protein coding sequences of the invention.

XX Sequence 521 BP; 167 A; 86 C; 131 G; 137 T; 0 other;

Query Match 75.5%; Score 249; DB 24; Length 521;
 Best Local Similarity 84.8%; Pred. No. 6.9e-73;
 Matches 279; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1 CATGGCATGTTATGATTAACCTTTCTTCTAAGAGTTGTGTGCGATGAGAGTGTGTC 60
 DB 92 CATGGAATTTATGACCGCTCTAGCTTCAAGAGCTCTGTGCGATGATGATGTGTC 151
 QY 61 TATACATTTCTGTGCAAGAGACAGCAAGACTCAATGCCCGAGCTGTAGTTCATC 120
 DB 152 TAACTATTTCTGTGCTAGTGTCTCAAGAGATTAATGATGATGATGATGATTCATT 211
 QY 121 AATGTCAAGAAAGGAGGAGAGATCTATGTTATTCAGAGCTGTATCAAGAAATGAGAGT 180
 DB 212 AAGGTAAAGAAAGGAGGAGAGATCTATGTTATTCAGAGCTGTATCAAGAAATGAGAGT 271
 QY 181 GGGGCAATCTGGGCTGGCAAGTGTATGTTAGTACACAGAGATGAGATGAGATGAGT 240
 DB 272 GGAAGATTTGGGCTGGCAAGTGTATGTTAGTACAGAGATGAGATGAGATGAGT 331
 QY 241 TATTTCCCAAGCACTGTGTTAGAGCAAGAGTGTACAGAGGCAAGAGAGAT 300
 DB 332 TATTTCCCAAGCACTGTGTTAGAGCAAGAGTGTACAGAGGCAAGAGAT 391
 QY 301 CCAACCAAGATATGACTTCTCTGTGA 329
 DB 392 CCCACCAAGATATGACTTCTCTGTGA 420

RESULT 15

AAH98228 standard; CDNA; 891 BP.

AAH98228;

12-OCT-2001 (first entry)

Human EST-derived coding sequence SEQ ID NO: 85.

Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;

KM tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
 KM diagnostics; forensic test; gene mapping; genetic disorder;
 KM biodiversity; gene therapy; nutrition; ss.

OS Homo sapiens.

XX W0200154477-A2.

XX 02-AUG-2001.

XX 25-JAN-2001; 2001WO-US02687.

XX 25-JAN-2000; 2000US-0491404.

XX 17-JUL-2000; 2000US-0617746.

XX 03-AUG-2000; 2000US-0631451.

XX 15-SEP-2000; 2000US-0663870.

XX (HSE-) HYSEQ INC.

XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
 PI Cao Y, Drmanac RA, Zhang J, Wehrman T;

XX WPI; 2001-476164/51.

XX P-PSDB; AAM23569.

XX Isolated polypeptide for treatment of diseases, diagnostics, raising
 PT antibodies and research use -

XX Claim 1; Page 236; 1275pp; English.

XX The present invention provides the protein and coding sequences of novel
 CC proteins from a variety of organisms, including human, dog, cat, horse,
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
 CC from the organism of interest. They can be used in diagnostics,
 CC forensics, gene mapping, identification of mutations, to assess
 CC biodiversity and for nutritional purposes. The present sequence is a CDNA
 CC of the invention.

XX Sequence 891 BP; 272 A; 146 C; 214 G; 259 T; 0 other;

Query Match 75.5%; Score 249; DB 22; Length 891;
 Best Local Similarity 84.8%; Pred. No. 8.8e-73;
 Matches 279; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1 CATGGCATGTTATGATTAACCTTTCTTCTAAGAGTTGTGTGCGATGAGAGTGTGTC 60
 DB 73 CATGGAATTTATGACCGCTCTAGCTTCAAGAGCTCTGTGCGATGATGATGTGTC 132
 QY 61 TATACATTTCTGTGCAAGAGACAGCAAGACTCAATGCCCGAGCTGTAGTTCATC 120
 DB 133 TAACTATTTCTGTGCTAGTGTCTCAAGAGATTAATGATGATGATGATGATTCATT 192
 QY 121 AATGTCAAGAAAGGAGGAGAGATCTATGTTATTCAGAGCTGTATCAAGAAATGAGAGT 180
 DB 193 AAGGTAAAGAAAGGAGGAGAGATCTATGTTATTCAGAGCTGTATCAAGAAATGAGAGT 252
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 DB 253 GGAAGATTTGGGCTGGCAAGTGTATGTTAGTACAGAGATGAGATGAGATGAGT 312
 QY 241 TATTTCCCAAGCACTGTGTTAGAGCAAGAGTGTACAGAGGCAAGAGAGAT 300
 DB 313 TATTTCCCAAGCACTGTGTTAGAGCAAGAGTGTACAGAGGCAAGAGAT 372
 QY 301 CCAACCAAGATATGACTTCTCTGTGA 329
 DB 373 CCCACCAAGATATGACTTCTCTGTGA 401

Search completed: December 30, 2003, 02:14:35
 Job time : 110.538 secs

GenCore version 5.1.6
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CM nucleic - nucleic search, using sw model

Run on: December 30, 2003, 04:08:13 ; Search time 270.994 Seconds
(without alignments)
4172.254 Million cell updates/sec

Title: US-10-019-455A-48

Perfect score: 330
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2244575 seqs, 1713117285 residues

Total number of hits satisfying chosen parameters: 4489150

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: Published Applications NA:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 249 | 75.5 | 426 | US-10-216-038-1 | Sequence 1, Appl |
| 2 | 249 | 75.5 | 521 | US-10-216-163-71 | Sequence 71, Appl |
| 3 | 249 | 75.5 | 521 | US-10-218-765-71 | Sequence 71, Appl |
| 4 | 249 | 75.5 | 521 | US-10-219-063-71 | Sequence 71, Appl |
| 5 | 249 | 75.5 | 521 | US-10-219-066-71 | Sequence 71, Appl |
| 6 | 249 | 75.5 | 521 | US-10-219-067-71 | Sequence 71, Appl |
| 7 | 249 | 75.5 | 521 | US-10-219-068-71 | Sequence 71, Appl |
| 8 | 249 | 75.5 | 521 | US-10-219-069-71 | Sequence 71, Appl |
| 9 | 249 | 75.5 | 521 | US-10-219-073-71 | Sequence 71, Appl |
| 10 | 249 | 75.5 | 521 | US-10-219-475-71 | Sequence 71, Appl |
| 11 | 249 | 75.5 | 521 | US-10-219-480-71 | Sequence 71, Appl |
| 12 | 249 | 75.5 | 521 | US-10-219-483-71 | Sequence 71, Appl |
| 13 | 249 | 75.5 | 521 | US-10-219-525-71 | Sequence 71, Appl |
| 14 | 249 | 75.5 | 521 | US-10-219-526-71 | Sequence 71, Appl |
| 15 | 249 | 75.5 | 521 | US-10-219-530-71 | Sequence 71, Appl |

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| 16 | 249 | 75.5 | 521 | US-10-219-531-71 | Sequence 71, Appl |
| 17 | 249 | 75.5 | 521 | US-10-219-532-71 | Sequence 71, Appl |
| 18 | 249 | 75.5 | 521 | US-10-219-533-71 | Sequence 71, Appl |
| 19 | 249 | 75.5 | 521 | US-10-223-081-359 | Sequence 359, App |
| 20 | 249 | 75.5 | 521 | US-10-230-437-71 | Sequence 71, Appl |
| 21 | 249 | 75.5 | 521 | US-10-232-228-71 | Sequence 71, Appl |
| 22 | 249 | 75.5 | 521 | US-10-223-082-359 | Sequence 359, App |
| 23 | 249 | 75.5 | 521 | US-10-227-884-71 | Sequence 71, Appl |
| 24 | 249 | 75.5 | 521 | US-10-230-163-71 | Sequence 71, Appl |
| 25 | 249 | 75.5 | 521 | US-10-230-338-71 | Sequence 71, Appl |
| 26 | 249 | 75.5 | 521 | US-10-230-414-71 | Sequence 71, Appl |
| 27 | 249 | 75.5 | 521 | US-10-216-159A-71 | Sequence 71, Appl |
| 28 | 249 | 75.5 | 521 | US-10-218-849-71 | Sequence 71, Appl |
| 29 | 249 | 75.5 | 521 | US-10-227-873-71 | Sequence 71, Appl |
| 30 | 249 | 75.5 | 521 | US-10-237-883-71 | Sequence 71, Appl |
| 31 | 249 | 75.5 | 521 | US-10-219-076-71 | Sequence 71, Appl |
| 32 | 249 | 75.5 | 521 | US-10-230-434-71 | Sequence 71, Appl |
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| 34 | 249 | 75.5 | 521 | US-10-219-075-71 | Sequence 71, Appl |
| 35 | 249 | 75.5 | 521 | US-10-219-464-71 | Sequence 71, Appl |
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| 37 | 249 | 75.5 | 521 | US-10-219-479-71 | Sequence 71, Appl |
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| 40 | 249 | 75.5 | 521 | US-10-232-231-71 | Sequence 71, Appl |
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| 42 | 249 | 75.5 | 521 | US-10-216-165-71 | Sequence 71, Appl |
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ALIGNMENTS

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RESULT 1
US-10-216-038-1
; Sequence 1, Application US/10216038
; Publication No. US20030124573A1
; GENERAL INFORMATION:
; APPLICANT: Mize, Nancy K
; APPLICANT: Boyle, Bryan J
; APPLICANT: Ford, John E
; APPLICANT: Arterburn, Matthew C
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Drmanac, Radoje T
; APPLICANT: Sjastad, Michael
; TITLE OF INVENTION: Methods and Materials Relating to No. US20030124573A1 Growth
; FILE REFERENCE: HVS-7CIP
; CURRENT APPLICATION NUMBER: US/10/216,038
; PRIOR FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: US 09/563,786
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 426
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (426)..(426)
; OTHER INFORMATION: n = A, T, G, or C
;
Query Match 75.5%; Score 249; DB 15; Length 426;
Best Local Similarity 84.8%; Pred. No. 2.8e-76;
Matches 279; Conservative 0; Mismatches 50; Indels 0;
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QY 1 CATGSCATGTTTATGTAATACTTCTTCTTAAGAGTTGGTGCAGATGAGTGTGTC 60
Db 73 CATGAAATATTTATGACCGCTAGCTTCCAGAACTCTGTGCAGATGATGAGTGTGTC 132
QY 61 TATACATTTCTCTGGCAGAGACAGAAAGTATGATGAGTGTGTC 120
Db 133 TATACATTTCTCTGGCAGAGACAGAAAGTATGATGAGTGTGTC 192
QY 121 AATGTCAGAAAGGCGACAGATCTATGTTTATCCAGTGTGTAACAGAAATGAGCT 180
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QY 181 GGGGCAATTCGGCTGGCAGTGTGTTATGATGAGCAGCAGATGAGTGTGTC 240
Db 253 GGAGAAATTTGGGCTGGCAGTGTGTTATGATGAGCAGCAGATGAGTGTGTC 312
QY 241 TATTTCCCGCAGCACTTGTTAGAGAGCAAGTGTGTAACAGAGGCGCAGAGAGATT 300
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QY 301 CCAACCAAGGATATTGACTTCTTCTGTGA 329
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RESULT 2

US-10-216-163-71
Sequence 71, Application US/10216163
Publication No. US20030149239A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Geritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C3
CURRENT APPLICATION NUMBER: US/10/216,163
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 71
LENGTH: 521
TYPE: DNA
ORGANISM: Homo Sapien

US-10-216-163-71

Query Match 75.5%; Score 249; DB 13; Length 521;
Best Local Similarity 84.8%; Pred. No. 3e-76;
Matches 279; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1 CATGSCATGTTTATGTAATACTTCTTCTTAAGAGTTGGTGCAGATGAGTGTGTC 60
Db 92 CATGAAATATTTATGACCGCTAGCTTCCAGAACTCTGTGCAGATGATGAGTGTGTC 151
QY 61 TATACATTTCTCTGGCAGAGACAGAAAGTATGATGAGTGTGTC 120
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QY 301 CCAACCAAGGATATTGACTTCTTCTGTGA 329
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RESULT 3

US-10-218-765-71
Sequence 71, Application US/10218765
Publication No. US20030187201A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Geritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C19
CURRENT APPLICATION NUMBER: US/10/218,765
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
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PRIOR APPLICATION NUMBER: 60/166361
PRIOR FILING DATE: 1999-11-16
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PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169495
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169835

Query Match 75.5%; Score 249; DB 13; Length 521;
Best Local Similarity 84.8%; Pred. No. 3e-76;
Matches 279; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1 CATGGCATGTTATGATTAACCTTTCTTAAGAGTTGTGCGAGTGAAGTGTGTC 60
DB 92 CATGGAATATTTATGACCGCTTACCTTCAAGAGCTCTGTGAGATGATGATGTGTC 151
QY 61 TATACATTTCTGTGCGAAGCAGACAGAGCTACATGCCCCGAGCTGAGTTATC 120
DB 152 TATACATTTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 211
QY 121 AATGTCAGAAAGGCGACAGATCTTATGTTTATTCACAGCTGTAACAGAAATGAGCT 180
DB 212 AAGCTTAAAGGCGACAGATCTTATGTTTATTCACAGCTGTAACAGAAATGAGCT 271
QY 181 GGGGCAATTCGCGCTGCGAGTGTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 240
DB 272 GGAAGATTTTGGCTGCGAGTGTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 331
QY 241 TATTTCCCGAGCACTGTTAGAGCAAGAGCTGTTACAGAGGCGCCAGAGAGATT 300
DB 332 TATTTCCCGAGCACTGTTAGAGCAAGAGCTGTTACAGAGGCGCCAGAGAGATT 391
QY 301 CCAACCAAGATATTGACTTCTTCTGTA 329
DB 392 CCAACCAAGATATTGACTTCTTCTGTA 420

RESULT 4
US-10-219-063-71

Sequence 71, Application US/10219063
Publication No. US20030187202A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530P1C24
CURRENT FILING DATE: 2002-08-13
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28

PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 71
LENGTH: 521
TYPE: DNA
ORGANISM: Homo Sapien
US-10-219-063-71

Query Match 75.5%; Score 249; DB 13; Length 521;
Best Local Similarity 84.8%; Pred. No. 3e-76;
Matches 279; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1 CATGGCATGTTATGATTAACCTTTCTTAAGAGTTGTGCGAGTGAAGTGTGTC 60
DB 92 CATGGAATATTTATGACCGCTTACCTTCAAGAGCTCTGTGAGATGATGATGTGTC 151
QY 61 TATACATTTCTGTGCGAAGCAGACAGAGCTACATGCCCCGAGCTGAGTTATC 120
DB 152 TATACATTTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 211
QY 121 AATGTCAGAAAGGCGACAGATCTTATGTTTATTCACAGCTGTAACAGAAATGAGCT 180
DB 152 TATACATTTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 211
QY 181 GGGGCAATTCGCGCTGCGAGTGTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 240
DB 272 GGAAGATTTTGGCTGCGAGTGTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 331
QY 241 TATTTCCCGAGCACTGTTAGAGCAAGAGCTGTTACAGAGGCGCCAGAGAGATT 300
DB 332 TATTTCCCGAGCACTGTTAGAGCAAGAGCTGTTACAGAGGCGCCAGAGAGATT 391
QY 301 CCAACCAAGATATTGACTTCTTCTGTA 329
DB 392 CCAACCAAGATATTGACTTCTTCTGTA 420

RESULT 5
US-10-219-066-71

Sequence 71, Application US/10219066
Publication No. US20030187203A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530P1C27
CURRENT FILING DATE: 2002-08-13
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-10-28

```

CURRENT APPLICATION NUMBER: US/10/219,067
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 71
LENGTH: 521

```

| | Query Match | Similarity | Score | DB | Length |
|------------|-------------|--------------|-------|------------|--------|
| Best Local | 84.8% | 75.5% | 249 | DB 13 | 200 |
| Matches | 219 | Conservative | 0 | Mismatches | 50 |
| | | | | Indels | 0 |
| | | | | Gaps | 0 |

| | Query | Match | Similarity | Score | DB | Length |
|----|-------|--|------------|-------|----|--------|
| Db | 1 | CATGGCATGTTATGGATAACTTCTCTAGAGAGTGTGTGCAGATGAGAGTGTGTC | 60 | | | |
| Db | 92 | CATGGAATTTATATGACCGCTTAGCTTCCAGAAAGCTCTGTGCAGATATATGAGTGTGTC | 151 | | | |
| Db | 61 | TATACCATTTCTGTGGCAGAGACACAGAAAGACTACATATGCCCGGACTGTAGATTATC | 120 | | | |
| Db | 152 | TATACATTTCTGTGCTATGTCTCAAGAAAGATTATATATGCCCGGACTGTAGATTATC | 211 | | | |
| Db | 121 | AATGTCAAGAAAGGCGAGCAGATCTATGTTTATTCAGAGTGTATACAGAAATGAGACT | 180 | | | |
| Db | 212 | AACGTTAAAAAAGGCGAGCAGATCTATGTACTCAAAAGTGTAAAGAAATGAGACT | 271 | | | |
| Db | 181 | GGGGCATTTGGGCTGGCAGTGTTTATGTGACACACAGGATAGATGGGAATTTGGGT | 240 | | | |
| Db | 272 | GGAAATTTTGGGCTGGCAGTGTTTATAGTGATGGCCGAGACGAGATGGAGTGTGGGT | 331 | | | |
| Db | 241 | TATTTCCCGACGAACTTGTTAGAGAGCAACGAGTATCCAGAGAGGCGACCAAGAGATT | 300 | | | |
| Db | 332 | TATTTCCCGACGAACTTGTTAGAGAGCAACGAGTGTATACAGAGAACTTACCAAGAAATT | 391 | | | |

```

QY      301  CCACCGAGATATTGACTTCTCTGCA 329
        |||||
        392  CCACCGAGATATTGACTTCTCTGCA 420
Db

RESULT 7
US-10-219-068-71
; Sequence 71, Application US/10219068
; Publication No. US20030187205A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Geritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stepan, Jean-Philippe F.

```

```

RESULT 8
US-10-219-069-71
; Sequence 71
; Publication NO. US00030187206A1
GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goodard, Audrey

```

RESULT 9
US-10-219-073-71
; Sequence 71, Application US/10219073
; Publication No. US20030187207A1

| Query Match | 75.5% | Score 249; | DB 13 | Length 521; |
|-----------------------|-------|--|-------|-------------------|
| Best Local Similarity | 84.8% | Pred. No. 3e-76; | | |
| Matches | 279; | Mismatches | 50; | Indels 0; Gaps 0; |
| QY | 1 | CATGGCAGCTTATGAGATMAACTTCTCTTAAAGAGTTGTGTGCAGATGAGAGAGTGTCT | 60 | |
| Db | 92 | CATGGAATATTTATGACCGCTCTAGCTTCCAAAGAGCTGTGCAGATGATATAGTGTGTC | 151 | |
| QY | 61 | TATACCAATTTCTCTGCGCAAGACACAGAAAGCTCAATAGCCCGAGCTGTAGGTTATC | 120 | |
| Db | 152 | TATACATATTTCTCTGCTAGTGTCTCAAGAAAGTTTAAAGCCCGAGCTGTGATTTCAT | 211 | |
| QY | 121 | AATGTCAAGAAAGGGGAGAGACATCTATGTTTATTCGAACTGGTAAACAGAAAATGAGCT | 180 | |
| Db | 212 | AACGTTAAAAAGGGGAGAGACATCTATGTTGTTACTCAAAGCTGGTAAAGAAAATGAGCT | 271 | |
| QY | 181 | GGGGCAATTCGTGGGCTGGCAGTGTTTATGTGTACCAACAGATATAGATGGGAATTTGGGCT | 240 | |
| Db | 272 | GGAGAAATTTGGGCTGCGAGTGTTTATGTGTGAAGGCGACAGATGGGAGTCGTGGGT | 331 | |
| QY | 241 | TATTTCCCAAGCACTTGTGTAAAGCAACGAGTGNACAGGAGGCCCAACGAGAGATT | 300 | |
| Db | 332 | TATTTCCCAAGCACTTGTGTAAAGCAACGAGTGTATCCAGGAAGGTACCAAGGAAGTT | 391 | |
| QY | 301 | CCAAACGAGATATGACTCTTCTGTGA | 329 | |
| Db | 392 | CCCAACGAGATATGACTCTTCTGTGA | 420 | |

| Query Match | 75.5% | Score 249 | DB 13 | Length 521 |
|-----------------------|-------|---|-----------|------------|
| Best Local Similarity | 84.8% | Pred. No. 3e-76 | | |
| Matches | 279 | Mismatches 0 | Indels 50 | Gaps 0 |
| QY | 1 | CATGCACGTGTTATGANTAACTTCTCTTAAGAAGTGTGTGCAGATGAGAGTGTGC | 60 | |
| Db | 92 | CATGAATAATTTATGACCGCTTAGCTTCCAGAAGCTCTGTGCAGATGATGAGTGTGC | 151 | |
| QY | 61 | TATACATTCTCTGGAAGAGCACAGAAAGACTACAAATGCCCGGACTGTAGTTCATC | 120 | |
| Db | 152 | TATACTATTCTCTGCTAGTGCCTCAAGAAAGATTATATGCCCGGACTGTATATTTCATT | 211 | |
| QY | 121 | AATGTCAAGAAAAGGCGACAGATCTAATGTTATTTCGAAGTGGTAAACAGAAAATGAGACT | 180 | |
| Db | 212 | AACGTAAAAAAAGGCGACAGATCTAATGTGTCAAGAGTGGTAAAGAAAATGAGACT | 271 | |
| QY | 181 | GGGGCATCTGGGCTGGAGAGTGTATATGTGTGACCAACAGAGATGAGATGGAAATTGGGT | 240 | |
| Db | 272 | GGAGAAATTTGGGCTGGCAGTGTTATATGTGTATGTGCCAGACAGAGATGGGAGTCTGGGT | 331 | |
| QY | 241 | TATTTTCCCGAGCACTTGTTAGAGAGCCAGATGTACCAAGAGGCCAATCCAAAGAGATT | 300 | |
| Db | 332 | TATTTTCCCGAGCACTTGTTCAAGAACAGGTGTGTATCCAGAAAGCTACCAAGAGATT | 391 | |

DR P-PSDB; AAB69126.
 XX Safe, low-toxicity secretory cell function-regulatory protein and
 XX encoded DNA, applicable as drugs, in diagnosis and development of
 PT promoters and inhibitors for preventing or treating e.g. bone and joint
 PT diseases -
 XX
 XX Claim 8; Page 97; 111pp; Japanese.
 XX
 XX The present invention describes novel MLP proteins and their encoding
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
 CC activities, and can be used in gene therapy and as secretory cell
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in
 CC the diagnosis and development of promoters and inhibitors for preventing
 CC or treating bone and joint diseases as well as pathologic angiogenesis.
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
 CC in the exemplification of the present invention.
 XX
 XX Sequence 330 BP; 91 A; 60 C; 91 G; 88 T; 0 other;
 SQ
 Query Match 100.0%; Score 330; DB 22; Length 330;
 Best Local Similarity 100.0%; Pred. No. 3.4e-97;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CATGGAATATTATGACCGCTAGCTTCCAGAAAGCTCTGTGCAATGATGATGTC 60
 Db 1 CATGGAATATTATGACCGCTAGCTTCCAGAAAGCTCTGTGCAATGATGATGTC 60
 QY 61 TATACATTTCTCTGGCTAGTGTCTCAAGAAATTAATGCCCGGACTGTATTCATT 120
 Db 61 TATACATTTCTCTGGCTAGTGTCTCAAGAAATTAATGCCCGGACTGTATTCATT 120
 QY 121 AACGTTAAAAAGGCGACAGATCTATGTGTACTCAAGCTGTAAAGAAAAATGAGCT 180
 Db 121 AACGTTAAAAAGGCGACAGATCTATGTGTACTCAAGCTGTAAAGAAAAATGAGCT 180
 QY 121 AACGTTAAAAAGGCGACAGATCTATGTGTACTCAAGCTGTAAAGAAAAATGAGCT 180
 Db 121 AACGTTAAAAAGGCGACAGATCTATGTGTACTCAAGCTGTAAAGAAAAATGAGCT 180
 QY 181 GGAGAAATTTGGGCTGGAGTGTATGTGTATGATGGCCAGACAGATGGAGTGGT 240
 Db 181 GGAGAAATTTGGGCTGGAGTGTATGTGTATGATGGCCAGACAGATGGAGTGGT 240
 QY 241 TATTTCCCGAGAACTTGTCAAGAACGCTGTGTACCAAGAACTTCAAGAAAGTT 300
 Db 241 TATTTCCCGAGAACTTGTGTCAAGAACGCTGTGTACCAAGAACTTCAAGAAAGTT 300
 QY 241 TATTTCCCGAGAACTTGTGTCAAGAACGCTGTGTACCAAGAACTTCAAGAAAGTT 300
 Db 241 TATTTCCCGAGAACTTGTGTCAAGAACGCTGTGTACCAAGAACTTCAAGAAAGTT 300
 QY 301 CCCACACGAGATATTGACTTCTTCTGGCAG 330
 Db 301 CCCACACGAGATATTGACTTCTTCTGGCAG 330
 RESULT 2
 AAF59065
 ID AAF59065 standard; DNA; 384 BP.
 XX
 AC AAF59065;
 XX
 DT 23-APR-2001 (first entry)
 XX
 DE Human MLP nucleotide sequence SEQ ID NO:4.
 XX
 XX MLP, MIA, melanoma inhibitory activity; cancer; bone disease;
 KM joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
 KM cardiant; gene therapy; secretory cell function regulator; promoter;
 KM inhibitor; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200102564-A1.
 XX
 PD 11-JAN-2001.
 XX
 PF 29-JUN-2000; 2000WO-JP04278.
 XX
 PR 30-JUN-1999; 99JP-0186718.

XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 XX Itoh Y, Nishi K, Ogi K, Okubo S, Mogi S, Noguchi Y, Yoshimura K;
 PI Tanaka H;
 XX
 XX WPI: 2001-159271/16.
 DR
 DR P-PSDB; AAB69123.
 XX
 XX Safe, low-toxicity secretory cell function-regulatory protein and
 PT encoded DNA, applicable as drugs, in diagnosis and development of
 PT promoters and inhibitors for preventing or treating e.g. bone and joint
 PT diseases -
 XX
 XX Example 1; Page 91; 111pp; Japanese.
 XX
 XX The present invention describes novel MLP proteins and their encoding
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
 CC activities, and can be used in gene therapy and as secretory cell
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in
 CC the diagnosis and development of promoters and inhibitors for preventing
 CC or treating bone and joint diseases as well as pathologic angiogenesis.
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
 CC in the exemplification of the present invention.
 XX
 XX Sequence 384 BP; 99 A; 70 C; 106 G; 109 T; 0 other;
 SQ
 Query Match 100.0%; Score 330; DB 22; Length 384;
 Best Local Similarity 100.0%; Pred. No. 3.6e-97;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CATGGAATATTATGACCGCTAGCTTCCAGAAAGCTCTGTGCAATGATGATGTC 60
 Db 55 CATGGAATATTATGACCGCTAGCTTCCAGAAAGCTCTGTGCAATGATGATGTC 114
 QY 61 TATACATTTCTCTGGCTAGTGTCTCAAGAAATTAATGCCCGGACTGTATTCATT 120
 Db 115 TATACATTTCTCTGGCTAGTGTCTCAAGAAATTAATGCCCGGACTGTATTCATT 174
 QY 121 AACGTTAAAAAGGCGACAGATCTATGTGTACTCAAGCTGTAAAGAAAAATGAGCT 180
 Db 175 AACGTTAAAAAGGCGACAGATCTATGTGTACTCAAGCTGTAAAGAAAAATGAGCT 234
 QY 181 GGAGAAATTTGGGCTGGAGTGTATGTGTATGATGGCCAGACAGATGGAGTGGT 240
 Db 235 GGAGAAATTTGGGCTGGAGTGTATGTGTATGATGGCCAGACAGATGGAGTGGT 294
 QY 241 TATTTCCCGAGAACTTGTCAAGAACGCTGTGTACCAAGAACTTCAAGAAAGTT 300
 Db 295 TATTTCCCGAGAACTTGTGTCAAGAACGCTGTGTACCAAGAACTTCAAGAAAGTT 354
 QY 301 CCCACACGAGATATTGACTTCTTCTGGCAG 330
 Db 355 CCCACACGAGATATTGACTTCTTCTGGCAG 384
 RESULT 3
 AAS17583
 ID AAS17583 standard; cDNA; 387 BP.
 XX
 AC AAS17583;
 XX
 DT 26-FEB-2002 (first entry)
 XX
 DE DNA encoding novel secreted protein #12.
 XX
 XX Secreted protein; cytosolic; immunosuppressive; vulnery; vaccine;
 KM antiinflammatory; neuroprotective; nephrotoxic; cardiovascular;
 KM human; cancer; autoimmune disease; wound healing disorder; infection;
 KM haematopoietic disorder; inflammatory disorder; infertility;
 KM neurological disease; psychiatric disease; cardiovascular disease;
 KM respiratory disease; renal; gastrointestinal; ss.
 XX

```

OS Homo sapiens.
XX Key Location/Qualifiers
XX Key 1..387
XX CDS /*tag= a
XX /product= "Human secreted protein"
XX
XX MO200179454-A1.
XX
XX 25-OCT-2001.
XX
XX 11-APR-2001; 2001WO-US11797.
XX
XX 13-APR-2000; 2000US-196603P.
XX
XX 24-APR-2000; 2000US-199417P.
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;
XX
XX WPI; 2002-061975/08.
XX
XX P-PSDB; AAU09871.
XX
XX New secreted proteins or polypeptides, useful for treating e.g. cancer,
XX autoimmune diseases, wound healing disorder, infections, haematopoietic
XX disorders, inflammatory disorders, infertility, cancer -
XX
XX Claim 2; Page 44; 92pp; English.
XX
XX The invention relates to an isolated novel secreted polypeptide (I) and
XX polynucleotide (II). (I) and (II) are useful for treating cancer,
XX autoimmune diseases, wound healing disorder, infections, haematopoietic
XX disorders, inflammatory disorders, infertility, neurological and
XX psychiatric diseases, cardiovascular diseases, respiratory diseases,
XX renal diseases, or gastrointestinal diseases. These may also be used to
XX treat diseases, abnormalities and disorders caused by abnormal
XX expression, production, function and/or metabolism of the genes, as
XX vaccines for inducing immunological response in a mammal, and in the
XX screening methods for detecting the effect of added compounds on the
XX production of mRNA and polypeptide in cells. The polypeptides can be used
XX as immunogens to produce antibodies immunospecific for the polypeptides,
XX and to identify membrane-bound or soluble receptors. The polynucleotides
XX may be used as diagnostic reagents, in chromosome localisation studies,
XX and in tissue expression studies. The present sequence represents the
XX coding sequence of novel human secreted protein #12.
XX
XX Sequence 387 BP; 101 A; 70 C; 106 G; 110 T; 0 other;
XX
XX Query Match 100.0%; Score 330; DB 24; Length 387;
XX Best Local Similarity 100.0%; Pred. No. 3.6e-97;
XX Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 CATGGAATATTATGAGACCGCTAGCTTCCAGAGAGCTGTGAGATGATGATGTC 60
XX 55 CATGGAATATTATGAGACCGCTAGCTTCCAGAGAGCTGTGAGATGATGATGTC 114
XX
XX 61 TATACATATTCTCTGGCTAGTGTCAAGAGATTAATATCCCGGAGCTAGATTCATT 120
XX 115 TATACATATTCTCTGGCTAGTGTCAAGAGATTAATATCCCGGAGCTAGATTCATT 174
XX
XX 121 AACGTTAAAAAGGGGCGACGATCTATGTGTACTCAAGAGCTGTGTAAGAAATGAGCT 180
XX 175 AACGTTAAAAAGGGGCGACGATCTATGTGTACTCAAGAGCTGTGTAAGAAATGAGCT 234
XX
XX 181 GGAAGATTTTGGGCTGGCAGTGTATTATGTGATGGCCAGAGACGAGATGGAGTGGTGGT 240
XX 235 GGAAGATTTTGGGCTGGCAGTGTATTATGTGATGGCCAGAGACGAGATGGAGTGGTGGT 294
XX
XX 241 TATTTCGCCAGAACTTGTCAGAGAAAGGCTGTGTACGAGAGAGCTTACCAAGAAATT 300
XX 295 TATTTCGCCAGAACTTGTCAGAGAAAGGCTGTGTGTACGAGAGAGCTTACCAAGAAATT 354

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```

XX 301 CCCACCAGGATATGACTTCTTGGCAG 330
XX |||||
XX 355 CCCACCAGGATATGACTTCTTGGCAG 384
XX
XX RESULT 4
XX AAH26341
XX ID AAH26341 standard; cDNA, 426 BP.
XX
XX AC AAH26341;
XX
XX DT 02-OCT-2001 (first entry)
XX
XX DE Human growth regulatory-like polypeptide clone 16372272.
XX
XX KW Growth regulatory-like polypeptide; human; cartilage; melanoma;
XX neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;
XX 88.
XX
XX OS Homo sapiens.
XX
XX PN MO200155332-A2.
XX
XX PD 02-AUG-2001.
XX
XX PF 25-JAN-2001; 2001WO-US02455.
XX
XX PR 25-JAN-2000; 2000US-0491404.
XX 02-MAY-2000; 2000US-0563786.
XX
XX (HYSE-) HYSEQ INC.
XX
XX PI Mize NK, Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C;
XX Drmanac RT;
XX
XX WPI; 2001-483333/52.
XX
XX DR 16372272, which was obtained from a human thymus cDNA library
XX using standard PCR with primers specific for vector sequences
XX flanking the inserts, sequencing by hybridisation sequence
XX signature analysis, and Sanger sequencing techniques. This
XX expressed sequence tag was used in the assembly of a full-length
XX cDNA sequence (see AAH26343) encoding a novel human growth
XX regulatory-like polypeptide (GRP, see AAB82671). The GRP
XX belongs to the same protein family as growth regulatory proteins,
XX growth factors, human melanoma derived growth regulatory protein
XX precursor (64% similarity and 45% identity over 111 amino acids)
XX or melanoma inhibitory activity, cattle cartilage-derived
XX retinoic acid sensitive protein (CD-RAP, 44% identity and 64%
XX similarity over 126 amino acids) and other retinoic acid-sensitive
XX proteins. GRP polypeptides and polynucleotides of the invention
XX can be used in the prophylaxis, treatment (including gene therapy)
XX and diagnosis of disorders and diseases caused by, or involving,
XX cartilage development and maintenance, inhibition of melanoma cell
XX growth and tumours, including neuroectodermal tumours such as
XX gliomas. The polynucleotides can also be used to design probes
XX and primers, for chromosome and gene mapping, in the recombinant
XX production of protein, in the generation of antisense, ribozyme and
XX peptide-nucleic acid molecules, and to produce transgenic animals.
XX
XX Sequence 426 BP; 119 A; 73 C; 113 G; 120 T; 1 other;
XX
XX Query Match 100.0%; Score 330; DB 22; Length 426;
XX Best Local Similarity 100.0%; Pred. No. 3.8e-97;
XX Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```


QY 1 CATGAAATATTTATGACCCGCTCTAGCTTCCAGAAAGCTCTGTGCAGATGATGAGTGTGTC 60
 Db 73 CATGAAATATTTATGACCCGCTCTAGCTTCCAGAAAGCTCTGTGCAGATGATGAGTGTGTC 132
 QY 61 TATCTATTTCTCTGGCTAGTGTCTCAAGAAATATATAATGCCCCGAGCTGATGATTCATT 120
 Db 133 TATCTATTTCTCTGGCTAGTGTCTCAAGAAATATATAATGCCCCGAGCTGATGATTCATT 192
 QY 121 AACGTTAAAAAGGCGACAGATCTATGTGTACTCAAAAGCTGTGTAAAAAGAAATGAGCT 180
 Db 193 AACGTTAAAAAGGCGACAGATCTATGTGTACTCAAAAGCTGTGTAAAAAGAAATGAGCT 252
 QY 181 GGAGAAATTTGGGCTGGCAGTGTCTTATGTATGCTGCGCAGAGAGATGGGAGTGTGGGT 240
 Db 253 GGAGAAATTTGGGCTGGCAGTGTCTTATGTATGCTGCGCAGAGAGATGGGAGTGTGGGT 312
 QY 241 TATTTCCCGAGAACTTGTCTCAAGAAAGCTGTGTCCAGAAAGCTTACCAAGAAAGTT 300
 Db 313 TATTTCCCGAGAACTTGTCTCAAGAAAGCTGTGTCTCAAGAAAGCTTACCAAGAAAGTT 372
 QY 301 CCCACACGAGATATTGACTTCTTCTGCGAG 330
 Db 373 CCCACACGAGATATTGACTTCTTCTGCGAG 402

RESULT 5
 ABL95740
 ID ABL95740 standard; cDNA; 521 BP.
 XX
 AC ABL95740;
 XX
 DT 19-JUL-2002 (first entry)
 XX

DE Human angiogenesis related cDNA PRO9873 SEQ ID NO: 359.

XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
 KM atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
 KM cardiac; cytosolic; antiangiogenic; hypotensive; vulnerary;
 KM antiarteriosclerotic; gene; ss.

OS Homo sapiens.

PN WO200208284-A2.

PD 31-JAN-2002.

PF 09-JUL-2001; 2001WO-US21735.

XX 20-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 25-JUL-2000; 2000US-220664P.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 02-AUG-2000; 2000US-222695P.
 PR 17-AUG-2000; 2000US-0643657.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 07-SEP-2000; 2000US-230978P.
 PR 15-SEP-2000; 2000US-000000P.
 PR 18-SEP-2000; 2000US-0664610.
 PR 18-SEP-2000; 2000US-0665350.
 PR 24-OCT-2000; 2000US-242922P.
 PR 08-NOV-2000; 2000US-0709238.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000US-0747259.
 PR 22-JAN-2001; 2001US-0767609.
 PR 28-FEB-2001; 2001US-0766498.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 09-MAR-2001; 2001US-0802706.

PR 14-MAR-2001; 2001US-0806689.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001US-0865628.
 PR 25-MAY-2001; 2001US-0866034.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 30-MAY-2001; 2001US-0870574.
 PR 30-MAY-2001; 2001WO-US17443.
 PR 01-JUN-2001; 2001WO-US19692.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 28-JUN-2001; 2001WO-US00000.
 XX
 PA (GENTH) GENENTECH INC.
 PA (BAKE) BAKER K P.
 PA (FERR) FERRARA N.
 PA (GERB) GERBER H.
 PA (GERR) GERRITSEN M E.
 PA (GODD) GODDARD A.
 PA (GODO) GODDARD P J.
 PA (GURN) GURNEY A L.
 PA (HILL) HILLMAN K J.
 PA (MARS) MARSTERS S A.
 PA (PANJ) PAN J.
 PA (PAON) PAONI N F.
 PA (STEP) STEPHAN J F.
 PA (WATA) WATANABE C K.
 PA (WILL) WILLIAMS P M.
 PA (WOOD) WOOD W I.
 PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W.
 DR WPI; 2002-171999/22.
 DR P-PSDB; ABB95602.
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal
 XX
 PS Claim 1; Fig 359; 567pp; English.
 XX The present invention provides the protein and coding sequences of human
 CC PRO proteins. These are useful for treating or diagnosing a
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac
 CC hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The present sequence is a coding sequence of the invention.
 XX
 SQ Sequence 521 BP; 167 A; 86 C; 131 G; 137 T; 0 other;

Query Match 100.0%; Score 330; DB 24; Length 521;
 Best Local Similarity 100.0%; Pred. No. 4.2e-97;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATGAAATATTTATGACCCGCTCTAGCTTCCAGAAAGCTCTGTGCAGATGATGAGTGTGTC 60
 Db 92 CATGAAATATTTATGACCCGCTCTAGCTTCCAGAAAGCTCTGTGCAGATGATGAGTGTGTC 151
 QY 61 TATCTATTTCTCTGGCTAGTGTCTCAAGAAATATATAATGCCCCGAGCTGATGATTCATT 120
 Db 152 TATCTATTTCTCTGGCTAGTGTCTCAAGAAATATATAATGCCCCGAGCTGATGATTCATT 211
 QY 121 AACGTTAAAAAGGCGACAGATCTATGTGTACTCAAAAGCTGTGTAAAAAGAAATGAGCT 180
 Db 212 AACGTTAAAAAGGCGACAGATCTATGTGTACTCAAAAGCTGTGTAAAAAGAAATGAGCT 271
 QY 181 GGAGAAATTTGGGCTGGCAGTGTCTTATGTATGCTGCGCAGAGATGGGAGTGTGGGT 240

```

Db      272 GGAGAAATTTGGGCTGACAGTGTATTGATGATGGCCAGACGAGATGGAGTCGTGGGT 331
QY      241 TATTTCCCGAGAACTTGTGCAAGAAACGCTGTGTACCGAAGCTTACCAAGAGATT 300
      332 TATTTCCCGAGAACTTGTGCAAGAAACGCTGTGTACCGAAGCTTACCAAGAGATT 391
Db      301 CCCACACGAGATATGACTTCTTCTCGGAG 330
      392 CCCACACGAGATATGACTTCTTCTCGGAG 421

RESULT 6
ABL88251
ID      ABL88251 standard; cDNA; 521 BP.
XX
AC      ABL88251;
XX
DT      16-MAY-2002 (first entry)
XX
DE      Human PR09873 cDNA sequence SEQ ID NO:359.
XX
KW      Human; angiogenesis; cardiant; cytosolic; antiangiogenic; hypotensive;
      KW vulnerable; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
      KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
      KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
      KW age-related macular degeneration; arterial restenosis; angina;
      KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
      KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
      KW wound healing; chromosome mapping; gene mapping; gene; ss.
XX
OS      Homo sapiens.
XX
PN      WO200206590-A2.
XX
PD      03-JAN-2002.
XX
PF      20-JUN-2001; 2001WO-US19692.
XX
PR      23-JUN-2000; 2000US-213637P.
PR      20-JUL-2000; 2000US-219556P.
PR      25-JUL-2000; 2000US-220624P.
PR      28-JUL-2000; 2000US-220644P.
PR      02-AUG-2000; 2000US-222695P.
PR      17-AUG-2000; 2000US-064365P.
PR      23-AUG-2000; 2000WO-US23532.
PR      24-AUG-2000; 2000WO-US23328.
PR      07-SEP-2000; 2000US-230978P.
PR      18-SEP-2000; 2000US-0664610.
PR      24-OCT-2000; 2000US-249232P.
PR      08-NOV-2000; 2000US-0709238.
PR      08-NOV-2000; 2000WO-US30952.
PR      10-NOV-2000; 2000WO-US30873.
PR      01-DEC-2000; 2000WO-US32678.
PR      20-DEC-2000; 2000US-0747259.
PR      20-DEC-2000; 2000WO-US34956.
PR      22-JAN-2001; 2001US-076769.
PR      28-FEB-2001; 2001US-0796498.
PR      28-FEB-2001; 2001WO-US06520.
PR      01-MAR-2001; 2001US-0806666.
PR      09-MAR-2001; 2001US-0802706.
PR      14-MAR-2001; 2001US-0806689.
PR      22-MAR-2001; 2001US-0816744.
PR      05-APR-2001; 2001US-0828366.
PR      10-MAY-2001; 2001US-0854209.
PR      10-MAY-2001; 2001US-0854280.
PR      25-MAY-2001; 2001US-0866038.
PR      25-MAY-2001; 2001US-0866034.
PR      25-MAY-2001; 2001WO-US17092.
PR      30-MAY-2001; 2001US-0870574.
PR      30-MAY-2001; 2001WO-US17443.
PR      01-JUN-2001; 2001WO-US17800.

```

```

XX      (GETH ) GENENTECH INC.
PA      Baker KP, Ferrara N, Gerber H, Gertlisen ME, Goddard A,
PI      Godowski PJ, Gueney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI      Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX      MPI; 2002-090516/12.
DR      P-FSDb; ABB84996.
XX
PT      One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT      useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT      infarction), endothelial or angiogenic disorders in a mammal -
XX
PS      Claim 2, Fig 359, 565pp; English.
XX
CC      ABL88072 to ABL88258 encode the PRO proteins given in ABB84917 to
CC      ABB85003. The PRO proteins and polynucleotides have cardiant, cytosolic,
CC      antiangiogenic, hypotensive, vulnerable and antiarteriosclerotic
CC      activities, and can be used in gene therapy. The PRO polynucleotides,
CC      proteins, agonists and antagonists are useful for treating or diagnosing
CC      a cardiovascular, endothelial or angiogenic disorder in a mammal,
CC      e.g. cardiac hypertrophy, trauma, cancer, age-related macular
CC      degeneration, atherosclerosis, hypertension, arterial restenosis,
CC      rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
CC      lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
CC      carcinoma) and wound healing. The PRO polynucleotides have applications
CC      in molecular biology, including use as hybridisation probes, and in
CC      chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
CC      probes used in the exemplification of the present invention.
XX
SQ      Sequence 521 BP; 167 A; 86 C; 131 G; 137 T; 0 other;
XX
Query Match      100.0%; Score 330; DB 24; Length 521;
Best Local Similarity 100.0%; Pred. No. 4,2e-97;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 CATGGAATATTTATGAGCGCTGTAGCTTCCAGAAAGCTCTGTGCAGATGAGTGTCTC 60
Db      92 CATGGAATATTTATGAGCGCTGTAGCTTCCAGAAAGCTCTGTGCAGATGAGTGTCTC 151
QY      61 TATTAATTTCTCTGCTAGTGTCTCAAGAAATTTATATGCCCGGACTGTAGTCAATT 120
Db      152 TATTAATTTCTCTGCTAGTGTCTCAAGAAATTTATATGCCCGGACTGTAGTCAATT 211
QY      121 AACGTTAAAAAGGCGACAGATCTATGTAAGTCAAGCTGTGTAAAGAAATGAGACT 180
Db      212 AACGTTAAAAAGGCGACAGATCTATGTAAGTGTCTAAAGCTGTGTAAAGAAATGAGACT 271
QY      181 GGAGAAATTTGGGCTGAGAGTGTATTGATGATGGCCAGACGAGATGGAGTCTGGGT 240
Db      272 GGAGAAATTTGGGCTGAGAGTGTATTGATGATGGCCAGACGAGATGGAGTCTGGGT 331
QY      241 TATTTCCCGAGAACTTGTGCAAGAAACGCTGTGTACCGAAGCTTACCAAGAGATT 300
Db      332 TATTTCCCGAGAACTTGTGCAAGAAACGCTGTGTACCGAAGCTTACCAAGAGATT 391
QY      301 CCCACACGAGATATGACTTCTTCTCGGAG 330
Db      392 CCCACACGAGATATGACTTCTTCTCGGAG 421

RESULT 7
ABK33571
ID      ABK33571 standard; cDNA; 521 BP.
XX
AC      ABK33571;
XX
DT      08-MAY-2002 (first entry)
XX
DE      cDNA encoding human PRO protein, Seq ID No 71.
XX
KW      Human; secreted protein; PRO; tumour; lung cancer; colon cancer;

```


XX Sequence 891 BP; 272 A; 146 C; 214 G; 259 T; 0 other;
SQ
Query Match 100.0%; Score 330; DB 22; Length 891;
Best Local Similarity 100.0%; Pred. No. 5.3e-97;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CATGGAATATTATGAGACCGCTAGCTTCCAGAAAGCTCTGTGAGATGATGAGTGTCT 60
DB 73 CATGGAATATTATGAGACCGCTAGCTTCCAGAAAGCTCTGTGAGATGATGAGTGTCT 132
QY 61 TATACATTTCTCTGCTAGTGTCTCAAGAAATTATATGCCCGGAGCTGTAGATTCTT 120
DB 133 TATACATTTCTCTGCTAGTGTCTCAAGAAATTATATGCCCGGAGCTGTAGATTCTT 192
QY 121 AACGTTAAAAAGGCGACAGATCTATGTACTCAAAAGTGTGTAAAGAAATGAGAGCT 180
DB 193 AACGTTAAAAAGGCGACAGATCTATGTACTCAAAAGTGTGTAAAGAAATGAGAGCT 252
QY 181 GGAGAAATTTGGGCTGGCAGTGTATTATGTATGCGCAGAGCAGATGGAGTGTGGCT 240
DB 253 GGAGAAATTTGGGCTGGCAGTGTATTATGTATGCGCAGAGCAGATGGAGTGTGGCT 312
QY 241 TATTTCCCGAGAACTTGGTCAAGAAAGCGTGTGTACCGAAAGCTTACCAAGAACTT 300
DB 313 TATTTCCCGAGAACTTGGTCAAGAAAGCGTGTGTACCGAAAGCTTACCAAGAACTT 372
QY 301 CCCACCAAGGATATTGACTTCTTCTGCGAG 330
DB 373 CCCACCAAGGATATTGACTTCTTCTGCGAG 402
RESULT 9
AAH26342
ID AAH26342 standard; cDNA; 891 BP.
XX AAH26342;
XX
DT 02-OCT-2001 (first entry)
XX
DE Human growth regulatory-like polypeptide partial cDNA clone.
XX
KW Growth regulatory-like polypeptide; human; cartilage; melanoma;
KW neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200155332-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US02455.
XX
PR 25-JAN-2000; 2000US-0491404.
PR 02-MAY-2000; 2000US-0563786.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Mize NK, Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C;
PI Drmanac RT;
XX
DR WPI; 2001-483233/52.
XX
XX Isolated human growth regulatory-like polypeptide useful for treating
XX e.g. Alzheimer's disease, cancer, autoimmune disorders,
XX hyperproliferative disorders, coagulation disorders, and nervous system
XX disorders -
XX
PS Claim 1; Page 115; 119pp; English.
XX
CC The present sequence is that of a novel nucleic acid that was
CC assembled from human thymus cDNA library-derived Hyseq clone

CC identification number 16372272 (see AAH26341). A recursive
CC algorithm was used to extend the clone by pulling additional
CC sequences from different databases. A full-length sequence (see
CC AAH26343) encoding novel human growth regulatory-like polypeptide
CC (GRIP, see AAB82671) was subsequently obtained. Human GRIP
CC belongs to the same protein family as growth regulatory proteins,
CC growth factors, human melanoma derived growth regulatory proteins,
CC precursor (64% similarity and 45% identity over 111 amino acids)
CC or melanoma inhibitory activity, cattle cartilage-derived
CC retinoic acid sensitive protein (CD-RAP, 44% identity and 64%
CC similarity over 126 amino acids) and other retinoic acid-sensitive
CC proteins. GRIP polypeptides and polynucleotides of the invention
CC can be used in the prophylaxis, treatment (including gene therapy)
CC and diagnosis of disorders and diseases caused by, or involving,
CC cartilage development and maintenance, inhibition of melanoma cell
CC growth and tumours, including neuroectodermal tumours such as
CC gliomas. The polynucleotides can also be used to design probes
CC and primers, for chromosome and gene mapping, in the recombinant
CC production of protein, in the generation of antisense, ribozyme and
CC peptide-nucleic acid molecules, and to produce transgenic animals.
SQ
Sequence 891 BP; 272 A; 146 C; 214 G; 259 T; 0 other;
Query Match 100.0%; Score 330; DB 22; Length 891;
Best Local Similarity 100.0%; Pred. No. 5.3e-97;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CATGGAATATTATGAGACCGCTAGCTTCCAGAAAGCTCTGTGAGATGATGAGTGTCT 60
DB 73 CATGGAATATTATGAGACCGCTAGCTTCCAGAAAGCTCTGTGAGATGATGAGTGTCT 132
QY 61 TATACATTTCTCTGCTAGTGTCTCAAGAAATTATATGCCCGGAGCTGTAGATTCTT 120
DB 133 TATACATTTCTCTGCTAGTGTCTCAAGAAATTATATGCCCGGAGCTGTAGATTCTT 192
QY 121 AACGTTAAAAAGGCGACAGATCTATGTACTCAAAAGTGTGTAAAGAAATGAGAGCT 180
DB 193 AACGTTAAAAAGGCGACAGATCTATGTACTCAAAAGTGTGTAAAGAAATGAGAGCT 252
QY 181 GGAGAAATTTGGGCTGGCAGTGTATTATGTATGCGCAGAGCAGATGGAGTGTGGCT 240
DB 253 GGAGAAATTTGGGCTGGCAGTGTATTATGTATGCGCAGAGCAGATGGAGTGTGGCT 312
QY 241 TATTTCCCGAGAACTTGGTCAAGAAAGCGTGTGTACCGAAAGCTTACCAAGAACTT 300
DB 313 TATTTCCCGAGAACTTGGTCAAGAAAGCGTGTGTACCGAAAGCTTACCAAGAACTT 372
QY 301 CCCACCAAGGATATTGACTTCTTCTGCGAG 330
DB 373 CCCACCAAGGATATTGACTTCTTCTGCGAG 402
RESULT 10
AAF59083
ID AAF59083 standard; DNA; 923 BP.
XX AAF59083;
XX
DT 23-APR-2001 (first entry)
XX
DE Human MLP nucleotide sequence SEQ ID NO:29.
XX
KW MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
KW cardiant; gene therapy; secretory cell function regulator; promoter;
KW inhibitor; ds.
XX
OS Homo sapiens.
XX
PN WO200102564-A1.
XX
PD 11-JAN-2001.

```

PF 29-JUN-2000; 2000CWO-JP04278.
XX 30-JUN-1999; 99JP-0186718.
PR (TAKE ) TAKEDA CHEM IND LTD.
PA
XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
PI Tanaka H;
XX WPI; 2001-159271/16.
XX
XX Safe, low-toxicity secretory cell function-regulatory protein and
XX encoded DNA, applicable as drugs, in diagnosis and development of
XX promoters and inhibitors for preventing or treating e.g. bone and joint
XX diseases -
XX
XX Example 1; Page 99-100; 11pp; Japanese.
XX
XX The present invention describes novel MLP proteins and their encoding
XX DNAs. The MLP proteins and DNAs have anti-inflammatory and cardiant
XX activities, and can be used in gene therapy and as secretory cell
XX function regulators. The MLP proteins and DNAs can be used in drugs, in
XX the diagnosis and development of promoters and inhibitors for preventing
XX or treating bone and joint diseases as well as pathologic angiogenesis.
XX AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
XX in the exemplification of the present invention.
XX
XX Sequence 923 BP; 303 A; 147 C; 213 G; 260 T; 0 other;
SQ
XX
XX Query Match 100.0%; Score 330; DB 22; Length 923;
XX Best Local Similarity 100.0%; Pred. No. 5.4e-97;
XX Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 CATGAAATTTATGAGCCGCTAGCTTCCAGAAAGCTGTGCGAGATGAGTGTCT 60
XX 88 CATGAAATTTATGAGCCGCTAGCTTCCAGAAAGCTGTGCGAGATGAGTGTCT 147
XX
XX 61 TATATCTATTTCTGTGCTAGTGTCTCAAGAAAGTATTAAGCCCGGAGCTGTGATTCA 120
XX 148 TATATCTATTTCTGTGCTAGTGTCTCAAGAAAGTATTAAGCCCGGAGCTGTGATTCA 207
XX
XX 121 AAGCTTAAAGAGGAGAGAGATCTATGTACTCAAGCTGTGTAAGAAATGAGACT 180
XX 208 AAGCTTAAAGAGGAGAGATCTATGTACTCAAGCTGTGTAAGAAATGAGACT 267
XX
XX 181 GGAGAAATTTGGGCTGCGAGTGTATGTATGATGCGCAGAGAGAGATGAGTGTGCT 240
XX 268 GGAGAAATTTGGGCTGCGAGTGTATGTATGATGCGCAGAGAGAGATGAGTGTGCT 327
XX
XX 241 TATTTCCCGAGAACTGTGTCAGAGAAAGCGTGTGTACAGAGAGCTTCAAGAGAGTT 300
XX 328 TATTTCCCGAGAACTGTGTCAGAGAAAGCGTGTGTACAGAGAGCTTCAAGAGAGTT 387
XX
XX 301 CCGACGACGAGATTTGACTTCTCTCGAG 330
XX 388 CCGACGACGAGATTTGACTTCTCTCGAG 417
XX
XX
XX RESULT 11
XX AAH26343
XX ID AAH26343 standard, cDNA; 1201 BP.
XX
XX AAH26343;
XX
XX 02-OCT-2001 (first entry)
XX
XX Human growth regulatory-like polypeptide cDNA.
XX
XX Growth regulatory-like polypeptide; human; cartilage; melanoma;
XX neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;
XX ss.
XX
XX Homo sapiens.

```

```

XX Key Location/Qualifiers
XX CDS 33..419
XX FT sig_peptide /*tag= a
XX FT mat_peptide /*tag= b
XX FT /tag= 102..416
XX FT /*tag= c
XX
XX W0200155332-A2.
XX
XX 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-US02455.
XX
XX 25-JAN-2000; 2000US-0491404.
XX 02-MAY-2000; 2000US-0563786.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Mize NK, Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C;
XX Dmanac RT;
XX
XX WPI; 2001-483233/52.
XX P-PSDB; AAB82671.
XX
XX Isolated human growth regulatory-like polypeptide useful for treating
XX e.g. Alzheimer's disease, cancer, autoimmune disorders,
XX hyperproliferative disorders, coagulation disorders, and nervous system
XX disorders -
XX
XX Claim 1; Page 115-116; 11pp; English.
XX
XX The present sequence is that of a novel nucleic acid encoding
XX human growth regulatory-like polypeptide (GRP, see AAB82671).
XX The sequence was assembled using human thymus cDNA library-derived
XX Hyseq clone identification number 16372272 (see AAH26341) as seed,
XX using software programs to pull additional sequences from Hyseq's
XX proprietary database containing expressed sequence tag sequences,
XX and by gel sequencing using primers to extend both 5' and 3' ends.
XX C. The predicted protein has a mol.wt. of 14 kDa unglycosylated. GRP
XX belongs to the same protein family as growth regulatory proteins,
XX growth factors, human melanoma derived growth regulatory proteins
XX precursor (64% similarity and 45% identity over 111 amino acids)
XX or melanoma inhibitory activity, cattle cartilage-derived
XX retinoic acid sensitive protein (CD-RAP, 44% identity and 64%
XX similarity over 126 amino acids) and other retinoic acid-sensitive
XX proteins. GRP polypeptides and polynucleotides of the invention
XX can be used in the prophylaxis, treatment (including gene therapy)
XX and diagnosis of disorders and diseases caused by, or involving,
XX cartilage development and maintenance, inhibition of melanoma cell
XX growth and tumours, including neuroectodermal tumours such as
XX gliomas. The polynucleotides can also be used to design probes
XX and primers, for chromosome and gene mapping, in the recombinant
XX production of protein, in the generation of antisense, ribozyme and
XX peptide-nucleic acid molecules, and to produce transgenic animals.
XX They may also have cytokine and cell proliferation or
XX differentiation activity, stem cell growth factor activity,
XX haematopoiesis regulating activity, tissue growth activity,
XX immunosuppressive or immunostimulant activity, activin/inhibin
XX activity, chemorectic/chemokinetic activity, haemostatic and
XX thrombolytic activity, use in cancer diagnosis and therapy,
XX drug screening, receptor/ligand activity, anti-inflammatory
XX activity, and treatment of leukaemia, nervous system disorders,
XX arthritis and inflammation.
XX
XX
XX Sequence 1201 BP; 357 A; 188 C; 275 G; 381 T; 0 other;
SQ
XX
XX Query Match 100.0%; Score 330; DB 22; Length 1201;
XX Best Local Similarity 100.0%; Pred. No. 6.1e-97;
XX Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 CATGAAATTTATGAGCCGCTAGCTTCCAGAAAGCTGTGCGAGATGAGTGTCT 60

```

| | | | |
|-----------|-----|--|-----|
| Db | 87 | CATGGAATATTATTTGACCGCTAGCTTCCAGAAAGCTCTGGCAGATGATGAGTGTCTC | 146 |
| Qy | 61 | TATACTATTCTCTGCTAGTGTCTCAAGAATTATATGCCCGGACTGTAGATTAT | 120 |
| Db | 147 | TATACTATTCTCTGCTAGTGTCTCAAGAATTATATATGCCCGGACTGTAGATTAT | 206 |
| Qy | 121 | AAGCTTAAAAAAGGCGACGACGATCTGTGTCTCTCAAAGCTGTGTAAAAAATGAGCT | 180 |
| Db | 207 | AACGTTAAAAAAGGCGACGACGATCTGTGTCTCTCAAAGCTGTGTAAAAAATGAGCT | 266 |
| Qy | 181 | GGAGAAATTTTGGGCTGGCAGTGTATTATGGTATGGCCAGAGACGAGATGGAGTGTGGGT | 240 |
| Db | 267 | GGAGAAATTTTGGGCTGGCAGTGTATTATGGTATGGCCAGAGACGAGATGGAGTGTGGGT | 326 |
| Qy | 241 | TATTTCCCGAGAACTTGTGTCAAGAAACGCGTGTGTACAGAAAGCTAACAGAAATT | 300 |
| Db | 327 | TATTTCCCGAGAACTTGTGTCAAGAAACGCGTGTGTACAGAAAGCTAACAGAAATT | 386 |
| Qy | 301 | CCGACCCAGGATATGTACTTCTTCTGCGAG | 330 |
| Db | 387 | CCGACCCAGGATATGTACTTCTTCTGCGAG | 416 |
| RESULT 12 | | | |
| AF59080 | ID | AF59080 standard; DNA; 330 BP. | |
| XX | AC | AF59080; | |
| XX | DT | 23-APR-2001 (first entry) | |
| XX | XX | Mouse MLP nucleotide sequence SEQ ID NO:25. | |
| DE | XX | MLP; MIA; melanoma inhibitory activity; cancer; bone disease; | |
| XX | XX | joint disease; pathologic angiogenesis; diagnosis; antiinflammatory; | |
| KM | XX | cardiac; gene therapy; secretory cell function regulator; promoter; | |
| KM | XX | inhibitor; ds. | |
| XX | XX | | |
| XX | OS | Mus musculus. | |
| XX | PN | WO200102564-A1. | |
| PD | XX | 11-JAN-2001. | |
| PF | XX | 29-JUN-2000; 2000WO-JP04278. | |
| XX | PR | 30-JUN-1999; 99JP-0186718. | |
| XX | XX | (TAKE) TAKEDA CHEM IND LTD. | |
| PA | XX | Itou Y, Nishi K, Ogi K, Okubo S, Mogi S, Noguchi Y, Yoshimura K, | |
| XX | PI | Tanaka H; | |
| XX | PI | WPI; 2001-159271/16. | |
| DR | XX | P-PSDB; AAB69127. | |
| PT | XX | Safe, low-toxicity secretory cell function-regulatory protein and | |
| PT | XX | encoded DNA, applicable as drugs, in diagnosis and development of | |
| XX | XX | promoters and inhibitors for preventing or creating e.g. bone and joint | |
| PT | XX | diseases | |
| PS | XX | Claim 10; Page 98; 11pp; Japanese. | |
| XX | XX | The present invention describes novel MLP proteins and their encoding | |
| CC | XX | DNA. The MLP proteins and DNAs have antiinflammatory and cardiant | |
| CC | XX | activities, and can be used in gene therapy and as secretory cell | |
| CC | XX | function regulators. The MLP proteins and DNAs can be used in drugs, in | |
| CC | XX | the diagnosis and development of promoters and inhibitors for preventing | |
| CC | XX | or creating bone and joint diseases as well as pathologic angiogenesis. | |
| CC | XX | AAB59063 to AAF59099 and AAB59122 to AAB69132 represent sequences used | |
| CC | XX | in the exemplification of the present invention. | |
| XX | XX | | |

SQ Sequence 330 BP; 91 A; 60 C; 92 G; 87 T; 0 other:

Query Match 76.4%; Score 252.2; DB 22; Length 330;
Best Local Similarity 85.4%; Pred. No. 7,3e-72;
Matches 281; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 CATGAAATATTATGACCGCTAGCTTCCAGAAGCTGTGCAGATGATGAGTGTC 60
Db 1 CATGGTTATTATTAAGATAAAGCTTCTTCAAGAGTTGTGGGATGAGAGTGTC 60

OY 61 TAATCTATTTCTCTGCGTAGTGCTCAAAGAAATTATAATCCCCCGACTGAATTTCAT 120
Db 61 TATACATTTTCTCTGGCAGAGAGCACAGAGAAATTACCATGCCAGCTGTAGGTCATC 120

OY 121 AACCTTAAAAAGGGGCGCAGATCTATGTGTACTCCAAAGTGGTAAAAGAAATGAGCT 180
Db 121 GATGTCAAGAAAGGGGCGCAGATCTATGTTTACTCCAAAGTGGTAAAGAAACGAGCT 180

OY 181 GGAGAAATTTTGCGCTGCGACAGTGTATTATGTGATGCGCAGAGCAGATGGAGTCTGGGT 240
Db 181 GGAGAGTTTTGGCTGCGACAGTGTATTATGTGATGACACAGAGATAGATGGGAATTTGAGGT 240

OY 241 TATTTTCCCAGGAACTTGTGTCAAAGAAACAGCGTGTGTACCAGAAAGCTAACCAAGAACTT 300
Db 241 TATTTTCCCAGCAACTGTGTGAAGAGCAGCGTGTATACACAGAGGCGCACCAAGAGATC 300

OY 301 CCCACCAAGGATATTGACTTCTTCTGGGA 329
Db 301 CCAAACCAAGGATATTGACTTCTTCTGTGA 329

RESULT 13
AFS9068
ID AFS9068 standard; DNA; 384 BP.
XX AFS9068;
AC
XX
XX AFS9068;
AC
XX
DT 23-APR-2001 (first entry)
XX
DE Mouse MLP nucleotide sequence SEQ ID NO:10.
XX
XX MLP: MIA; melanoma inhibitory activity; cancer; bone disease;
KM joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
KM cardiac; gene therapy; secretory cell function regulator; promoter;
XX inhibitor; ds.
XX
OS Mus musculus.
XX
PN WO200102564-A1.
XX
PD 11-JAN-2001.
XX
PF 29-JUN-2000; 2000WO-JP04278.
PR 30-JUN-1999; 99JP-0186718.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Itoh Y, Nishi K, Ogi K, Okkubo S, Mogi S, Noguchi Y, Yoshimura K;
PI Tanaka H;
XX
DR WPI; 2001-159271/16.
XX P-PsDB; AAB69125.

PT Safe, low-toxicity secretory cell function-regulatory protein and
PT encoded DNA, applicable as drugs, in diagnosis and development of
PT promoters and inhibitors for preventing or treating e.g. bone and joint
diseases -
XX
PS Claim 11; Page 93; 11pp; Japanese.
CC The present invention describes novel MLP proteins and their encoding
DNAs. The MLP proteins and DNAs have antiinflammatory and cardiac

CC activities, and can be used in gene therapy and as secretory cell
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in
 CC the diagnosis and development of promoters and inhibitors for preventing
 CC or treating bone and joint diseases as well as pathologic angiogenesis.
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
 CC in the exemplification of the present invention.

SO Sequence 384 BP; 98 A; 68 C; 111 G; 107 T; 0 other;

Query Match

Best Local Similarity 76.4%; Score 252.2; DB 22; Length 384;

Matches 281; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 CATGAAATATTATGACCGCTAGCTCCAAAGAGCTCTGGAGATGATGATGCTGTC 60
 Db 55 CATGGTGTATTATGAGATTAACCTTCTTAAGAGTGTGTGGATGAGAGTGTGTC 114
 QY 61 TATACTATTCTCTGCTAGTGTCTCAAGAGATTATATGCCCCGACTGTAGATTGATT 120
 Db 115 TATACTATTCTCTGCTAGTGTCTCAAGAGATTATATGCCCCGACTGTAGATTGATT 174
 QY 121 AACGTTAAAAAGGCGACAGATCTATGTGTACTCAAACTGTGTAAAAAATGAGCT 180
 Db 175 GATGCAAGAAAGGCGACAGATCTATGTGTACTCAAACTGTGTAAAAAAGGAGCT 234
 QY 181 GGAGAAATTTGGGCTGGCAGTGTATGTGTATGCGCCAGAGAGATGGGAGTGTGGCT 240
 Db 235 GGAGAGTTTGGGCTGGCAGTGTATGTGTATGCGCCAGAGATGGGAGTGTGGCT 294
 QY 241 TATTTCCCGCAGAACTTGGTCAAGAGAGCGTGTGTACCAAGAGTACCAAGAAATT 300
 Db 295 TATTTCCCGCAGAACTTGGTCAAGAGAGCGTGTGTATACCAAGAGTACCAAGAAATT 354
 QY 301 CCCACACGAGATATTGACTTCTTCTGCGA 329
 Db 355 CCACACGAGATATTGACTTCTTCTGCGA 383

RESULT 14

AAF59084 ID AAF59084 standard; DNA; 947 BP.

XX AAF59084;

XX 23-APR-2001 (first entry)

DE Mouse MLP nucleotide sequence SEQ ID NO:30.

XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
 KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
 KW cardiant; gene therapy; secretory cell function regulator; promoter;
 KW inhibitor; ds.

XX Mus musculus.

XX WO200102564-A1.

XX 11-JAN-2001.

XX 29-JUN-2000; 2000WO-JP04278.

XX 30-JUN-1999; 99JP-0186718.

XX (TAKE) TAKEDA CHEM IND LTD.

PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;

XX Tanaka H;

XX MPI; 2001-159271/16.

PT Safe, low-toxicity secretory cell function-regulatory protein and
 PT encoded DNA, applicable as drugs, in diagnosis and development of
 PT promoters and inhibitors for preventing or treating e.g. bone and joint

PT diseases -
 XX Example 2; Page 100-101; 11np; Japanese.

CC The present invention describes novel MLP proteins and their encoding
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
 CC activities, and can be used in gene therapy and as secretory cell
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in
 CC the diagnosis and development of promoters and inhibitors for preventing
 CC or treating bone and joint diseases as well as pathologic angiogenesis.
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
 CC in the exemplification of the present invention.

SO Sequence 947 BP; 279 A; 158 C; 221 G; 289 T; 0 other;

Query Match

Best Local Similarity 76.4%; Score 252.2; DB 22; Length 947;

Matches 281; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 CATGAAATATTATGACCGCTAGCTCCAAAGAGCTCTGGAGATGATGATGCTGTC 60
 Db 65 CATGGTGTATTATGAGATTAACCTTCTTAAGAGTGTGTGGATGAGAGTGTGTC 124
 QY 61 TATACTATTCTCTGCTAGTGTCTCAAGAGATTATATGCCCCGACTGTAGATTGATT 120
 Db 125 TATACTATTCTCTGCTAGTGTCTCAAGAGATTATATGCCCCGACTGTAGATTGATT 184
 QY 121 AACGTTAAAAAGGCGACAGATCTATGTGTACTCAAACTGTGTAAAAAATGAGCT 180
 Db 185 GATGCAAGAAAGGCGACAGATCTATGTGTACTCAAACTGTGTAAAAAAGGAGCT 244
 QY 181 GGAGAAATTTGGGCTGGCAGTGTATGTGTATGCGCCAGAGAGATGGGAGTGTGGCT 240
 Db 245 GGAGAGTTTGGGCTGGCAGTGTATGTGTATGCGCCAGAGATGGGAGTGTGGCT 304
 QY 241 TATTTCCCGCAGAACTTGGTCAAGAGAGCGTGTGTACCAAGAGTACCAAGAAATT 300
 Db 305 TATTTCCCGCAGAACTTGGTCAAGAGAGCGTGTGTATACCAAGAGTACCAAGAAATT 364
 QY 301 CCCACACGAGATATTGACTTCTTCTGCGA 329
 Db 365 CCACACGAGATATTGACTTCTTCTGCGA 393

RESULT 15

AAF59099 ID AAF59099 standard; DNA; 330 BP.

XX AAF59099;

XX 23-APR-2001 (first entry)

DE Rat MLP nucleotide sequence SEQ ID NO:48.

XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
 KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
 KW cardiant; gene therapy; secretory cell function regulator; promoter;
 KW inhibitor; ds.

XX Rattus sp.

XX WO200102564-A1.

XX 11-JAN-2001.

XX 29-JUN-2000; 2000WO-JP04278.

XX 30-JUN-1999; 99JP-0186718.

XX (TAKE) TAKEDA CHEM IND LTD.

PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;

XX Tanaka H;

XX WPI; 2001.159271/16.
DR P-PSDB; AAB69131.
XX

PT Safe, low-toxicity secretory cell function-regulatory protein and
PT encoded DNA, applicable as drugs, in diagnosis and development of
PT promoters and inhibitors for preventing or treating e.g. bone and joint
PT diseases

PS Claim 12; Page 107; 11np; Japanese.

XX
CC The present invention describes novel MIP proteins and their encoding
CC DNAs. The MIP proteins and DNAs have anti-inflammatory and cardiant
CC activities, and can be used in gene therapy and as secretory cell
CC function regulators. The MIP proteins and DNAs can be used in drugs, in
CC the diagnosis and development of promoters and inhibitors for preventing
CC or treating bone and joint diseases as well as pathologic angiogenesis.
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
CC in the exemplification of the present invention.

XX Sequence 330 BP; 91 A; 62 C; 91 G; 86 T; 0 other;

Query Match 75.5%; Score 249; DB 22; Length 330;
Best Local Similarity 84.8%; Pred. No. 8e-71;
Matches 279; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1 CATGGAATATTATGACCGCTCTAGCTCCAGAAGCTCTGTGCAGATGAGTGTGTC 60
DB 1 CATGCAATGTTATGATTAACCTTCTCTAAGAAGTTGTGTGCAGATGAGAGTGTGTC 60
QY 61 TATACATTTCTCTGGCTAGTCTCAAGAGATTATATGCCCCGAGCTGAGTTGATT 120
DB 61 TATACATTTCTCTGGCAAGACACAGAGAACTACATGCCCGAGCTGAGTTGATT 120
QY 121 AACGTTAAAGGGGCGACAGATCTATGTCTCAAGCTGTAAAGAAATGAGAGCT 180
DB 121 AATGCAAGAAAGGGCGACAGATCTATGTCTTATTCAGAGCTGTACAGAAATGAGAGCT 180
QY 181 GGAGATTTTGGGCTGGCAGTGTATGATGAGCCAGAGATGAGAGTGTGGGT 240
DB 181 GGGGATTTCTGGGCTGGCAGTGTATGATGAGCCAGAGATGAGAGTGTGGGT 240
QY 241 TATTTCCCGAGAACTGTGTCAGAGAACGGGTGTATCAGAGAGCTTACCAAGAAATT 300
DB 241 TATTTCCCGAGAACTGTGTCAGAGAACGGGTGTATCAGAGAGCTTACCAAGAAATT 300
QY 301 CCCACCAAGGATATTGACTTCTTCTGCGA 329
DB 301 CCAACCAAGGATATTGACTTCTTCTGTA 329

Search completed: December 30, 2003, 02:14:32
Job time : 109.538 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 30, 2003, 04:08:13 ; Search time 270.994 Seconds

(without alignments)
4172.254 Million cell updates/sec

Title: US-10-019-455A-23

Perfect score: 330

Sequence: 1 catggaattctatgacgcg.....atatgactctctctcgag 330

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 2244575 seqs, 171317285 residues

Total number of hits satisfying chosen parameters: 4489150

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing First 45 summaries

Database : Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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8: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
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10: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
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13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB_PUBCOMB.seq:*
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15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match Length | DB ID | Description |
|------------|-------|--------------|-------------------------|-------------------|
| 1 | 330 | 100.0 | 426 15 US-10-216-038-1 | Sequence 1, Appl |
| 2 | 330 | 100.0 | 521 13 US-10-216-163-71 | Sequence 71, Appl |
| 3 | 330 | 100.0 | 521 13 US-10-218-765-71 | Sequence 71, Appl |
| 4 | 330 | 100.0 | 521 13 US-10-219-063-71 | Sequence 71, Appl |
| 5 | 330 | 100.0 | 521 13 US-10-219-066-71 | Sequence 71, Appl |
| 6 | 330 | 100.0 | 521 13 US-10-219-067-71 | Sequence 71, Appl |
| 7 | 330 | 100.0 | 521 13 US-10-219-068-71 | Sequence 71, Appl |
| 8 | 330 | 100.0 | 521 13 US-10-219-069-71 | Sequence 71, Appl |
| 9 | 330 | 100.0 | 521 13 US-10-219-073-71 | Sequence 71, Appl |
| 10 | 330 | 100.0 | 521 13 US-10-219-475-71 | Sequence 71, Appl |
| 11 | 330 | 100.0 | 521 13 US-10-219-480-71 | Sequence 71, Appl |
| 12 | 330 | 100.0 | 521 13 US-10-219-483-71 | Sequence 71, Appl |
| 13 | 330 | 100.0 | 521 13 US-10-219-525-71 | Sequence 71, Appl |
| 14 | 330 | 100.0 | 521 13 US-10-219-526-71 | Sequence 71, Appl |
| 15 | 330 | 100.0 | 521 13 US-10-219-530-71 | Sequence 71, Appl |

| | | | | |
|----|-----|-------|--------------------------|-------------------|
| 16 | 330 | 100.0 | 521 13 US-10-219-531-71 | Sequence 71, Appl |
| 17 | 330 | 100.0 | 521 13 US-10-219-532-71 | Sequence 71, Appl |
| 18 | 330 | 100.0 | 521 13 US-10-219-533-71 | Sequence 71, Appl |
| 19 | 330 | 100.0 | 521 13 US-10-223-081-359 | Sequence 359, App |
| 20 | 330 | 100.0 | 521 13 US-10-230-437-71 | Sequence 71, Appl |
| 21 | 330 | 100.0 | 521 13 US-10-233-228-71 | Sequence 71, Appl |
| 22 | 330 | 100.0 | 521 13 US-10-227-082-359 | Sequence 359, App |
| 23 | 330 | 100.0 | 521 15 US-10-227-884-71 | Sequence 71, Appl |
| 24 | 330 | 100.0 | 521 15 US-10-230-163-71 | Sequence 71, Appl |
| 25 | 330 | 100.0 | 521 15 US-10-230-338-71 | Sequence 71, Appl |
| 26 | 330 | 100.0 | 521 15 US-10-218-631-71 | Sequence 71, Appl |
| 27 | 330 | 100.0 | 521 15 US-10-230-414-71 | Sequence 71, Appl |
| 28 | 330 | 100.0 | 521 15 US-10-216-159A-71 | Sequence 71, Appl |
| 29 | 330 | 100.0 | 521 15 US-10-218-849-71 | Sequence 71, Appl |
| 30 | 330 | 100.0 | 521 15 US-10-227-873-71 | Sequence 71, Appl |
| 31 | 330 | 100.0 | 521 15 US-10-227-883-71 | Sequence 71, Appl |
| 32 | 330 | 100.0 | 521 15 US-10-219-076-71 | Sequence 71, Appl |
| 33 | 330 | 100.0 | 521 15 US-10-230-434-71 | Sequence 71, Appl |
| 34 | 330 | 100.0 | 521 15 US-10-219-003-71 | Sequence 71, Appl |
| 35 | 330 | 100.0 | 521 15 US-10-219-075-71 | Sequence 71, Appl |
| 36 | 330 | 100.0 | 521 15 US-10-219-464-71 | Sequence 71, Appl |
| 37 | 330 | 100.0 | 521 15 US-10-219-466-71 | Sequence 71, Appl |
| 38 | 330 | 100.0 | 521 15 US-10-219-479-71 | Sequence 71, Appl |
| 39 | 330 | 100.0 | 521 15 US-10-219-481-71 | Sequence 71, Appl |
| 40 | 330 | 100.0 | 521 15 US-10-230-260-71 | Sequence 71, Appl |
| 41 | 330 | 100.0 | 521 15 US-10-233-231-71 | Sequence 71, Appl |
| 42 | 330 | 100.0 | 521 15 US-10-232-233-71 | Sequence 71, Appl |
| 43 | 330 | 100.0 | 521 15 US-10-216-165-71 | Sequence 71, Appl |
| 44 | 330 | 100.0 | 521 15 US-10-218-956-71 | Sequence 71, Appl |
| 45 | 330 | 100.0 | 521 15 US-10-219-468-71 | Sequence 71, Appl |

ALIGNMENTS

RESULT 1
US-10-216-038-1
Sequence 1, Application US/10216038
Publication No. US20030124573A1
GENERAL INFORMATION:
APPLICANT: Mize, Nancy K
APPLICANT: Boyle, Bryan J
APPLICANT: Ford, John B
APPLICANT: Arterburn, Matthew C
APPLICANT: Tang, Y Tom
APPLICANT: Liu, Chenghua
APPLICANT: Drmanac, Radoje T
APPLICANT: Song, Yong
APPLICANT: Stataad, Michael
TITLE OF INVENTION: Methods and Materials Relating to No. US20030124573A1 Growth
TITLE OF INVENTION: Polypeptides and Polynucleotides
FILE REFERENCE: HVS-7C1P
CURRENT APPLICATION NUMBER: US/10/216,038
PRIOR FILING DATE: 2002-08-08
PRIOR APPLICATION NUMBER: US 09/563,786
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR FILING DATE: 2000-01-25
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 426
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (426)..(426)
OTHER INFORMATION: n = A, T, G, or C
US-10-216-038-1
Query Match 100.0%; Score 330; DB 15; Length 426;
Best Local Similarity 100.0%; Pred. No. 6.5e+100;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATGAAATATTATGACCGCTAGCTTCCAAGAAGCTCTGTGAGATGATGATGTC 60
DB 73 CATGAAATATTATGACCGCTAGCTTCCAAGAAGCTCTGTGAGATGATGATGTC 132
QY 61 TATACATTTCTCTGCTAGTGTCTCAGAGATTATTAATGCCCCGAGCTGATGATCATT 120
DB 133 TATACATTTCTCTGCTAGTGTCTCAGAGATTATTAATGCCCCGAGCTGATGATCATT 192
QY 121 AACGTTAAAAAGGCGACAGATCTATGTGTCTAAAGCTGTGTAAAGAAATGAGACT 180
DB 193 AACGTTAAAAAGGCGACAGATCTATGTGTCTAAAGCTGTGTAAAGAAATGAGACT 252
QY 181 GGAGAAATTTTGGGCTGGCAGTGTCTATGTTGATGGCCAGAGAGATGGAGTGGTGGT 240
DB 253 GGAGAAATTTTGGGCTGGCAGTGTCTATGTTGATGGCCAGAGAGATGGAGTGGTGGT 312
QY 241 TATTTCCCGAGAACTTGTGTCAAGAGACGCTGTGTATCCAGAAAGCTACCAAGAACTT 300
DB 313 TATTTCCCGAGAACTTGTGTCAAGAGACGCTGTGTATCCAGAAAGCTACCAAGAACTT 372
QY 301 CCCACCAAGGATATTGACTTCTTCTGCGAG 330
DB 373 CCCACCAAGGATATTGACTTCTTCTGCGAG 402

RESULT 2
US-10-216-163-71
Sequence 71, Application US/10216163
Publication No. US20030149239A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530P1C3
CURRENT APPLICATION NUMBER: US/10/216,163
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 71
LENGTH: 521
TYPE: DNA
ORGANISM: Homo Sapien

US-10-216-163-71

Query Match 100.0%; Score 330; DB 13; Length 521;
Best Local Similarity 100.0%; Pred. No. 7.2e-100;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATGAAATATTATGACCGCTAGCTTCCAAGAAGCTCTGTGAGATGATGATGTC 60
DB 92 CATGAAATATTATGACCGCTAGCTTCCAAGAAGCTCTGTGAGATGATGATGTC 151
QY 61 TATACATTTCTCTGCTAGTGTCTCAGAGATTATTAATGCCCCGAGCTGATGATCATT 120
DB 152 TATACATTTCTCTGCTAGTGTCTCAGAGATTATTAATGCCCCGAGCTGATGATCATT 211
QY 121 AACGTTAAAAAGGCGACAGATCTATGTGTCTAAAGCTGTGTAAAGAAATGAGACT 180
DB 212 AACGTTAAAAAGGCGACAGATCTATGTGTCTAAAGCTGTGTAAAGAAATGAGACT 271
QY 181 GGAGAAATTTTGGGCTGGCAGTGTCTATGTTGATGGCCAGAGAGATGGAGTGGTGGT 240
DB 272 GGAGAAATTTTGGGCTGGCAGTGTCTATGTTGATGGCCAGAGAGATGGAGTGGTGGT 331
QY 241 TATTTCCCGAGAACTTGTGTCAAGAGACGCTGTGTATCCAGAAAGCTACCAAGAACTT 300
DB 332 TATTTCCCGAGAACTTGTGTCAAGAGACGCTGTGTATCCAGAAAGCTACCAAGAACTT 391
QY 301 CCCACCAAGGATATTGACTTCTTCTGCGAG 330
DB 392 CCCACCAAGGATATTGACTTCTTCTGCGAG 421

RESULT 3
US-10-218-765-71

Sequence 71, Application US/10218765
Publication No. US20030187201A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530P1C19
CURRENT APPLICATION NUMBER: US/10/218,765
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 71
LENGTH: 521
TYPE: DNA
ORGANISM: Homo Sapien

Tue Dec 30 10:20:39 2003

us-10-019-455a-23.rmpb

PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/086392
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089905
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090691
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/095302
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/095318
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/095916
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/096446
PRIOR FILING DATE: 1998-08-11
PRIOR APPLICATION NUMBER: 60/096791
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 60/097986
PRIOR FILING DATE: 1998-08-26
PRIOR APPLICATION NUMBER: 60/098544
PRIOR FILING DATE: 1998-08-31
PRIOR APPLICATION NUMBER: 60/099596
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099598
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099803
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099811
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099812
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099816
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/100038
PRIOR FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: 60/100385
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100390
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100627
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100848
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/100919
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/101477
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101738
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101741
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101786
PRIOR FILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: 60/101916
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101922
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/106178
PRIOR FILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: 60/106248
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 60/106464
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 60/106905
PRIOR FILING DATE: 1998-11-03
PRIOR APPLICATION NUMBER: 60/108787
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/108801
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/108849
PRIOR FILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: 60/112422
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/113296
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/113605
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113621
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/115558
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115565
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115733
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/119549
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/123618
PRIOR FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: 60/125259
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 60/125775
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 60/126773
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: 60/127887
PRIOR FILING DATE: 1999-04-05
PRIOR APPLICATION NUMBER: 60/130232
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/131022
PRIOR FILING DATE: 1999-04-26
PRIOR APPLICATION NUMBER: 60/131270
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131291
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131445
PRIOR FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 60/134287
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/140650
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/140723
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/141037
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 60/144758
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/145698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: 60/146222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: 60/146963
PRIOR FILING DATE: 1999-08-03
PRIOR APPLICATION NUMBER: 60/149320

QY 301 CCAACCGAGATATTGACTTCTTCTGTA 329
DB 392 CCCACGAGATATTGACTTCTTCTGCGA 420

RESULT 11
US-10-219-480-71
Sequence 71, Application US/10219480
Publication No. US20030187209A1
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Macanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530P1C38
CURRENT APPLICATION NUMBER: US/10/219,480
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 71
LENGTH: 521
TYPE: DNA
ORGANISM: Homo Sapien
US-10-219-480-71

Query Match 75.5%; Score 249; DB 13; Length 521;
Best Local Similarity 84.8%; Pred. No. 3e-76;
Matches 279; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1 CATGCAGATTTATGATTAACCTTCTTCTAGAAAGTGTGAGATGAGAGTGTGTC 60
DB 92 CATGAATATTATGACCGCTTACCTTCAAGAGCTGTGTGAGATGAGATGAGTGTGTC 151
QY 61 TATACCATTTCTCTGCAAGAGACAGAGAACTAATGCCCCGAGCTGTAGTTCATC 120
DB 152 TATACATTTCTCTGCTAGTGTCTCAAGAAATTAATGCCCCGAGCTGTAGTTCATC 211
QY 121 AATGTCAGAAAGGAGCAGATCTATGTTTATTCAGAGCTGTAAACAGAAATGAGACT 180
DB 212 AACGTTAAAGGAGCAGAGATCTATGTTTAAAGCTGTAAAGAAATGAGACT 271
QY 181 GGGGAGATTTCTGGGCTGGAGTGTATATGTCAGCCAGATGAGATGAGATTTGAGCT 240

DB 272 GGAGATTTTGGCTGGAGATGTTATGCTGATGCCAGACGAGATGGAGTCTGTGCT 331
QY 241 TATTTCCCGAGCACTTGCTTAGAGAGCAACGAGTACCGAGAGCCAGAGAGAT 300
DB 332 TATTTCCCGAGCACTTGCTTAGAGAGCAACGAGTGTGTACAGAGAGCTACCGAGAGAT 391
QY 301 CCAACCGAGATATTGACTTCTTCTGTA 329
DB 392 CCCACGAGATATTGACTTCTTCTGCGA 420

RESULT 12
US-10-219-483-71
Sequence 71, Application US/10219483
Publication No. US20030187210A1
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Macanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530P1C43
CURRENT APPLICATION NUMBER: US/10/219,483
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 71
LENGTH: 521
TYPE: DNA
ORGANISM: Homo Sapien
US-10-219-483-71

Query Match 75.5%; Score 249; DB 13; Length 521;
Best Local Similarity 84.8%; Pred. No. 3e-76;
Matches 279; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1 CATGCAGATTTATGATTAACCTTCTTCTAGAAAGTGTGAGATGAGAGTGTGTC 60
DB 92 CATGAATATTATGACCGCTTACCTTCAAGAGCTGTGTGAGATGAGATGAGTGTGTC 151
QY 61 TATACCATTTCTCTGCAAGAGACAGAGAACTAATGCCCCGAGCTGTAGTTCATC 120
DB 152 TATACATTTCTCTGCTAGTGTCTCAAGAAATTAATGCCCCGAGCTGTAGTTCATC 211
QY 121 AATGTCAGAAAGGAGCAGATCTATGTTTATTCAGAGCTGTAAACAGAAATGAGACT 180

Db 212 AACGTTAAAAAGGCGAGACATCTATGTACTCAAGCTGGTAAAGAAAATGAGCT 271
Qy 181 GGGGCAATTCCTGGGCTGGAGCTGTTTATGTGACACCAAGATGAGATGGGAATTCGGCT 240
Db 272 GGAAGAAATTTGGGCTGGAGCTGTTTATGTGATGGCCAGAGCGAGATGGAGTCTGGGT 331
Qy 241 TATTTCCCAAGCACTTGGTGTAGAGAGCAAGCTGTACAGAGAGCCCAAGAGAT 300
Db 332 TATTTCCCAAGCACTTGGTGTAGAGAGCAAGCTGTGTACAGAGAGCTACAGAGAGT 391
Qy 301 CCAACCAAGGATATTGACTTCTTGTGA 329
Db 392 CCCACCAAGGATATTGACTTCTTGTGGA 420

RESULT 13

US-10-219-525-71
; Sequence 71, Application US/10219525
; Publication No. US2003018721A1
; GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.

APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530P1C29
CURRENT APPLICATION NUMBER: US/10/219,525
CURRENT FILING DATE: 2002-08-13

PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 71
LENGTH: 521
TYPE: DNA
ORGANISM: Homo Sapien
US-10-219-525-71

Query Match 75.5%; Score 249; DB 13; Length 521;
Best Local Similarity 84.8%; Pred. No. 3e-76;
Matches 279; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Qy 1 CATGGCAATGTTTATGATAAATTTCTTCTAGAGAGTTGTGCGAGATGAGAGTGTGTC 60
Db 92 CATGGAAATTTTATGAGACCGCTGCTTCCAGAGAGCTGTGTGAGATGATGATGTGTC 151

Qy 61 TATACATTTCTCTGGCAAGACAGAGAGATCAATATCCCGGACTGTAGTTATC 120
Db 152 TATACATTTCTCTGGCTAGTGTCTCAAGAAAGATTAATAGCCCGGACTGTAGTTATC 211
Qy 121 AATGTAAAGAAAGGAGAGAGATCTATGTTTATTCAGAGCTGTATACAGAAATGAGCT 180
Db 212 AACGTTAAAAAGGCGAGACATCTATGTACTCAAGCTGGTAAAGAAAATGAGCT 271
Qy 181 GGGGCAATTCCTGGGCTGGAGCTGTTTATGTGACCAAGATGAGATGGGAATTCGGCT 240
Db 272 GGAAGAAATTTGGGCTGGAGCTGTTTATGTGATGGCCAGAGCGAGATGGAGTCTGGGT 331
Qy 241 TATTTCCCAAGCACTTGGTGTAGAGAGCAAGCTGTACAGAGAGCCCAAGAGAT 300
Db 332 TATTTCCCAAGCACTTGGTGTAGAGAGCAAGCTGTGTACAGAGAGCTACAGAGAGT 391
Qy 301 CCAACCAAGGATATTGACTTCTTGTGA 329
Db 392 CCCACCAAGGATATTGACTTCTTGTGGA 420

RESULT 14

US-10-219-526-71
; Sequence 71, Application US/10219526
; Publication No. US2003018721A1
; GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.

APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530P1C41
CURRENT APPLICATION NUMBER: US/10/219,526
CURRENT FILING DATE: 2002-08-13

PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 71
LENGTH: 521
TYPE: DNA
ORGANISM: Homo Sapien
US-10-219-526-71

Query Match 75.5%; Score 249; DB 13; Length 521;
Best Local Similarity 84.8%; Pred. No. 3e-76;
Matches 279; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Qy 1 CATGGCAATGTTTATGATAAATTTCTTCTAGAGAGTTGTGCGAGATGAGAGTGTGTC 60
Db 92 CATGGAAATTTTATGAGACCGCTGCTTCCAGAGAGCTGTGTGAGATGATGATGTGTC 151

QY 1 CATGCGATGTTTATGATATAAATTCTTCTTACAGAGTGTGACAGATGAGAGTGTGTC 60
DB 92 CATGGAATATTTATGACCGCTTAGCTTCCAGAGACCTGTGTCAATGATGAGTGTGTC 151
QY 61 TATACCATTTCTCTGGCAGAGCAAGAGAACTACAAATGCCCCGAGCTGTAGTTTCATC 120
DB 152 TATACATATTTCTCTGGCTAGTGTCTCAAGAAATTAATGAGTGTGAGTGTGATTCATT 211
QY 121 AATGCAAGAAAGGAGGAGAGATCTATGTTTATTCAGAGTGTGTAACAAGAAATGAGGT 180
DB 212 AACGTTAAAAAGGAGAGAGATCTATGTTACTCAAGAGTGTGTAAGAAAGAAATGAGGT 271
QY 181 GGGGCAATTCGGCTGGCAGTGTGTTATGTTAGTACACAGAGATGAGATGGAAATGGAGT 240
DB 272 GGAGAAATTTGGGCTGGCAGTGTGTTATGTTAGTACAGAGAGAGAGAGTGTGGGT 331
QY 241 TATTTCCCGACGAACTTGTTAGAGAGCAAGAGTGTACAGAGAGGCCCAAGAGAGATT 300
DB 332 TATTTCCCGACGAACTTGTTAGAGAGCAAGAGTGTGTACAGAGAGAGTGTCAAGAGAGATT 391
QY 301 CCAACCAAGGATATTGACTTCTCTGTGA 329
DB 392 CCCACCAAGGATATTGACTTCTCTGTGA 420

RESULT 15

US-10-219-530-71
Sequence 71, Application US/10219530
Publication No. US20030187213A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerltsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: B530P1C54
CURRENT APPLICATION NUMBER: US/10/219,530
PRIOR FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 71
LENGTH: 521
TYPE: DNA
ORGANISM: Homo Sapien

US-10-219-530-71
Query Match 75.5%; Score 249; DB 13; Length 521;
Best Local Similarity 84.8%; Pred. No. 3e-76;
Matches 279; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 1 CATGCGATGTTTATGATATAAATTCTTCTTACAGAGTGTGACAGATGAGAGTGTGTC 60
DB 92 CATGGAATATTTATGACCGCTTAGCTTCCAGAGACCTGTGTCAATGATGAGTGTGTC 151
QY 61 TATACCATTTCTCTGGCAGAGCAAGAGAACTACAAATGCCCCGAGCTGTAGTTTCATC 120
DB 152 TATACATATTTCTCTGGCTAGTGTCTCAAGAAATTAATGAGTGTGAGTGTGATTCATT 211
QY 121 AATGCAAGAAAGGAGGAGAGATCTATGTTTATTCAGAGTGTGTAACAAGAAATGAGGT 180
DB 212 AACGTTAAAAAGGAGAGAGATCTATGTTACTCAAGAGTGTGTAAGAAAGAAATGAGGT 271
QY 181 GGGGCAATTCGGCTGGCAGTGTGTTATGTTAGTACACAGAGATGAGATGGAAATGGAGT 240
DB 272 GGAGAAATTTGGGCTGGCAGTGTGTTATGTTAGTACAGAGAGAGAGAGTGTGGGT 331
QY 241 TATTTCCCGACGAACTTGTTAGAGAGCAAGAGTGTACAGAGAGGCCCAAGAGAGATT 300
DB 332 TATTTCCCGACGAACTTGTTAGAGAGCAAGAGTGTGTACAGAGAGAGTGTCAAGAGAGATT 391
QY 301 CCAACCAAGGATATTGACTTCTCTGTGA 329
DB 392 CCCACCAAGGATATTGACTTCTCTGTGA 420

Search completed: December 30, 2003, 10:03:04
Udb time: 271.994 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model1

Run on: December 30, 2003, 01:34:27 ; Search time 26.6527 Seconds
(without alignments)
5464.997 Million cell updates/sec

Title: US-10-019-455A-48

Perfect score: 330
Sequence: 1 catgcatgttctatgataa.....atattgacttctctgtgaa 330

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents NA:
1: /cgn2_6/ptodata/2/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCtus.COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|---------------------------------------|
| 1 | 64 | 19.4 | 581 | 1 | US-08-578-649-4 Sequence 4, Appli |
| 2 | 63.4 | 19.2 | 459 | 1 | US-08-578-649-1 Sequence 1, Appli |
| 3 | 62.4 | 18.9 | 330 | 1 | US-08-578-649-18 Sequence 18, Appli |
| 4 | 57.4 | 17.4 | 305 | 1 | US-08-578-649-8 Sequence 8, Appli |
| 5 | 35.6 | 10.8 | 596 | 1 | US-08-578-649-24 Sequence 24, Appli |
| 6 | 35.6 | 10.8 | 3565 | 1 | US-08-578-649-3 Sequence 3, Appli |
| 7 | 33.8 | 9.9 | 7218 | 1 | US-08-233-463-14 Sequence 14, Appli |
| 8 | 33.8 | 9.6 | 2075 | 1 | US-08-167-628-1 Sequence 1, Appli |
| 9 | 31.6 | 9.6 | 2075 | 1 | US-08-386-680-1 Sequence 1, Appli |
| 10 | 31.6 | 9.6 | 2075 | 1 | US-08-459-717-1 Sequence 1, Appli |
| 11 | 31.6 | 9.6 | 2075 | 1 | US-08-712-302-1 Sequence 1, Appli |
| 12 | 31.6 | 9.6 | 2075 | 2 | US-08-880-031-1 Sequence 1, Appli |
| 13 | 31.6 | 9.6 | 2075 | 3 | US-09-097-179-1 Sequence 1, Appli |
| 14 | 31.6 | 9.6 | 2075 | 3 | US-09-090-715-1 Sequence 1, Appli |
| 15 | 31.6 | 9.6 | 2075 | 4 | US-09-142-569-7 Sequence 7, Appli |
| 16 | 31.6 | 9.6 | 2075 | 4 | US-09-461-688-1 Sequence 1, Appli |
| 17 | 31.6 | 9.6 | 2075 | 5 | PCT-US96-08140-1 Sequence 1, Appli |
| 18 | 31.6 | 9.6 | 2998 | 3 | US-09-054-368-1 Sequence 1, Appli |
| 19 | 31.6 | 9.6 | 2998 | 3 | US-09-054-274-1 Sequence 1, Appli |
| 20 | 31.6 | 9.6 | 2998 | 3 | US-09-056-704-1 Sequence 1, Appli |
| 21 | 31.6 | 9.6 | 4214 | 4 | US-09-122-135-1 Sequence 1, Appli |
| 22 | 29.8 | 9.0 | 3169 | 4 | US-09-620-312D-713 Sequence 713, App |
| 23 | 29.6 | 9.0 | 3505 | 1 | US-07-718-575-3 Sequence 3, Appli |
| 24 | 29.6 | 9.0 | 3505 | 1 | US-08-481-206-3 Sequence 3, Appli |
| 25 | 29.6 | 9.0 | 3505 | 2 | US-08-486-269A-3 Sequence 3, Appli |
| 26 | 29.6 | 9.0 | 36138 | 4 | US-08-311-731A-136 Sequence 136, App |
| 27 | 29.4 | 8.9 | 591 | 4 | US-09-107-532A-1482 Sequence 1482, Ap |

| | | | | | |
|----|------|-----|---------|---|--------------------------------------|
| 28 | 29.2 | 8.8 | 8789 | 1 | US-08-328-254-5 Sequence 5, Appli |
| 29 | 29.2 | 8.8 | 10136 | 1 | US-08-353-700-2 Sequence 2, Appli |
| 30 | 29.2 | 8.8 | 10136 | 5 | PCT-US95-16216-2 Sequence 2, Appli |
| 31 | 29.2 | 8.8 | 1230025 | 4 | US-09-198-452A-1 Sequence 1, Appli |
| 32 | 28.8 | 8.7 | 681 | 5 | PCT-US96-10602-13 Sequence 13, Appli |
| 33 | 28.6 | 8.7 | 2649 | 3 | US-08-400-067-2 Sequence 2, Appli |
| 34 | 28.4 | 8.6 | 1136 | 3 | US-08-860-820-1 Sequence 1, Appli |
| 35 | 28.2 | 8.5 | 647 | 2 | US-08-392-771-20 Sequence 20, Appli |
| 36 | 28 | 8.5 | 1108 | 4 | US-09-702-705-1249 Sequence 1249, Ap |
| 37 | 28 | 8.5 | 1108 | 4 | US-09-736-457-1249 Sequence 1249, Ap |
| 38 | 28 | 8.5 | 2938 | 3 | US-08-969-815-3 Sequence 3, Appli |
| 39 | 28 | 8.5 | 2938 | 3 | US-09-120-025-3 Sequence 3, Appli |
| 40 | 28 | 8.5 | 2938 | 4 | US-09-710-481-3 Sequence 3, Appli |
| 41 | 28 | 8.5 | 2938 | 4 | US-09-553-875-3 Sequence 3, Appli |
| 42 | 28 | 8.5 | 2938 | 4 | US-09-768-670-3 Sequence 3, Appli |
| 43 | 28 | 8.5 | 4403765 | 3 | US-09-103-840A-2 Sequence 2, Appli |
| 44 | 28 | 8.5 | 4411529 | 3 | US-09-103-840A-1 Sequence 1, Appli |
| 45 | 27.8 | 8.4 | 1778 | 1 | US-08-416-870C-3 Sequence 3, Appli |

ALIGNMENTS

RESULT 1
US-08-578-649-4
Sequence 4, Application US/08578649
Patent No. 5770366
GENERAL INFORMATION:
APPLICANT: Ulrich Bogdan
APPLICANT: Reinhard Butner
APPLICANT: Brigitte Kaluza
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felte & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 MB storage diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-July-1993
ATTORNEY/AGENT INFORMATION:
NAME: Andrew L. Tiajoloif
REGISTRATION NUMBER: 31,575
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 638-3864
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 581 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 110..499
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 110..178
FEATURE:

NAME/KEY: mat_peptide
LOCATION: 179..499
US-08-578-649-4

Query Match 19.4%; Score 64; DB 1; Length 581;
Best Local Similarity 54.7%; Pred. No. 2.6e-12;
Matches 174; Conservative 0; Mismatches 135; Indels 9; Gaps 2;

QY 12 TATGGATAAAGCTTCTTCTAAGAGTTGTGTGAGATGAGTGTATACCATTC 71
DB 184 TATGCCAAGCTGCTGACTGAGACTGTGTGCGACGAGATGAGCACTTATCTC 243
QY 72 TCTGCAAGAGCAGACAGAAAGACTACATGCCCCGACCTAGATTTCATCATGACAGA 131
DB 244 CATGGCTGTGCCCCCTCCAGACACTGATGCCCCCTGATTCGCGCTTCTATATATAG 303
QY 132 AGGGCAGCAGATTTATGTTTATTCAGACTGTGTAACAGAAATGAGCTGGGGCATTCG 191
DB 304 GGGCCAAAGTGTATGTCTTCTCCAAAGTTG-----AAGGGCCGTGGGCGCTTTCTG 357
QY 192 GGTGCGACAGTTTATGTGTACACACAGATGAGATGGGA---ATTGTGGTTATTTCCC 248
DB 358 GGGAGGAGAGTTCAGAGGAGTTTACTATGAGAGCTGGACGCCCTGGCTATTTCCC 417
QY 249 CAGCACTTGTTAGAGAGCAAGAGTGTACAGAGGCCACCAAGAGATTCCAACCA 308
DB 418 CAGTAGCATTTGTCGGGAGAGACTGAACTGAAACCTGGCAAAATGATATGAGACCGA 477
QY 309 GGATATTGACTTCTTCTG 326
DB 478 TCATGGGATTCTACTG 495

RESULT 2
US-08-578-649-1
Sequence 1, Application US/08578649
Patent No. 5770366

GENERAL INFORMATION:
APPLICANT: Ulrich Bogdan
APPLICANT: Reinhard Butner
APPLICANT: Brigitte Kaluza
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10023
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578.649
FILING DATE: 29-July-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-July-1993
ATTORNEY/AGENT INFORMATION:
NAME: Andrew L. Tiajoleff
REGISTRATION NUMBER: 31,575
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-9884
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 459 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 40..432
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 40..111
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 112..432
US-08-578-649-1

Query Match 19.2%; Score 63.4; DB 1; Length 459;
Best Local Similarity 58.2%; Pred. No. 3.7e-12;
Matches 153; Conservative 0; Mismatches 101; Indels 9; Gaps 2;

QY 12 TATGGATAAAGCTTCTTCTAAGAGTTGTGTGAGATGAGTGTCTATACCATTC 71
DB 117 TATGCCAAGCTGCTGACTGACCGAAGCTGTGTGCGACGAGATGAGCACTTATCTC 176
QY 72 TCTGCAAGAGCAGACAGAAAGACTACATGCCCCGACCTAGATTTCATCATGACAGA 131
DB 177 CATGCTGTGCCCCCTTCAAGACTGACATGCCCCCGACTGCCGATTCCTGACATTCACG 236
QY 132 AGGGAGCAGATTTATGTTTATTCAGACTGTGTAACAGAAATGAGCTGGGGCATTCG 191
DB 237 GGGCCAAAGTGTATGTCTTCTCCAAAGCTG-----AAGGGCCGTGGGCGCTTCTG 290
QY 192 GGTGCGACAGTTTATGTGTACACACAGATGAGATGGGAAT---GTGGTTATTTCCC 248
DB 291 GGGAGGAGCAGCTTCAGGAGATTACTATGAGATCTGCTGCTGGGCTATTTCCC 350
QY 249 CAGCACTTGTTAGAGAGCAAC 271
DB 351 CAGTAGCATTTGTCGAGAGAGAC 373

RESULT 3
US-08-578-649-18
Sequence 18, Application US/08578649
Patent No. 5770366

GENERAL INFORMATION:
APPLICANT: Ulrich Bogdan
APPLICANT: Reinhard Butner
APPLICANT: Brigitte Kaluza
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578.649
FILING DATE: 29-July-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-July-1993
ATTORNEY/AGENT INFORMATION:
NAME: Andrew L. Tiajoleff
REGISTRATION NUMBER: 31,575
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
TELECOMMUNICATION INFORMATION:

RESULT 4 858-649-8
 : Sequence 8, Application US/08578649
 : Patent No. 5770366
 : GENERAL INFORMATION:
 : APPLICANT: Ulrich Bogdan
 : APPLICANT: Reinhard Butner
 : APPLICANT: Brigitte Kalza
 : TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
 : NUMBER OF SEQUENCES: 24
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Felfe & Lynch
 : STREET: 605 Third Avenue
 : CITY: New York
 : STATE: New York
 : COUNTRY: USA
 : ZIP: 10022
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
 : COMPUTER: IBM PS/2
 : OPERATING SYSTEM: PC-DOS
 : SOFTWARE: Wordperfect
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/578,649
 : FILING DATE: 29-July-1994
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: DE P 43 24 247.2
 : FILING DATE: 20-July-1993
 : ATTORNEY/AGENT INFORMATION:
 :

```

RESULT 5
US-08-578-649-24
; Sequence 24, Application US/08578649
; Patent No. 5770366
;
GENERAL INFORMATION:
;
APPLICANT: Ulrich Bogdan
;
APPLICANT: Reinhard Butner
;
APPLICANT: Brigitte Kaluza
;
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
;
NUMBER OF SEQUENCES: 24
;
CORRESPONDENCE ADDRESS:
;
ADDRESSER: Felle & Lynch
;
STREET: 805 Third Avenue
;
CITY: New York
;
STATE: New York
;
COUNTRY: USA
;
ZIP: 10022
;
COMPUTER READABLE FORM:
;
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
;
COMPUTER: IBM PS/2
;
OPERATING SYSTEM: PC-DOS
;
SOFTWARE: Wordperfect
;
CURRENT APPLICATION DATA:
;
APPLICATION NUMBER: US/08/578,649
;
FILING DATE: 29-July-1994
;
CLASSIFICATION: 435
;
PRIOR APPLICATION DATA:
;
APPLICATION NUMBER: DE P 43 24 247.2
;
FILING DATE: 20-July-1993
;

```

ATTORNEY/AGENT INFORMATION:
NAME: Andrew L. Tiajolo
REGISTRATION NUMBER: 31,575
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 596 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: join(40..111, 40..166, 214..347, 393..503, 549
LOCATION: ..569)
FEATURE:
NAME/KEY: sig peptide
LOCATION: 40..111
FEATURE:
NAME/KEY: exon
LOCATION: 40..166
FEATURE:
NAME/KEY: exon
LOCATION: 214..347
FEATURE:
NAME/KEY: exon
LOCATION: 393..503
FEATURE:
NAME/KEY: exon
LOCATION: 549..569
NAME/KEY: -
LOCATION: one-of(194, 369, 527)
OTHER INFORMATION: /note= "N in positions 194, 369
OTHER INFORMATION: and 527 denotes an indefinite number and sequence
OTHER INFORMATION: of nucleotides "
US-08-578-649-24

Query Match 10.8%; Score 35.6; DB 1; Length 596;
Best Local Similarity 60.2%; Pred. No. 0.016;
Matches 59; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 65 CCATTCTCTGCAAGACAGACAGAACTACAAATGCCCGGACTGTAGTTTCATCATG 124
DB 217 CTATCTCCATGCTGTGGCCCTTCAGACTACATGCGCCCGGACTGCGATTCCTGACCA 276
QY 125 TCAAGAAAGGCGACAGATCTATGTTTATTCGAAGCTG 162
DB 277 TTCACGGGGGCCAAGTGTGTATGTTCTTCTCCAAAGCTG 314

RESULT 6
US-08-578-649-3
Sequence 3, Application US/08578649
GENERAL INFORMATION:
APPLICANT: Ulrich Bogdan
APPLICANT: Reinhard Buttner
APPLICANT: Brigitte Kaluza
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette

COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-July-1993
ATTORNEY/AGENT INFORMATION:
NAME: Andrew L. Tiajolo
REGISTRATION NUMBER: 31,575
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3565 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: sig peptide
LOCATION: 1378..1449
FEATURE:
NAME/KEY: exon
LOCATION: 1378..1504
FEATURE:
NAME/KEY: exon
LOCATION: 1586..1719
FEATURE:
NAME/KEY: exon
LOCATION: 2804..2914
FEATURE:
NAME/KEY: exon
LOCATION: 3232..3252
NAME/KEY: -
LOCATION: one-of(2216)
OTHER INFORMATION: /note= "N in position 2216
OTHER INFORMATION: denotes an indefinite number and sequence of
OTHER INFORMATION: nucleotides "
US-08-578-649-3

Query Match 10.8%; Score 35.6; DB 1; Length 3565;
Best Local Similarity 60.2%; Pred. No. 0.04;
Matches 59; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 65 CCATTCTCTGCAAGACAGACAGAACTACAAATGCCCGGACTGTAGTTTCATCATG 124
DB 1589 CTATCTCCATGCTGTGGCCCTTCAGACTACATGCGCCCGGACTGCGATTCCTGACCA 1648
QY 125 TCAAGAAAGGCGACAGATCTATGTTTATTCGAAGCTG 162
DB 1649 TTCACGGGGGCCAAGTGTGTATGTTCTTCTCCAAAGCTG 1686

RESULT 7
US-08-232-463-14/c
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/386,680
FILING DATE: 10-FEB-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/167,628
FILING DATE:
APPLICATION NUMBER: US/07/752,427
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr. Ph.D., John W.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-1294
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-455-5100
TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2075 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: DB60R32
FEATURE:
NAME/KEY: CDS
LOCATION: 130..1177
US-08-386-680-1

Query Match
Best Local Similarity 53.2%; Pred. No. 0.74;
Matches 67; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 99 TGGCCCGGACTGTAGGTTCTCATGTGCAAGAAAGGCGACAGATTTATGTTTCCAA 158
DB 1354 TTCCCCAGACACTGGTTTGAAGATGTTAAGACTTGACAGTGAAGTACATTAGTACACA 1413

QY 159 GCTGTGTAACAGAAATGAGCTGGGCACTTCTGGCTGGAGTGTATGTTAGTACACCA 218
DB 1414 GCACCGAATGTATTTAATTAAGGTGGCTTTAGAGAGAGTGGGAGGTACCGCGCGTTA 1473

QY 219 GGATGA 224
DB 1474 GTATCA 1479

RESULT 10
US-08-459-717-1
Sequence 1, Application US/08459717
Patent No. 5770209
GENERAL INFORMATION:
APPLICANT: Grotendorst, Gary R.
APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Juba & Lubitz
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,717
FILING DATE: 02-JUN-1995

CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/752,427
FILING DATE: 30-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr. Ph.D., John W.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-1294
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-455-5100
TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2075 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: DB60R32
FEATURE:
NAME/KEY: CDS
LOCATION: 130..1177
US-08-459-717-1

Query Match
Best Local Similarity 53.2%; Pred. No. 0.74;
Matches 67; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 99 TGGCCCGGACTGTAGGTTCTCATGTGCAAGAAAGGCGACAGATTTATGTTTCCAA 158
DB 1354 TTCCCCAGACACTGGTTTGAAGATGTTAAGACTTGACAGTGAAGTACATTAGTACACA 1413

QY 159 GCTGTGTAACAGAAATGAGCTGGGCACTTCTGGCTGGAGTGTATGTTAGTACACCA 218
DB 1414 GCACCGAATGTATTTAATTAAGGTGGCTTTAGAGAGAGTGGGAGGTACCGCGCGTTA 1473

QY 219 GGATGA 224
DB 1474 GTATCA 1479

RESULT 11
US-08-712-302-1
Sequence 1, Application US/08712302
Patent No. 5783187
GENERAL INFORMATION:
APPLICANT: Grotendorst, Gary R.
APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Juba & Lubitz
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/712,302
FILING DATE: 11-SEP-1996
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/386,680
FILING DATE: 10-FEB-1995
APPLICATION NUMBER: US/08/167,628
FILING DATE:
APPLICATION NUMBER: US/07/752,427

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr. Ph.D., John W.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-1294
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-455-5100
TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2075 base pairs
TYPE: nucleic acid
STRADEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: DB60R32
FEATURE:
NAME/KEY: CDS
LOCATION: 130..1177
US-08-712-302-1

Query Match
Best Local Similarity 9.6%; Score 31.6; DB 1; Length 2075;
Matches 67; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 99 TCCCCGAGCTAGTTCATCAATGTCAGAAAGGCGACAGATCTATGTTATTCGA 158
DB 1354 TTCCCCAGACACTGTTTGAAGATGTTAGACTTGACAGTGAACACTAGTACACA 1413
QY 159 GCTGTACAGAAATGAGACTGGGCACTTCTGGCTGGCACTTTATGTGACACCA 218
DB 1414 GCACCAAGATGATATTAAGTGTGCTTTAGAGACAGTGGAGGGTACCGCCCGGTTA 1473
QY 219 GGATGA 224
DB 1474 GTATCA 1479

RESULT 12
US-08-880-031-1
Sequence 1, Application US/08880031
GENERAL INFORMATION:
APPLICANT: Groendorst, Gary R.
APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,031
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/167,628
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr. Ph.D., John W.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-1294
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-455-5100

TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2075 base pairs
TYPE: nucleic acid
STRADEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: DB60R32
FEATURE:
NAME/KEY: CDS
LOCATION: 130..1177
US-08-880-031-1

Query Match
Best Local Similarity 9.6%; Score 31.6; DB 2; Length 2075;
Matches 67; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 99 TCCCCGAGCTAGTTCATCAATGTCAGAAAGGCGACAGATCTATGTTATTCGA 158
DB 1354 TTCCCCAGACACTGTTTGAAGATGTTAGACTTGACAGTGAACACTAGTACACA 1413
QY 159 GCTGTACAGAAATGAGACTGGGCACTTCTGGCTGGCACTTTATGTGACACCA 218
DB 1414 GCACCAAGATGATATTAAGTGTGCTTTAGAGACAGTGGAGGGTACCGCCCGGTTA 1473
QY 219 GGATGA 224
DB 1474 GTATCA 1479

RESULT 13
US-09-097-179-1
Sequence 1, Application US/09097179
GENERAL INFORMATION:
APPLICANT: Groendorst, Gary R.
APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,179
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/386,680
FILING DATE: 10-FEB-1995
APPLICATION NUMBER: US/08/167,628
FILING DATE:
APPLICATION NUMBER: US/07/752,427
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr. Ph.D., John W.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-1294
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-455-5100
TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 2075 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: DB60R32
FEATURE:
NAME/KEY: CDS
LOCATION: 130..1177
US-09-097-179-1

Query Match
Best Local Similarity 53.2%; Pred. No. 0.74; Length 2075;
Matches 67; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 99 TGCCCCGAGTGTAGTTCATCAATGTCAGAAAGGCGAGCATCTTATGTTTATCCAA 158
DB 1354 TTCCCCAGACACTGTGTTGAAGATGTTAAGACTTGACAGTGAACATTAAGTACACA 1413
QY 159 GCTGTAAACAGAAATGAGCTGGGGCATCTGGGCTGGCAGTGTATGTCACACCA 218
DB 1414 GCACCGAATGTATATTAAAGGTGTGCTTTAGAGCAGTGGAGGTAACCGCCGGTTA 1473
QY 219 GGATGA 224
DB 1474 GTATCA 1479

RESULT 14
US-09-080-715-1
Sequence 1, Application US/09080715
Patent No. 6190884
GENERAL INFORMATION:
APPLICANT: Grotenhorst, Gary R.
APPLICANT: Bradham Jr., Douglas M.
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,715
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/167,628
FILING DATE:
APPLICATION NUMBER: US/07/752,427
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr. Ph.D., John W.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-1294
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-455-5110
TELEFAX: 619-455-5100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2075 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

IMMEDIATE SOURCE:
CLONE: DB60R32
FEATURE:
NAME/KEY: CDS
LOCATION: 130..1177
US-09-080-715-1

Query Match
Best Local Similarity 53.2%; Pred. No. 0.74; Length 2075;
Matches 67; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 99 TGCCCCGAGTGTAGTTCATCAATGTCAGAAAGGCGAGCATCTTATGTTTATCCAA 158
DB 1354 TTCCCCAGACACTGTGTTGAAGATGTTAAGACTTGACAGTGAACATTAAGTACACA 1413
QY 159 GCTGTAAACAGAAATGAGCTGGGGCATCTGGGCTGGCAGTGTATGTCACACCA 218
DB 1414 GCACCGAATGTATATTAAAGGTGTGCTTTAGAGCAGTGGAGGTAACCGCCGGTTA 1473
QY 219 GGATGA 224
DB 1474 GTATCA 1479

RESULT 15
US-09-142-569-7
Sequence 7, Application US/09142569
Patent No. 6413735
GENERAL INFORMATION:
APPLICANT: Lau, Lester F.
TITLE OF INVENTION: Extracellular Matrix Signalling Molecules
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshhall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/142,569
FILING DATE: 02-Apr-1999
CLASSIFICATION: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28758/33766
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2075 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: "CTGF cDNA coding sequence"
US-09-142-569-7

Query Match
Best Local Similarity 53.2%; Pred. No. 0.74; Length 2075;
Matches 67; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 99 TCCCCGAGCTAGTTCATCAATGCAGAAAAGGACAGATCTATGTTATTCAA 158
 Db 1354 TTCCCCAGACACTGGTTTGAAGATGTTAGACTTGACAGTGAACCTACATTAGTACACA 1413
 QY 159 GCTGCTAACAGAAATGAGAGCTGGGGCATTCTGGGCTGGCAGTGTATTATGTGACCA 218
 Db 1414 GCACCAAGATGTATTATTAAGTGTGGCTTACGAGCAGTGGAGAGGTACCGGCCGGTTA 1473
 QY 219 GGATGA 224
 Db 1474 GTATCA 1479

Search completed: December 30, 2003, 06:10:59
 Job time : 31.6527 secs

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|---------|----------------------|
| 1 | 264.5 | 44.8 | 131 | 2 | I38019 | melanoma-derived |
| 2 | 93.5 | 15.8 | 844 | 1 | TWMSVY | transforming protein |
| 3 | 91.5 | 15.5 | 839 | 1 | TVHUVV | transforming protein |
| 4 | 84.5 | 14.3 | 878 | 2 | I51940 | gene VAVP protein |
| 5 | 82.5 | 14.0 | 1589 | 1 | RGBVYS | cell division con |
| 6 | 77 | 13.0 | 413 | 2 | TJ1051 | transposase homolo |
| 7 | 75.5 | 12.8 | 1215 | 2 | TJ32734 | myosin-IIA - Acanti |
| 8 | 74 | 12.5 | 695 | 2 | S66662 | protein-glutamine |
| 9 | 74 | 12.5 | 994 | 2 | T21356 | hypothetical prot |
| 10 | 73.5 | 12.4 | 847 | 1 | A53800 | mixed-lineage prot |
| 11 | 73 | 12.4 | 670 | 2 | S67383 | probable signal tr |
| 12 | 71.5 | 12.1 | 344 | 2 | C81920 | hypothetical protei |
| 13 | 71 | 12.0 | 585 | 2 | G96695 | ATP-dependent RNA |
| 14 | 71 | 12.0 | 954 | 1 | S68178 | mixed-lineage pro |
| 15 | 70 | 11.8 | 308 | 2 | T48525 | hypothetical prot |
| 16 | 70 | 11.8 | 414 | 2 | C90364 | transposase ISCl3 |
| 17 | 70 | 11.8 | 782 | 2 | B83966 | formate dehydrogen |
| 18 | 69.5 | 11.8 | 223 | 2 | F70469 | enolase-phosphatasa |
| 19 | 69.5 | 11.8 | 461 | 2 | AF2340 | sugar ABC transpor |
| 20 | 69.5 | 11.8 | 636 | 2 | T06793 | receptor kinase ho |
| 21 | 69.5 | 11.8 | 1097 | 2 | T31504 | hypothetical prote |
| 22 | 69 | 11.7 | 722 | 2 | G86746 | hypothetical prote |
| 23 | 68.5 | 11.6 | 727 | 2 | A55628 | translation initiat |
| 24 | 68.5 | 11.6 | 839 | 2 | G96719 | probable chromeme |
| 25 | 68.5 | 11.6 | 868 | 2 | G71691 | hypothetical prote |
| 26 | 68 | 11.5 | 373 | 2 | T39655 | VHS domain contain |
| 27 | 67.5 | 11.4 | 333 | 2 | A84055 | transcription regu |
| 28 | 67.5 | 11.4 | 413 | 2 | T02593 | S-receptor kinase |
| 29 | 67.5 | 11.4 | 505 | 1 | S24550 | protein-tyrosine k |

| | | | | | | |
|----|------|------|------|---|--------|---------------------|
| 30 | 67.5 | 11.4 | 506 | 1 | S24553 | protein-tyrosine k |
| 31 | 67.5 | 11.4 | 618 | 2 | G58432 | Madcap protein [m |
| 32 | 67.5 | 11.4 | 1560 | 2 | T30282 | calcium-binding pr |
| 33 | 67 | 11.3 | 229 | 2 | AG5737 | acetyltransferase |
| 34 | 67 | 11.3 | 229 | 2 | E97518 | probable acetyltra |
| 35 | 67 | 11.3 | 259 | 2 | G64427 | hypothetical prote |
| 36 | 67 | 11.3 | 541 | 2 | G64439 | asparagine synthas |
| 37 | 67 | 11.3 | 816 | 2 | T17257 | hypothetical prote |
| 38 | 66 | 11.2 | 415 | 2 | AG0391 | conserved hypothet |
| 39 | 66 | 11.2 | 639 | 2 | T11511 | adapter protein CM |
| 40 | 66 | 11.2 | 1173 | 2 | T08610 | major core capsid |
| 41 | 65.5 | 11.1 | 164 | 2 | F66968 | hypothetical prote |
| 42 | 65.5 | 11.1 | 227 | 2 | T28531 | hypothetical prote |
| 43 | 65.5 | 11.1 | 344 | 2 | E81183 | copper ABC transpo |
| 44 | 65.5 | 11.1 | 377 | 2 | S08636 | nick protein - huma |
| 45 | 65.5 | 11.1 | 383 | 2 | S24156 | polysialacturonase |

ALIGNMENTS

RESULT 1
18019
melanoma-derived growth regulatory protein M1A - human
C.Species: Homo sapiens (man)
C.Date: 17-May-1996 #sequence_revision 17-May-1996 #ext_change 04-Mar-2000
C.Accession: 18018, 540238
R.Blesch, A.; Bosserhoff, A.K.; Apfel, R.; Behl, C.; Hesseboerfer, B.; Schmitt, A.; Jac
Cancer Res. 54, 5695-5701, 1994
A>Title: Cloning of a novel malignant melanoma-derived growth-regulatory protein, M1A.
A.Reference number: 18019; PMID:95007612; PMID:7923218
A.Accession: 18019
A.Status: preliminary/
A.Molecule type: mRNA
A.Residues: 1-131 <RES>
C.Cross-references: EMBL:X75450; NID:g438057; PIDN:CAA53203.1; PID:g438058
C.Genetics:
A.Gene: m1a
C.Superfamily: human melanoma-derived growth regulatory protein M1A

| | | | | |
|-----------------------|------------------|--------------------|-----------|-------------|
| Query Match | 44.8% | Score 264.5; | DB 2; | Length 131; |
| Best Local Similarity | 46.3%; | Pred. No. 4.8e-21; | | |
| Matches 50; | Conservative 23; | Mismatches 30; | Indels 5; | Gaps 3 |

```

QY      5 MDKLSKKKCADEACVYITSLARAOEDYNAPDCRFLNVKKQQQIYYYSKLVTEANG-AF 6
Db      27 MPKLADKLCADQECSPHISMAVALDYNAPDCRFLTIHQGVVYVFSKL---KGGRLP 83
QY      64 MASVYGDHDDMGKI-VGYEFSNLVBEQRYYCATATEIFPTDIDFCE 110
Db      84 WGSVQGDYDGLAARGVFPSSIVEDDTLKGKRDVKTDMKDFCQ 131

```

transforming protein vav - mouse
 t:MSVSV
 RESULT 2
 C:Species: Mus musculus (house mouse)
 C:Date: 03-May-1994 #sequence revision 16-Feb-1996 #text_change 18-Jun-1999
 C:Accession: A61187; A39576; S36941; S23669
 R:Coppola, J.; Bryant, S.; Koda, T.; Conway, D.; Bartracid, M.
 Cell Growth Differ. 2, 95-105, 1991
 A>Title: Mechanism of activation of the vav proto-oncogene.
 A:Reference number: A61187; MUID:91299578; PMID:2069873
 A:Accession: A61187
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-644 <COP>
 R:Katzay, S.; Cleveland, J.T.; Heslop, H.E.; Pulido, D.
 Mol. Cell. Biol. 11, 1912-1920, 1991
 A>Title: Loss of the amino-terminal helix-loop-helix domain of the vav proto-oncogene c
 A:Reference number: A39576; MUID:91172176; PMID:2005887
 A:Accession: A39576
 A:Molecule type: mRNA

A;Residues: 1-28, 'E', 30-93 <KAT>
 A;Cross-references: GB:M59833; NID:g202343; PIDN:AAA63402.1; PID:g202344
 R;Adams, J.M.
 Submitted to the EMBL Data Library, January 1992
 A;Reference number: S36941
 A;Accession: S36941
 A;Molecule type: mRNA
 A;Residues: 1-323, 'DLWVPMQVRVKKYHLLLOELVK', 346-347, 'QDAT', 352, 'K', 354, 'N', 355-453, 'R', 45
 A;Cross-references: EMBL:X64361; NID:g55220; PIDN:CAA45713.1; PID:g55221
 R;Adams, J.M.; Houston, H.; Allen, J.; Lints, T.; Harvey, R.
 Oncogene 7, 611-618, 1992
 A;Title: The hematopoietically expressed vav proto-oncogene shares homology with the dbl
 A;Reference number: S23669; MUID:92228488; PMID:1565462
 A;Contents: annotation; the authors note the frameshift difference with sequence in A611
 A;Note: the complete sequence was submitted to Genbank; see S36941
 C;Genetics:
 A;Gene: vav
 C;Superfamily: vav transforming protein; CDC24 homology; protein kinase C zinc-binding
 C;Keywords: phosphoprotein; transforming protein; zinc finger
 F;32-102/Region: leucine-rich
 F;132-176/Region: acidic
 F;194-458/Domain: CDC24 homology <CD24>
 F;336-340/Region: proline-rich
 F;486-493/Region: nuclear location signal
 F;515-563/Domain: protein kinase C zinc-binding repeat homology <K21>
 F;528-548/Region: zinc finger HCCC motif
 F;553-566/Region: zinc finger HCCC motif
 F;575-582/Region: nuclear location signal
 F;604-654/Domain: SH3 homology <SH3A>
 F;606-609/Region: proline-rich
 F;670-761/Domain: SH2 homology <SH2>
 F;788-831/Domain: SH3 homology <SH3B>
 F;439/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

Query Match 15.8%; Score 93.5; DB 1; Length 844;
 Best Local Similarity 32.9%; Pred. No. 0.08; Mismatches 20; Indels 13; Gaps 3;
 Matches 23; Conservative 14; Mismatches 13; Indels 13; Gaps 3;

QY 26 ARAQEDYNAPDCRFINVKKGQOIYVYSKLTENGAGAFWAGSVYGDHDEMGIYGFPSN 85
 Db 786 AKARYDFCARDRELSLKEGDI-----KILNKGQGGWRRGETYGR-----IGWFPN 834
 QY 86 LVREQRYOE 95
 Db 835 YVEED--YSE 842

RESULT 3
 TVHUV
 transforming protein vav - human (fragments)
 N;Alternate names: finger protein vav
 C;Species: Homo sapiens (man)
 C;Date: 31-Mar-1991 #sequence_revision 03-May-1996 #ext_change 18-Jun-1999
 C;Accession: B39576; S05382
 R;Adams, S.; Cleveland, J.L.; Heslop, H.E.; Pulido, D.
 Mol. Cell. Biol. 11, 1912-1920, 1991
 A;Title: Loss of the amino-terminal helix-loop-helix domain of the vav proto-oncogene ac
 A;Reference number: A39576; MUID:91172176; PMID:2005687
 A;Accession: B39576
 A;Molecule type: mRNA
 A;Residues: 1-61 <KAT>
 A;Cross-references: GB:M59834; NID:g340189; PIDN:AAA63267.1; PID:g340190
 A;Note: the authors translated the codon CAA for residue 6 as Glu, CAG for residue 13 as
 R;Adams, S.; Martin-zanca, D.; Barbacid, M.
 EMBO J 8, 2283-2290, 1989
 A;Title: vav, a novel human oncogene derived from a locus ubiquitously expressed in hema
 A;Reference number: S05382; MUID:90005432; PMID:2477241
 A;Accession: S05382
 A;Molecule type: mRNA
 A;Residues: 62-839 <KAT2>
 A;Cross-references: EMBL:X16316
 R;Adams, J.M.; Houston, H.; Allen, J.; Lints, T.; Harvey, R.
 Oncogene 7, 611-618, 1992

A;Title: The hematopoietically expressed vav proto-oncogene shares homology with the d
 A;Reference number: S23669; MUID:92228488; PMID:1565462
 A;Contents: annotation
 A;Note: in the sequence from mouse the authors find three additional nucleotides that
 occurred in the published human sequences
 C;Comment: in comparing these sequences with the mouse (see PIR:TVMSV), there appear
 C;Genetics:
 A;Gene: GDB:VAV1; VAV
 A;Cross-references: GDB:127112; OMIM:164875
 A;Map position: 19p13.3-19p13.3
 C;Superfamily: vav transforming protein; CDC24 homology; protein kinase C zinc-binding
 C;Keywords: phosphoprotein; transforming protein; zinc finger
 F;126-170/Region: acidic
 F;188-452/Domain: CDC24 homology <CD24>
 F;509-557/Domain: protein kinase C zinc-binding repeat homology <K22>
 F;522-542/Region: zinc finger HCCC motif
 F;547-560/Region: zinc finger HCCC motif
 F;598-648/Domain: SH3 homology <SH3A>
 F;664-756/Domain: SH2 homology <SH2>
 F;783-831/Domain: SH3 homology <SH3B>
 F;433/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

Query Match 15.5%; Score 91.5; DB 1; Length 839;
 Best Local Similarity 32.9%; Pred. No. 0.13; Mismatches 20; Indels 13; Gaps 3;
 Matches 23; Conservative 14; Mismatches 20; Indels 13; Gaps 3;

QY 26 ARAQEDYNAPDCRFINVKKGQOIYVYSKLTENGAGAFWAGSVYGDHDEMGIYGFPSN 85
 Db 781 AKARYDFCARDRELSLKEGDI-----KILNKGQGGWRRGETYGR-----VGWFPN 829
 QY 86 LVREQRYOE 95
 Db 830 YVEED--YSE 837

RESULT 4
 151940
 gene VAV2 protein - human
 C;Species: Homo sapiens (man)
 C;Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #ext_change 16-Jul-1999
 C;Accession: 151940
 R;Henske, E.P.; Short, M.P.; Jozwiak, S.; Bovey, C.M.; Ramlakhan, S.; Haines, J.L.; Kw
 Ann. Hum. Genet. 59, 25-37, 1995
 A;Title: Identification of VAV2 on 9q34 and its exclusion as the tuberous sclerosis ge
 A;Reference number: 151940; MUID:9528235; PMID:7762982
 A;Accession: 151940
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-878 <RES>
 A;Cross-references: GB:676992; NID:g913345; PIDN:AA634377.1; PID:g913346
 C;Genetics:
 A;Gene: GDB:VAV2
 A;Cross-references: GDB:370880; OMIM:600428
 A;Map position: 9q34-q934
 C;Superfamily: vav transforming protein; CDC24 homology; protein kinase C zinc-binding
 F;198-462/Domain: CDC24 homology <CD24>
 F;524-572/Domain: protein kinase C zinc-binding repeat homology <K2>
 F;673-764/Domain: SH2 homology <SH2>
 F;823-872/Domain: SH3 homology <SH3>

Query Match 14.3%; Score 84.5; DB 2; Length 878;
 Best Local Similarity 27.6%; Pred. No. 0.77; Mismatches 22; Indels 13; Gaps 3;
 Matches 21; Conservative 20; Mismatches 22; Indels 13; Gaps 3;

QY 20 VYT---ISLAAQEDYNAPDCRFINVKKGQOIYVYSKLTENGAGAFWAGSVYGDHDEM 76
 Db 812 VFTPRVIGTAVVAVNFAARMRELSLREGDVAVIYRIGDQG---WKKG-----ETN 861
 QY 77 GIVGYFPSNLVREQRY 92
 Db 862 GRIGWFPSTVEEGE 877

RESULT 5

RBYCS

cell division control protein CDC25 - yeast (*Saccharomyces cerevisiae*)
N/Alternate names: protein L2142.6; protein YLR310C

C/Species: *Saccharomyces cerevisiae*

C/Date: 31-Mar-1988 #sequence_revision 31-Mar-1993 #text_change 21-Jul-2000

C/Accession: A26596; S51442; A23444; S43051; S47990

R/Broek, D.; Toda, T.; Michaeli, T.; Levin, L.; Bitchmeier, C.; Zoller, M.; Powers, S.;

Cell 48, 789-799, 1987

A/Title: The *S. cerevisiae* CDC25 gene product regulates the Ras/adenylate cyclase pathway

A/Reference number: A26596; MUID:87131091; PMID:3545497

A/Accession: A26596

A/Molecule type: DNA

A/Residues: 1-1589 <BRO>

A/Cross-references: EMBL:M5458; NID:g171184; PIDN:AAA34478.1; PID:g171185

R/Paulley, A.

submitted to the EMBL Data Library, November 1994

A/Description: The sequence of *S. cerevisiae* cosmid L2142.

A/Reference number: S51437

A/Accession: S51442

A/Molecule type: DNA

A/Residues: 1-1589 <PAU>

A/Cross-references: EMBL:U17247; NID:9577216; PIDN:AA67360.1; PID:9577222; GSPDB:GN0001

R/Camons, J.H.; Kalekine, M.; Gondre, B.; Garreau, H.; Boy-Marcotte, E.; Jaquet, M.

EMBO J. 5, 375-380, 1986

A/Title: Characterization, cloning and sequence analysis of the CDC25 gene which control

A/Reference number: A23444; MUID:86220116; PMID:3011405

A/Accession: A23444

A/Molecule type: DNA

A/Residues: 1-496, 'Y', 498-953, 'LSYINKLSR', 964-1589 <CAM>

A/Cross-references: EMBL:X03579; NID:g3483; PIDN:CAA27255.1; PID:g3484

R/Daniel, J.H.

Curr. Genet. 10, 879-885, 1986

A/Title: The CDC25 "start" gene of *Saccharomyces cerevisiae*: sequencing of the active C-

A/Reference number: S43051; MUID:88194639; PMID:3329037

A/Accession: S43051

A/Molecule type: DNA

A/Residues: 877-1589 <DAN>

A/Cross-references: EMBL:X03579

C/Genetics:

A/Gene: SGD: CDC25; CTN1; MIPS: YLR310C

A/Cross-references: SGD: S0004301; MIPS: YLR310C

A/Map position: 12R

C/Function:

A/Description: positive control of level of cellular cAMP at the stage at which the cell

C/Superfamily: budding yeast CDC25; CDC25-type guanine nucleotide exchange activator hom

C/Keywords: cell cycle control; transmembrane protein

F:65-123/Domain: SH3 homology <SH3>

F:1301-1542/Domain: CDC25-type guanine nucleotide exchange activator homology <SOS>

Query Match

Best Local Similarity 14.0%; Score 82.5; DB 1; Length 1589;

Matches 25; Conservative 18; Mismatches 35; Indels 11; Gaps 4;

QY 8 LSSKLCADBECCYTTISLARAQEDYNAP-----DCRFINVKKGQGIYYSKLVTEAGAGA 62

DB 45 LSSSSTSELTSLIRPIGIVAAVDENYPIKXSSQLSLVQGGRTIYLTK-----NSSG- 99

QY 63 FWAGSYGDHGDGEMGIVGYPNSLVREQR 91

DB 100 WMDGLVYDDSNKVN-RGWFQNGFPLR 127

RESULT 6

T31051

transposase homolog - *Sulfolobus* sp. plasmid pNOB8
N/Alternate names: hypothetical protein 413

C/Species: *Sulfolobus* sp.

C/Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 30-Sep-2002

C/Accession: T31051

R/She, O.; Phan, H.; Garrett, R.A.; Albers, S.V.; Stedman, K.M.; Zillig, W.

Extremophiles 2, 417-425, 1998

A/Title: Genetic profile of pNOB8 from *Sulfolobus*: the first conjugative plasmid from an

A/Reference number: Z20959; MUID:99044580; PMID:9627331

A/Accession: T31051

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-413 <SHE>

A/Cross-references: EMBL:NJ010405; NID:e1351926; PID:e1351973; PIDN:CAA09157.1

C/Genetics:

A/Superfamily: Mycobacterium tuberculosis probable IS1081 transposase

Query Match

Best Local Similarity 13.0%; Score 77; DB 2; Length 413;

Matches 27; Conservative 15; Mismatches 31; Indels 12; Gaps 5;

QY 11 KKLCADECCYTTISLARAQEDYNAPD-CRFINVKKGQGIYYSKLVTEAGAGFAGSV 68

DB 236 KAISLSQVDPFAPRAKRLDADKCAFLNPREVRHYLY-----TNTISESF--NST 349

QY 69 YGDHGDGEMGIVGYPNSLVREQRVY 93

DB 350 LARFEEELG--GYFPS--LRSLEYV 370

QY 132734

myosin-1A - *Acanthamoeba castellanii*

C/Species: *Acanthamoeba castellanii*

C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 08-Sep-2000

C/Accession: T32734

R/lee, W.L.; Ostap, E.M.; Zol, H.G.; Pollard, T.D.

submitted to the EMBL Data Library, August 1998

A/Description: Hydrodynamic and ligand binding properties of *Acanthamoeba* myosin-1A GP

A/Reference number: Z12126

A/Accession: T32734

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-1215 <LEE>

A/Cross-references: EMBL:AF085185; NID:g3599477; PID:g3599478; PIDN:AA035357.1

A/Experimental source: strain Neff

C/Genetics:

A/Gene: MIA

A/Insertions: 1/3; 41/3; 72/2; 103/2; 162/3; 184/1; 217/1; 296/1; 340/3; 447/3; 50

C/Superfamily: protozoan myosin heavy chain 1B; myosin motor domain homology; SH3 homo

F:14-674/Domain: myosin motor domain homology <MHO>

Query Match

Best Local Similarity 12.8%; Score 75.5; DB 2; Length 1215;

Matches 20; Conservative 12; Mismatches 25; Indels 13; Gaps 2;

QY 20 VTTISLARAQEDYNAPD-CRFINVKKGQGIYYSKLVTEAGAGFAGSVYGDHGDGEMGIV 79

DB 1158 VPTVGRCALVDYGAQADELTREGDVIDIVK-----SGWEETGLNGK-----T 1204

QY 80 GYFPSNLVRE 89

DB 1205 GVFPANTVED 1214

QY 86662

protein-glutamine gamma-glutamyltransferase (EC 2.3.2.13) - red sea bream

N/Alternate names: transglutaminase

C/Species: *Chrysophrys major* (red sea bream)

C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 18-Jun-1999

C/Accession: S66662

R/Yasuda, H.; Nakanishi, K.; Kunazawa, Y.; Nagase, K.; Motoki, M.; Matsui, H.

Eur J. Biochem. 232, 411-419, 1995

A/Title: Tissue-type transglutaminase from red sea bream (*Parus major*). Sequence anal

A/Reference number: S66662; MUID:96035874; PMID:7556189

A/Accession: S66662

A/Molecule type: mRNA

A/Residues: 1-695 <YAS>

A:Cross-references: GB:S79761; NID:g1176434; PIDN:AA85370.1; PID:g1176435
 C:Superfamily: protein-glutamine gamma-glutamyltransferase
 C:Keywords: aminocylitransferase
 F:272/Active site: Cys #status predicted

Query Match 12.5%; Score 74; DB 2; Length 695;
 Best Local Similarity 25.2%; Pred. No. 7.9;
 Matches 21; Conservative 21; Mismatches 28; Indels 10; Gaps 3;
 QY 31 DYNAPDCRFINVKKGQOIYVYSKLVTEAGAG--FWAGSVYGDHDEMGIYGFPSNLV 87
 DB 393 EVANADTIYWIYQXGQGR-----RKITEDHASVGNISTKSYVGNHREDVTLHKYKPEGSQ 447
 QY 88 REORVYQDAITKEI--PTTDI 105
 DB 448 KEREVYKAGRRVTEPSNEI 467

RESULT 9
 T21356
 hypothetical protein F25H2.13 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T21356; T21540
 R:Wilkinson, J.
 submitted to the EMBL Data Library, September 1996
 A:Reference number: Z19411
 A:Accession: T21356
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-994 <WIL>
 A:Cross-references: EMBL:Z79755; PIDN:CAB02102.1; GSPDB:GN00019; CESP:F25H2.13
 R:Wilkinson, J.
 submitted to the EMBL Data Library, December 1996
 A:Reference number: Z19437
 A:Accession: T21540
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-994 <WIL>
 A:Cross-references: EMBL:Z83224; PIDN:CAB05720.1; GSPDB:GN00019; CESP:F25H2.13
 A:Experimental source: clone F25H2
 R:Wilkinson, J.
 submitted to the EMBL Data Library, September 1996
 A:Reference number: Z19437
 A:Accession: T21540
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-994 <WIL>
 A:Cross-references: EMBL:Z83224; PIDN:CAB05720.1; GSPDB:GN00019; CESP:F25H2.13
 A:Experimental source: clone F29C6
 C:Genetics:
 A:Gene: CESP:F25H2.13
 A:Map position: 1
 A:Introns: 129/2; 177/1; 206/2; 349/3; 436/3; 506/2; 626/3; 689/3; 772/3; 845/3; 903/3;
 A:Introns: 129/2; 177/1; 206/2; 349/3; 436/3; 506/2; 626/3; 689/3; 772/3; 845/3; 903/3;

Query Match 12.5%; Score 74; DB 2; Length 994;
 Best Local Similarity 27.8%; Pred. No. 12;
 Matches 37; Conservative 20; Mismatches 46; Indels 30; Gaps 8;
 QY 5 MDKL-SSKLL-----CADEECYTTISLAPQEDYVAPDCRFINVKKGQIYVYSK- 53
 DB 339 MDLTFSSQJAKSVPPSGKASDGE-ILLETTLAKGADNANSE-RLVDVLDALSYLSKN 396
 QY 54 --LVTEAGAG--AFWAGSVYGDH-QDEMGIVG-----YFSPNLVBEORVYCEA 96
 DB 397 EEVALTEKGDGMEKAVDFLLSTYSTHQAQVAAVGBETVKLVDVRVPKVAVANCLYIOK 456
 QY 97 TREIPTTDDIFC 109
 DB 457 DXKNEKLTIKYFC 469

RESULT 10
 A53800
 mixed-lineage protein kinase (EC 2.7.1.1) 3 - human
 N:Alternate names: protein kinase PTK1; protein kinase SPRK
 C:Species: Homo sapiens (man)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A53800; I56395
 R:Galio, K.A.; Mark, M.R.; Seadden, D.T.; Wang, Z.; Gu, Q.; Godowski, P.J.
 J. Biol. Chem. 269, 15092-15100, 1994

A:Title: Identification and characterization of SPRK, a novel src-homology 3 domain-cc
 A:Reference number: A53800; MUID:94253068; PMID:8195146
 A:Accession: A53800
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-847 <GAL>
 A:Cross-references: GB:U07747; NID:g464027; PIDN:AAA19647.1; PID:g464028
 R:ing, Y.L.; Leung, I.W.; Heng, H.H.; Tsui, L.C.; Lassar, N.J.
 Oncogene 9, 1745-1750, 1994
 A:Title: MLK-3: identification of a widely-expressed protein kinase bearing an SH3 dor
 A:Reference number: I56395; MUID:94239754; PMID:8183572
 A:Accession: I56395
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-847 <RES>
 A:Cross-references: GB:L32976; NID:g468295; PIDN:AAA59859.1; PID:g468296
 C:Genetics:
 A:Gene: GDB:MLK3; PTK1; SPRK
 A:Cross-references: GDB:134755; OMIM:600050
 A:Map position: 11q13.1-11q13.3
 C:Superfamily: mixed-lineage protein kinase 3; protein kinase homology; SH3 homology
 C:Keywords: ATP; leucine zipper; phosphotransferase; serine/threonine-specific protein
 F:468-100/Domain: SH3 homology <SH3>
 F:115-383/Domain: protein kinase homology <KIN>
 F:123-131/Region: protein kinase ATP-binding motif
 F:403-424/Region: leucine zipper motif
 F:438-459/Region: leucine zipper motif
 F:468-482/Region: basic

Query Match 12.4%; Score 73.5; DB 1; Length 847;
 Best Local Similarity 33.3%; Pred. No. 11;
 Matches 19; Conservative 8; Mismatches 23; Indels 7; Gaps 1;
 QY 31 DYNAPDCRFINVKKGQOIYVYSKLVTEAGAGAFWAGSVYGDHDEMGIYGFPSNLV 87
 DB 51 DYPSGDELALRKGDREVLISRDPAISGDGMAWGQVQGO-----VGIFPSNYV 100

RESULT 11
 S67383
 probable signal transduction protein - fission yeast (Schizosaccharomyces pombe)
 N:Alternate names: FCH domain and SH3 domain containing protein
 C:Species: Schizosaccharomyces pombe
 C:Date: 19-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000
 C:Accession: T39317; S67383
 R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Beck, A.; Reinhardt, R.
 submitted to the EMBL Data Library, September 1998
 A:Reference number: Z21844
 A:Accession: T39317
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-670 <WOO>
 A:Cross-references: EMBL:AL031528; PIDN:CAA20684.1; GSPDB:GN00067; SPDB:SPEC11C11.02
 A:Experimental source: strain 972h-; cosmid c11c11
 C:Genetics:
 A:Gene: SPB11C11.02
 A:Map position: 2
 A:Introns: 23/3; 54/2; 612/1
 C:Superfamily: SH3 homology
 F:614-665/Domain: SH3 homology <SH3>

Query Match 12.4%; Score 73; DB 2; Length 670;
 Best Local Similarity 39.1%; Pred. No. 9.7;
 Matches 25; Conservative 6; Mismatches 21; Indels 12; Gaps 4;
 QY 31 DYNAPDCRFINVKKGQOIYVYSKLVTEAGAGAFWAGSVYGDHDEMGIYGFPSNLV 88
 DB 617 DYDAIEEISFRKGDITAVLK-LYEDG--WMEGVVEDDHNH-----GQFPSTVFR 666
 QY 89 EQRV 92
 DB 667 EIEV 670

RESULT 12

C81920

hypothetical protein NMA0762 [imported] - *Neisseria meningitidis* (strain Z2491 serogroup C)
 C/Species: *Neisseria meningitidis*
 C/Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
 C/Accession: C81920

R/Parhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, N.; Holroyd, S.; Jagsch, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000
 A/Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.
 A/Reference number: A81775; MUID:20222556; PMID:10761919
 A/Accession: C81920

A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-344 <PAR>
 A/Cross-references: GB:AL62754; GB:AL57959; NID:G7379424; PIDN:CAB84045.1; PID:G737948
 A/Experimental source: serogroup A, strain Z2491
 C/Genetics:
 A/Gene: NMA0762

Query Match 12.1%; Score 71.5; DB 2; Length 344;
 Best Local Similarity 29.4%; Pred. No. 6.6;
 Matches 25; Conservative 14; Mismatches 39; Indels 7; Gaps 4;

QY 6 DKLSKKUCADDECVYTTISLAQEDYNAPDRCFINVKKGOIYYSKLV--TENGAQAF 63
 DB 182 DKLSANHF--ENCQIGHFTAIETGSLHDSFIN-NEQYKYVSTFLDMSSEGHNY 237

QY 64 WA-GSVYGDHODEMGIVGFPSNLV 87
 DB 238 WSDNSAFDLNGDGFSDSAVRPGIT 262

RESULT 13

G96995

ATP-dependent RNA helicase, superfamily II [imported] - *Clostridium acetobutylicum*
 C/Species: *Clostridium acetobutylicum*
 C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001

R/Nolling, U.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Bacteriol. 183, 4833-4838, 2001
 A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld
 A/Reference number: A96900; MUID:21359325; PMID:21359325
 A/Accession: G96995

A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-585 <KUR>
 A/Cross-references: GB:AE001437; PIDN:AAK78754.1; PID:G15023664; GSPDB:GND0168
 A/Experimental source: *Clostridium acetobutylicum* ATCC824
 C/Genetics:
 A/Gene: CAC0778

Query Match 12.0%; Score 71; DB 2; Length 585;
 Best Local Similarity 29.4%; Pred. No. 14;
 Matches 30; Conservative 12; Mismatches 38; Indels 22; Gaps 5;

QY 12 KLCADDE---ECVYTTISLAQEDYNAPDRCFINVKKGOIYYVSK-----LVTEAGAGA 62
 DB 272 KDCDEVEIKYKRAIPLEVEDESFNYKD---IKGDAVYVFSKKRVLLEIAQSYSG 326

QY 63 FWAGSVYGDHODEMGIVGFPSNLVREQRYQEAFTKPIPTD 104
 DB 327 IKASIIYGDLPPEVRKQY-----EQFIKKE-TKVLVITTD 360

RESULT 14

S68178

mixed-lineage protein kinase 2 (EC 2.7.1.1) - human
 C/Species: *Homo sapiens* (man)
 C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 11-Jun-1999
 C/Accession: S68178; I38044; S32468

Query Match 11.8%; Score 70; DB 2; Length 308;
 Best Local Similarity 37.2%; Pred. No. 8.4;
 Matches 16; Conservative 6; Mismatches 19; Indels 2; Gaps 1;

R/Dorow, D.S.; Deyereux, L.; Tu, G.F.; Price, G.; Nicholl, J.K.; Sutherland, G.R.; Sim, Eur. J. Biochem. 234, 492-500, 1995
 A/Title: Complete nucleotide sequence, expression, and chromosomal localization of hum
 A/Reference number: S68178; MUID:96128179; PMID:8536694
 A/Accession: S68178

A/Molecule type: mRNA
 A/Residues: 1-954 <DOR>
 A/Cross-references: EMBL:X90846; NID:9971419; PIDN:CAA62351.1; PID:9971420
 R/Kachon, M.; Hirai, M.; Sugimura, T.; Terada, M.
 Oncogene 10, 1447-1451, 1995

A/Title: Cloning and characterization of MST, a novel (putative) serine/threonine kina
 A/Reference number: I38044; MUID:95249256; PMID:7731697
 A/Accession: I38044
 A/Status: translated from GB/EMBL/DD8J
 A/Molecule type: mRNA
 A/Residues: 1-461, 'A', 'V', '465-470', 'S', '472-806', 'R', '808-817', 'A', '819-954 <RES>
 A/Cross-references: EMBL:Z48615; NID:9758592; PIDN:CAA8831.1; PID:9758593
 R/Dorow, D.S.; Deyereux, L.; Dietzsch, E.; de Kreter, T.
 Eur. J. Biochem. 213, 701-710, 1993

A/Title: Identification of a new family of human epithelial protein kinases containing
 A/Reference number: S32467; MUID:93238756; PMID:8477742
 A/Accession: S32468
 A/Molecule type: mRNA
 A/Residues: 244-464, 'AQAAGRQPHQPALML' <DO2>
 C/Genetics:
 A/Gene: GDB:MLK2; GDB:MST
 A/Cross-references: GDB:362654; GDB:624810; OMIM:600137

A/Map position: 19q13.1-19q13.2
 C/Superfamily: mixed-lineage protein kinase 2; protein kinase homology; SH3 homology
 C/Keywords: ATP; leucine zipper; phosphotransferase; serine/threonine-specific protein
 F/23-76/Domain: SH3 homology <SH3>
 F/96-364/Domain: protein kinase homology <SH3>
 F/104-112/Region: protein kinase homology <SH3>
 F/184-405/Region: protein kinase ATP-binding motif
 F/419-440/Region: leucine zipper motif
 F/449-463/Region: leucine zipper motif
 F/145,145,222,224/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 12.0%; Score 71; DB 1; Length 954;
 Best Local Similarity 31.6%; Pred. No. 24;
 Matches 18; Conservative 9; Mismatches 24; Indels 6; Gaps 1;

QY 31 DYNAPDRCFINVKKGOIYYVSKLVTEAGAFWAGSVYGDHODEMGIVGFPSNLV 87
 DB 26 DYNAQDEULTLRGRVQVLSQDCVSGDECMWTC-----OLPSGRVGFPSNYV 76

RESULT 15

T48525

hypothetical protein T22P22.50 - *Arabidopsis thaliana*
 C/Species: *Arabidopsis thaliana* (mouse-ear cress)
 C/Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000

R/Bevan, M.; Hilbert, H.; Brann, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft
 submitted to the Protein Sequence Database, April 2000
 A/Reference number: Z24490
 A/Accession: T48525

A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-308 <BEV>
 A/Cross-references: EMBL:AL163814
 A/Experimental source: cultivar Columbia; BAC clone T22P22
 C/Genetics:
 A/Map position: 5
 A/Introns: 63/3; 117/3; 135/3; 180/3
 A/Note: T22P22.50

Query Match 11.8%; Score 70; DB 2; Length 308;
 Best Local Similarity 37.2%; Pred. No. 8.4;
 Matches 16; Conservative 6; Mismatches 19; Indels 2; Gaps 1;

Tue Dec 30 10:20:52 2003

us-10-019-455a-49.rpr

Page 6

Db 168 KGCERAVYASIVCEKIDGNMWTVDVRYDRPDVH--IGYWPKEJ, 208

Search completed: December 29, 2003, 16:10:41
Job time : 11.4006 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 29, 2003, 16:03:18 ; Search time 4.31373 Seconds

(without alignments)
1199.181 Million cell updates/sec

Title: US-10-019-455a-49

Perfect score: 591
Sequence: 1 HGVEMDKLSSKKLCADECEV.....RVYQATKKEIPTIDIFCE 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 segs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt 41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 574 | 97.1 | 128 | 1 | OTOR_MOUSE |
| 2 | 541 | 91.5 | 128 | 1 | OTOR_HUMAN |
| 3 | 461.5 | 78.1 | 132 | 1 | OTOR_CHICK |
| 4 | 395 | 66.8 | 133 | 1 | OTOR_RANCA |
| 5 | 264.5 | 44.8 | 131 | 1 | MIA_HUMAN |
| 6 | 263.5 | 44.6 | 130 | 1 | MIA_BOVIN |
| 7 | 263.5 | 44.6 | 130 | 1 | MIA_RAT |
| 8 | 248.5 | 42.0 | 130 | 1 | MIA_MOUSE |
| 9 | 93.5 | 15.8 | 843 | 1 | VAV_RAT |
| 10 | 93.5 | 15.8 | 845 | 1 | VAV_MOUSE |
| 11 | 93.5 | 15.8 | 847 | 1 | VAV_MOUSE |
| 12 | 91.5 | 15.5 | 845 | 1 | VAV_HUMAN |
| 13 | 91.5 | 15.5 | 847 | 1 | VAV_HUMAN |
| 14 | 85.5 | 14.5 | 868 | 1 | VAV2_MOUSE |
| 15 | 84.5 | 14.3 | 878 | 1 | VAV2_HUMAN |
| 16 | 82.5 | 14.0 | 1589 | 1 | CC25_YEAST |
| 17 | 79 | 13.4 | 2161 | 1 | SHK1_HUMAN |
| 18 | 77 | 13.0 | 2167 | 1 | SHK1_RAT |
| 19 | 74 | 12.5 | 695 | 1 | TGM2_PAGMA |
| 20 | 73 | 12.4 | 670 | 1 | YB2 SCHPO |
| 21 | 72 | 12.2 | 1815 | 1 | SHK3_RAT |
| 22 | 71 | 12.0 | 776 | 1 | ARH6_HUMAN |
| 23 | 71 | 12.0 | 933 | 1 | ZO3_HUMAN |
| 24 | 71 | 12.0 | 934 | 1 | M3TA_HUMAN |
| 25 | 70 | 11.8 | 1217 | 1 | ITNI_RAT |
| 26 | 69 | 11.7 | 380 | 1 | NCK2_HUMAN |
| 27 | 68.5 | 11.6 | 727 | 1 | IF2M_HUMAN |
| 28 | 68 | 11.5 | 427 | 1 | AROA_STRP8 |
| 29 | 68 | 11.5 | 430 | 1 | AROA_STRP8 |
| 30 | 68 | 11.5 | 646 | 1 | PIXB_HUMAN |
| 31 | 68 | 11.5 | 733 | 1 | VINE_MOUSE |
| 32 | 67.5 | 11.4 | 505 | 1 | SRK1_SPOLA |
| 33 | 67.5 | 11.4 | 506 | 1 | SRK4_SPOLA |

ALIGNMENTS

| RESULT 1 | ID | OTOR_MOUSE | STANDARD | PRT | 128 AA. |
|----------|--|------------|----------|------------|---------|
| AC | 091E3 | | | | |
| DT | 16-OCT-2001 (Rel. 40, Created) | | | | |
| DT | 16-OCT-2001 (Rel. 40, Last sequence update) | | | | |
| DT | 28-FEB-2003 (Rel. 41, Last annotation update) | | | | |
| DE | Otoraplin precursor (Melanoma inhibitory activity-like protein). | | | | |
| GN | OTOR OR MIAL | | | | |
| OS | Mus musculus (Mouse). | | | | |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. | | | | |
| OX | NCB1_TaxID=10090; | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RX | MEDLINE=20334619; PubMed=10873378; | | | | |
| RA | Robertson N.G., Heller S., Lin J.S., Resendes B.L., Wermowicz S., | | | | |
| RA | Denis C.S., Bell A.M., Hudepeth A.J., Morton C.C.; | | | | |
| RT | "A novel conserved cochlear gene, OTOR: identification, expression | | | | |
| RT | analysis, and chromosomal mapping."; | | | | |
| RL | Genomics 66:242-248(2000). | | | | |
| RN | [2] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | Tissue=Fetal; | | | | |
| RX | MEDLINE=21100875; PubMed=11161796; | | | | |
| RA | Rendtorff N.D., Frodin M., Attie-Bitach T., Vekemans M., Tommerup N., | | | | |
| RT | "Identification and characterization of an inner ear-expressed human | | | | |
| RT | melanoma inhibitory activity (MIA)-like gene (MIAL) with a frequent | | | | |
| RT | polymorphism that abolishes translation."; | | | | |
| RL | Genomics 71:40-52(2001). | | | | |
| CC | - SUBCELLULAR LOCATION: Secreted (Potential). | | | | |
| CC | - TISSUE SPECIFICITY: HIGHLY EXPRESSED IN COCHLEA. | | | | |
| CC | - SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY. | | | | |
| CC | - SIMILARITY: Contains 1 SH3 domain. | | | | |
| CC | - This SWISS-PROT entry is copyright. It is produced through a collaboration | | | | |
| CC | between the Swiss Institute of Bioinformatics and the EMBL Outstation - | | | | |
| CC | the European Bioinformatics Institute. There are no restrictions on its | | | | |
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| CC | entities requires a license agreement (See http://www.isb-sib.ch/announce/ | | | | |
| CC | or send an email to license@isb-sib.ch). | | | | |
| DR | EMBL; AF233333; AAR82079.1; - | | | | |
| DR | EMBL; AJ243939; CAC27444.1; - | | | | |
| DR | HSSP; Q16674; 111J. | | | | |
| DR | MCD; MG1:1888678; Otor. | | | | |
| DR | GO; GO:0001502; P:carilage condensation; IMP. | | | | |
| DR | InterPro; IPR001452; SH3. | | | | |
| DR | Pfam; PF00018; SH3; 1. | | | | |
| DR | SMART; SM00326; SH3; 1. | | | | |
| DR | PROSITE; PS50002; SH3; 1. | | | | |
| KW | Signal; SH3 domain. | | | | |
| FT | SIGNAL | 1 | 18 | POTENTIAL. | |
| FT | CHAIN | 19 | 128 | OTORAPLIN. | |
| FT | DOMAIN | 39 | 110 | SH3. | |

```

FT DISULFID 32 37 BY SIMILARITY.
SQ SEQUENCE 128 AA; 14328 MW; 3DD47D4C77CA7ED CRC64;

Query Match 97.1%; Score 574; DB 1; Length 128;
Best Local Similarity 96.4%; Pred. No. 6.4e-53;
Matches 106; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 HGMEMDKLSKSLKLCADCECVYTISLARAQEDYNAPDCRFINVKKGQOIYVYSKLVTENGA 60
DB 19 HGVEMDKLSKSLKLCADCECVYTISLARAQEDYNAPDCRFIDVKKGQOIYVYSKLVTENGA 78
QY 61 GAFWAGSVYGDHGDQEMGIVGYPNSLVREORVYQEAATKEIPTDIDFFCE 110
DB 79 GEFWAGSVYGDHGDQEMGIVGYPNSLVREORVYQEAATKEIPTDIDFFCE 128

RESULT 2
OTOR HUMAN STANDARD; PRT; 128 AA.
AC Q9NRG9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Otoraplin precursor (fibrocyte-derived protein) (Melanoma inhibitory
DE activity like protein).
GN OTOR OR FDP OR MIAL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RC TISSUE=Cochlea;
RP MEDLINE=20334619; PubMed=10873378;
RX Robertson N.G., Heller S., Lin J.S., Resendes B.L., Wermowicz S.,
RA Denis C.S., Bell A.M., Hudspeth A.J., Morton C.C.;
RT "A novel conserved cochlear gene, OTOR: identification, expression
RT analysis, and chromosomal mapping.";
RL Genomics 66:242-248(2000).
RN SEQUENCE FROM N.A.
RX MEDLINE=20568254; PubMed=10998416;
RA Cohen-Salmon M., Frenz D., Liu W., Verpy E., Voegelings S., Petit C.;
RT "Fdp, a new fibrocyte-derived protein related to MIA/CD-RAP, has an
RT in vitro effect on the early differentiation of the inner ear
RT mesenchyme.";
RL J. Biol. Chem. 275:40036-40041(2000).
RN SEQUENCE FROM N.A.
RC TISSUE=Brain, and Cochlea;
RP MEDLINE=21100875; PubMed=1161796;
RX Rendicoff N.D., Frodin M., Attie-Bitach T., Vekemans M., Tommerup N.;
RT "Identification and characterization of an inner ear-expressed human
RT melanoma inhibitory activity (MIA)-like gene (MIAL) with a frequent
RT polymorphism that abolishes translation.";
RL Genomics 71:40-52(2001).
RN SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagunlay C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Griffin D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,

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RA Lehaesjaino M.H., Leversha M.A., Lloyd D.M., Lovell J.D.,
RA Maeh V.L., Martin S.L., McCormachie L.J., McLeay K., McMurtry A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsey H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkhen R., Sims S.,
RA Skuce C.D., Smith M., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
CC -1- SUBCELLULAR LOCATION: Secreted (potential).
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN COCHLEA.
CC -1- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
CC -1- SIMILARITY: Contains 1 SH3 domain.
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DR EMBL: AF233261; AAF82078.1; -
DR EMBL: AF243505; AAG42356.1; -
DR EMBL: AJ242552; CAC27443.1; -
DR EMBL: AJ252324; CAC28085.1; -
DR EMBL: AJ252325; CAC28085.1; JOINED.
DR EMBL: AJ252326; CAC28085.1; JOINED.
DR EMBL: AJ252327; CAC28085.1; JOINED.
DR EMBL: AL034428; CAC16848.1; -
DR HSSP: Q16674; 111D.
DR GeneW; HGNC:8517; OTOR.
DR MIM; 606067; -
DR GO; GO:0007605; P.hearing; TAS.
DR InterPro; IPR001452; SH3.
DR Pfam; PF00018; SH3; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS50002; SH3; FALSE_NEG.
KM SIGNAL; SH3 domain.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 128 OTORAPLIN.
FT DOMAIN 39 110 SH3.
FT DISULFID 32 37 BY SIMILARITY.
FT DISULFID 55 127 BY SIMILARITY.
SQ SEQUENCE 128 AA; 14332 MW; 9BB52C7F5D4F8700 CRC64;

Query Match 91.5%; Score 541; DB 1; Length 128;
Best Local Similarity 89.1%; Pred. No. 1.7e-49;
Matches 98; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 HGMEMDKLSKSLKLCADCECVYTISLARAQEDYNAPDCRFINVKKGQOIYVYSKLVTENGA 60
DB 19 HGVEMDKLSKSLKLCADCECVYTISLARAQEDYNAPDCRFIDVKKGQOIYVYSKLVTENGA 78
QY 61 GAFWAGSVYGDHGDQEMGIVGYPNSLVREORVYQEAATKEIPTDIDFFCE 110
DB 79 GEFWAGSVYGDHGDQEMGIVGYPNSLVREORVYQEAATKEIPTDIDFFCE 128

RESULT 3
OTOR CHICK STANDARD; PRT; 132 AA.
AC Q918F6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Otoraplin precursor.
GN OTOR.

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OS Gallus gallus (Chicken).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
CC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20334619; PubMed=10873378;
RA Robertson N.G., Heller S., Lin T.S., Resendes B.L., Weremowicz S.,
RA Denis C.S., Bell A.M., Hudspeth A.J., Morton C.C.;
RT "A novel conserved cochlear gene, OTOR: identification, expression
RT analysis, and chromosomal mapping."
RL Genomics 66:242-248(2000).
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN COCHLEA.
CC -1- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
CC -1- SIMILARITY: Contains 1 SH3 domain.
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CC -----
DR EMBL; AF33518; AAF82727.1; -
DR HSSP; Q16674; 1117.
DR InterPro; IPR001452; SH3.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS50002; SH3; 1.
KM Signal; SH3 domain.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 132 OTORAPLIN.
FT DOMAIN 42 114 SH3.
FT DISULFID 35 40 BY SIMILARITY.
FT DISULFID 58 131 BY SIMILARITY.
SQ SEQUENCE 132 AA; 15177 MW; 9D1CB07D353CE1C CRC64;

Query Match 78.1%; Score 461.5; DB 1; Length 132;
Best Local Similarity 77.3%; Pred. No. 3,4e-41;
Matches 85; Conservative 11; Mismatches 13; Indels 1; Gaps 1;

QY 2 GMEFMDKLSKRLCADDECVTTISLARAQEDYNAPDCRFNVKGGQIYVSKLVTEGAG 61
DB 23 GTFMDKLSKRLCADDECVTTISLARAQEDYNAPDCRFNVKGGQIYVSKLVTEGAG 82
QY 62 AFWAGSYVYG-DHODEMGIYGFPPSNLYREQRYQEAATKEIPTDIDPFCE 110
DB 83 EFWAGSYVGEYEDHMGTVGFPRSLVSEOHVQEAANKITPTDIDPFCE 132

RESULT 4
OTOR_RANCA STANDARD; PRT; 133 AA.
AC Q9185;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Otoraplin precursor.
GN OTOR.
OS Rana catesbeiana (Bull frog).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20334619; PubMed=10873378;
RA Robertson N.G., Heller S., Lin T.S., Resendes B.L., Weremowicz S.,
RA Denis C.S., Bell A.M., Hudspeth A.J., Morton C.C.;
RT "A novel conserved cochlear gene, OTOR: identification, expression
RT analysis, and chromosomal mapping."
RL Genomics 66:242-248(2000).

```

```

CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
CC -1- SIMILARITY: Contains 1 SH3 domain.
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CC -----
DR EMBL; AF33519; AAF82728.1; -
DR HSSP; Q16674; 1117.
DR InterPro; IPR001452; SH3.
DR Pfam; PF00018; SH3; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS50002; SH3; 1.
KM Signal; SH3 domain.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 133 OTORAPLIN.
FT DOMAIN 48 115 SH3.
FT DISULFID 35 40 BY SIMILARITY.
FT DISULFID 58 132 BY SIMILARITY.
SQ SEQUENCE 133 AA; 15243 MW; 25440C1A3CF911AE CRC64;

Query Match 66.8%; Score 395; DB 1; Length 133;
Best Local Similarity 59.8%; Pred. No. 2,9e-34;
Matches 67; Conservative 26; Mismatches 17; Indels 2; Gaps 2;

QY 1 HGFMDKLSKRLCADDECVTTISLARAQEDYNAPDCRFNVKGGQIYVSKLVTEGAG 59
DB 22 YGVYQKSDKDKLCAHDECIYVAFSGRAEDYDNPDCRFNVKGGQIYVSKLVTEGAG 81
QY 60 AFWAGSYVYG-DHODEMGIYGFPPSNLYREQRYQEAATKEIPTDIDPFCE 110
DB 82 AEFWSGSVYSQYRDQGLVGFPPSLVTELVYKDELQELPTTAVDFCD 133

RESULT 5
MIA_HUMAN STANDARD; PRT; 131 AA.
AC Q16574;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Melanoma derived growth regulatory protein precursor (Melanoma
DE inhibitory activity).
GN MIA.
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=95007612; PubMed=7923218;
RA Bleesch A., Bosserhoff A.-K., Apfel R., Behl C., Hesseboer B.,
RA Schmitt A., Jachmickak P., Lottspeich F., Buettnner R., Bogdan U.,
RT "Cloning of a novel malignant melanoma-derived growth-regulatory
RT protein, MIA."
RL Cancer Res. 54:5695-5701(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96132947; PubMed=8550608;
RA Bosserhoff A.-K., Hein R., Bogdan U., Buettnner R.;
RT "Structure and promoter analysis of the gene encoding the human
RT melanoma-inhibiting protein MIA."
RL J. Biol. Chem. 271:490-495(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Skin;
RL MEDLINE=22388257; PubMed=12477932;

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RA  Strausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA  Klausner R.D., Collins F.S., Wagner L., Sheman C.M., Schuler G.D.,
RA  Altshul S.F., Zeeberg B., Buecaw K.H., Schaefer C.F., Bhac N.K.,
RA  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang U., Hsieh F.,
RA  Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA  Stepleton M., Soares M.B., Bonaldi M.F., Cavaert T.L., Scheetz T.E.,
RA  Brownstein M.J., Usdin T.B., Toshiyuki S., Cantini P., Prange C.,
RA  Rana S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA  Bosak S.A., McEwan P.J., McKernan K.O., Malek J.A., Gunaratne P.H.,
RA  Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Halys S.W.,
RA  Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA  Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA  Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA  Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA  Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
RA  Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA  Schermer A., Schein J.E., Jones S.J.M., Marra M.A.;
RT  "Generation and initial analysis of more than 15,000 full-length
RT  human and mouse cDNA sequences." ;
RL  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN  [4]
RP  X-RAY CRYSTALLOGRAPHY (1.39 ANGSTROMS) OF 25-131.
RX  MEDLINE:21244635, PubMed:11331761,
RA  Longhead J.C., Holton J.M., Alber T., Bazan J.F., Handel T.M.;
RT  "Structure of melanoma inhibitory activity protein, a member of a
RT  recently identified family of secreted proteins." ;
RL  Proc. Natl. Acad. Sci. U.S.A. 98:5515-5520 (2001).
CC  - FUNCTION: ELICITS GROWTH INHIBITION ON MELANOMA CELLS IN VITRO
CC  - AS WELL AS SOME OTHER NEUROENDOCRINAL TUMORS, INCLUDING GLIOMAS.
CC  - SUBCELLULAR LOCATION: Secreted.
CC  - TISSUE SPECIFICITY: ALL MALIGNANT MELANOMA CELL LINES TESTED AND
CC  - INRECUENTLY IN GLIOMA CELL LINES.
CC  - PTM: MAY POSSESS TWO INTRAMOLECULAR DISULFIDE BONDS.
CC  - SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
CC  - SIMILARITY: Contains 1 SH3 domain.
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CC  EMBL; X75450; CAA53203.1; -.
DR  EMBL; X84707; CAA59195.1; -.
DR  EMBL; BC005910; AAH05910.1; -.
DR  PIR; J38019; I38019.
DR  PDB; 1IUJ; 16-MAY-01.
DR  PDB; 1HJD; 29-JUN-02.
DR  PDB; 1K0X; 24-JUL-02.
DR  Genew; HGNC:7076; MIA.
MIM; 601340; -.
DR  GO; GO:0005615; C:extracellular space; TAS.
DR  GO; GO:0008283; P:cell proliferation; TAS.
DR  InterPro; IPR001452; SH3.
DR  Pfam; PF00018; SH3; 1.
DR  SMART; SM00326; SH3; 1.
DR  PROSITE; PS50002; SH3; 1.
KM  Growth factor; Signal; SH3 domain; 3D-structure.
FT  SIGNAL 1 24
FT  CHAIN 25 131
FT  DOMAIN 43 113
FT  DISULFID 36 41
FT  DISULFID 59 130
FT  STRAND 33 36
FT  TURN 39 40
FT  STRAND 46 50
FT  STRAND 54 54
FT  TURN 59 60
FT  STRAND 61 61
FT  STRAND 64 64

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FT TURN 66 67
FT STRAND 69 76
FT HELIX 78 80
FT TURN 81 82
FT STRAND 83 89
FT TURN 93 94
FT STRAND 96 96
FT STRAND 101 104
FT HELIX 105 107
FT STRAND 108 113
FT STRAND 119 122
FT HELIX 126 128
SQ SEQUENCE 131 AA; 14509 MW; 4D3B830BD6008BDC CRC64;

Query Match 44.8%; Score 264.5; DB 1; Length 131;
Best Local Similarity 46.3%; Pred. No. 1.1e-20;
Matches 50; Conservative 23; Mismatches 30; Indels 5; Gaps 3;

Qy 5 MDKSSKTLCADECEVYITISLRAGQEDYNADPCSPINKKQOQIYVYSKLTVENTAG-AF 63
Db 27 MPKCLADRLCADQCSCSHPIISMAVALQDMADPCFLLTHRQGVVYVSKL--KGRGLF 83

Qy 64 WAGSVYGGHODEMGI-VGPPSNIVREQRYVGEATKEIPTDIDPFCE 110
Db 84 WGSVYGGDYGDLLARLGLGFPSSIVREDQTLKPKGVKDVKTDMDFYCO 131

RESULT 6
MIA_BOVIN
ID MIA_BOVIN STANDARD; PRT; 130 AA.
AC Q28038;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Melanoma derived growth regulatory protein precursor (Melanoma
DE inhibitory activity) (Cartilage-derived retinoic acid-sensitive
DE protein) (CD-RAP).
GN MIA OR CDRAP.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96216414; PubMed=8621736;
RA Dietz U.H., Sandell L.J.,
RT "Cloning of a retinoic acid-sensitive mRNA expressed in cartilage and
RT during chondrogenesis."
J. Biol. Chem. 271:3311-3316(1996).
RL -1- FUNCTION: MAY FUNCTION DURING CARTILAGE DEVELOPMENT AND
CC MAINTENANCE.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: CARTILAGE PRIMORDIA AND CARTILAGE.
CC -1- INDUCTION: Repressed by retinoic acid.
CC -1- PTM: MAY POSSESS TWO INTRAMOLECULAR DISULFIDE BONDS.
CC -1- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
CC -1- SIMILARITY: Contains 1 SH3 domain.
CC -----
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CC -----
DR EMBL; U51437; AAC48523.1; --
DR HSSP; O16674; 111J
DR InterPro; IPR001452; SH3.
DR Pfam; PF00018; SH3; 1.
DR SMART; SMO0326; SH3; 1.
DR PROSITE; PSS00002; SH3; 1.

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 CC -----
 CC DR EMBL; X94322; CAA65983.1; -
 CC DR EMBL; U85612; AAB42082.1; -
 CC DR EMBL; X97965; CAA66608.1; -
 CC DR HSSP; Q16674; 111J
 CC DR MCD; MGT109615; Ma.
 CC DR GO; GO:0007160; P:cell-matrix adhesion; IMP.
 CC DR GO; GO:0030198; P:extracellular matrix organization and bioge. .; IMP.
 CC DR InterPro; IPR001452; SH3.
 CC DR Pfam; PF00018; SH3; 1.
 CC DR SMART; SM00326; SH3; 1.
 CC DR PROSITE; PS50002; SH3; FALSE_NEG.
 CC DR Growth factor; Signal; SH3 domain.
 CC FT SIGNAL 1 22 POTENTIAL.
 CC FT CHAIN 23 130 MELANOMA DERIVED GROWTH REGULATORY
 CC FT DOMAIN 42 112 SH3.
 CC FT DISULFID 35 40 BY SIMILARITY.
 CC FT DISULFID 58 129 BY SIMILARITY.
 CC FT CONFLICT 112 113 TL -> NS (IN REF. 1).
 CC SQ SEQUENCE 130 AA; 14593 MW; 16C957459C5B5F9 CRC64;
 CC
 CC Query Match 42.0%; Score 248.5; DB 1; Length 130;
 CC Best Local Similarity 46.3%; Pred. No. 5e-19;
 CC Matches 50; Conservative 20; Mismatches 33; Indels 5; Gaps 3;
 CC
 CC QY 5 MDKLSKXLCADCECVYITSLARQEDYVAPDGRFINVKGGQIYVYSKLVLENAGG-AF 63
 CC Db 26 MPKLADMKLCADCECHSPISMAYALQDYVAPDGRFLTRIGQVYVFSK---KGRGRUF 82
 CC QY 64 MAGSYVGDHDEMGV-VGYFPNVLVEQRYQYQATKEIPTDIDPFCE 110
 CC Db 83 WGSYVGGYGYDYLARLGYPPSSIVREDTLKXGKIDMTDQWDFYCO 130
 CC
 CC RESULT 9
 CC VAV_RAT STANDARD; PRT; 843 AA.
 CC ID VAV_RAT
 CC AC P54100;
 CC DT 01-OCT-1996 (Rel. 34, Created)
 CC DT 01-OCT-1996 (Rel. 34, Last sequence update)
 CC DT 15-SEP-2003 (Rel. 42, Last annotation update)
 CC DE Vav proto-oncogene (p95).
 CC GN VAV1 OR VAV.
 CC OS Rattus norvegicus (Rat).
 CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC OX NCBI_TaxID=10116;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE=99323974; PubMed=10395673;
 CC RA Song J.S., Halsem-Smith H., Arudchandran R., Gomez J., Scott P.M.,
 CC RA Mill J.F., Fan T.-H., Rivera U.;
 CC RT "Tyrosine phosphorylation of Vav stimulates IL-6 production in mast
 CC RT cells by a Rac/c-Jun N-terminal kinase-dependent pathway.";
 CC RL J. Immunol. 163:802-810(1999).
 CC CC - FUNCTION: Couples tyrosine kinase signals with the activation of
 CC CC the Rho/Rac GTPases, thus leading to cell differentiation and/or
 CC CC proliferation.
 CC CC - SUBUNIT: Interacts with SLA (By similarity).
 CC CC - PTM: Phosphorylated on tyrosine residues.
 CC CC - SIMILARITY: Contains 1 calponin-homology (CH) domain.
 CC CC - SIMILARITY: Contains 1 Dbl-homology (DH) domain.
 CC CC - SIMILARITY: Contains 1 PH domain.
 CC CC - SIMILARITY: Contains 1 zinc-dependent phospho-ester and DAG
 CC CC binding domain.
 CC CC - SIMILARITY: Contains 1 SH2 domain.
 CC CC - SIMILARITY: Contains 2 SH3 domains.
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 CC -----
 CC DR EMBL; U39476; AAA98606.1; -
 CC DR HSSP; P29354; IGR1.
 CC DR InterPro; IPR001715; Calponin-like.
 CC DR InterPro; IPR003247; CH type.
 CC DR InterPro; IPR002319; DAG PE-bind.
 CC DR InterPro; IPR001331; GDS_CDCC24.
 CC DR InterPro; IPR001849; PH.
 CC DR InterPro; IPR000219; RHOGEF.
 CC DR InterPro; IPR000980; SH2.
 CC DR InterPro; IPR001452; SH3.
 CC DR InterPro; IPR001096; SM22_calponin.
 CC DR Pfam; PF00307; CH; 1.
 CC DR Pfam; PF00130; DAG_PE-bind; 1.
 CC DR Pfam; PF00169; PH; 1.
 CC DR Pfam; PF00621; RHOGEF; 1.
 CC DR Pfam; PF00017; SH2; 1.
 CC DR Pfam; PF00019; SH3; 2.
 CC DR PRINTS; PR00401; SH2DOMAIN.
 CC DR PRINTS; PR00452; SH3DOMAIN.
 CC DR PRINTS; PR00888; SM22CALPONIN.
 CC DR ProDom; PD001527; CH type; 1.
 CC DR ProDom; PD000093; SH2; 1.
 CC DR ProDom; PD000066; SH3; 1.
 CC DR SMART; SM0109; CH; 1.
 CC DR SMART; SM0033; CH; 1.
 CC DR SMART; SM00233; PH; 1.
 CC DR SMART; SM00325; RHOGEF; 1.
 CC DR SMART; SM00252; SH2; 1.
 CC DR SMART; SM00326; SH3; 2.
 CC DR PROSITE; PS50021; CH; 1.
 CC DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
 CC DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
 CC DR PROSITE; PS50010; DH 2; 1.
 CC DR PROSITE; PS00741; DH 1; 1.
 CC DR PROSITE; PS50003; PH_DOMAIN; 1.
 CC DR PROSITE; PS50001; SH2; 1.
 CC DR PROSITE; PS50002; SH3; 2.
 CC KW Guanine-nucleotide releasing factor; Repeat; Phosphorylation.
 CC FT DOMAIN 1 119 CH.
 CC FT DOMAIN 194 373 DH.
 CC FT DOMAIN 402 504 PH.
 CC FT DOMAIN 516 564 PHORBOL-ESTER AND DAG BINDING.
 CC FT DOMAIN 615 658 SH3 1.
 CC FT DOMAIN 669 763 SH2 1.
 CC FT DOMAIN 780 840 SH3 2.
 CC SQ SEQUENCE 843 AA; 97953 MW; CAA5CADC45FCB80E CRC64;
 CC
 CC Query Match 15.8%; Score 93.5; DB 1; Length 843;
 CC Best Local Similarity 32.9%; Pred. No. 0.053;
 CC Matches 23; Conservative 14; Mismatches 20; Indels 13; Gaps 3;
 CC
 CC QY 26 ARAQEDYNAPDREINVKKGGQIYVYSKLVLENAGAFVAGSYVGDHDEMGVGYFPN 85
 CC Db 785 AKARYDFCARSRLSKEGDII-----KILNKKGGQGWGELYGR-----IGMFPN 833
 CC QY 86 LVREQRYQOE 95
 CC Db 834 YVEED--YSE 841
 CC
 CC RESULT 10
 CC VAV_MOUSE STANDARD; PRT; 845 AA.
 CC ID VAV_MOUSE
 CC AC P27870;
 CC DT 01-AUG-1992 (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Vav proto-oncogene.
 GN VAV1 OR VAV.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9222848; PubMed=1555462;
 RA Adams J.A., Houston H., Allen J., Lints T., Harvey R.;
 RT "The hematopoietically expressed vav proto-oncogene shares homology
 RT with the db1 GDP-GTP exchange factor, the bcr gene and a yeast gene
 RT (CDC24) involved in cytoskeletal organization.";
 RL Oncogene 7:611-618(1992).
 RN (2)
 RP SEQUENCE OF 1-93 FROM N.A.
 RX MEDLINE=91172176; PubMed=2005887;
 RA Katrav S., Cleveland J.L., Heslop H.E., Pulido D.;
 RT "Loss of the amino-terminal helix-loop-helix domain of the vav proto-
 RT oncogene activates its transforming potential.";
 RL Mol. Cell. Biol. 11:1912-1920(1991).
 RN (3)
 RP INTERACTION WITH SLA.
 RX MEDLINE=20130290; PubMed=10662792;
 RA Sosinowski T., Pandey A., Dixit V.M., Weiss A.;
 RT "Src-like adaptor protein (SLAP) is a negative regulator of T cell
 RT receptor signaling.";
 RL J. Exp. Med. 191:463-474(2000).
 CC -1- FUNCTION: Couples tyrosine kinase signals with the activation of
 CC the Rho/Rac GTPases, thus leading to cell differentiation and/or
 CC proliferation.
 CC -1- SUBUNIT: Interacts with SLA.
 CC -1- TISSUE SPECIFICITY: Widely expressed in hematopoietic cells but
 CC not in other cell types.
 CC -1- PTM: Phosphorylated on tyrosine residues (by similarity).
 CC -1- SIMILARITY: Contains 1 calponin-homology (CH) domain.
 CC -1- SIMILARITY: Contains 1 DBL-homology (DH) domain.
 CC -1- SIMILARITY: Contains 1 PH domain.
 CC -1- SIMILARITY: Contains 1 zinc-dependent phospho-ester and DAG
 CC binding domain.
 CC -1- SIMILARITY: Contains 1 SH2 domain.
 CC -1- SIMILARITY: Contains 2 SH3 domains.
 CC -----
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 CC -----
 DR EMBL; X64361; CA45713.1; -
 DR EMBL; M59833; AAA63402.1; -
 DR PTR; A61187; TMSV.
 DR PDB; 1FSY; 15-SEP-00.
 DR PDB; 1GCP; 28-JAN-03.
 DR PDB; 1GCO; 28-JAN-03.
 DR PDB; 1K1Z; 18-DEC-02.
 DR TRANSFAC; T01230; -
 DR MGD; MGI:98923; Vav1.
 DR InterPro; IPR001715; Calponin-like.
 DR InterPro; IPR003247; CH type.
 DR InterPro; IPR002219; DAG_PE-bind.
 DR InterPro; IPR001331; GDS_CDCC4.
 DR InterPro; IPR001849; PH.
 DR InterPro; IPR000219; RhogEF.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR InterPro; IPR003096; SM22-calponin.
 DR Pfam; PF001307; CH; 1.
 DR Pfam; PF00130; DAG_pe-bind; 1.

DR Pfam; PF00169; PH; 1.
 DR Pfam; PF00621; RhogEF; 1.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 2.
 DR PRINTS; PRO0401; SH2DOMAIN.
 DR PRINTS; PRO0452; SH3DOMAIN.
 DR PRINTS; PRO0688; SM22CALPONIN.
 DR ProDom; P001527; CH_type; 1.
 DR ProDom; P000093; SH2; 1.
 DR ProDom; P000066; SH3; 1.
 DR SMART; SM0109; C1; 1.
 DR SMART; SM00033; CH; 1.
 DR SMART; SM00233; PH; 1.
 DR SMART; SM0325; RhogEF; 1.
 DR SMART; SM0252; SH2; 1.
 DR SMART; SM00326; SH3; 2.
 DR PROSITE; PS50021; CH; 1.
 DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
 DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
 DR PROSITE; PS50010; DH_2; 1.
 DR PROSITE; PS00741; DH_1; 1.
 DR PROSITE; PS50003; PH_DOMAIN; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 2.
 KW Proto-oncogene; Phorbol-ester binding; Zinc; SH2 domain; SH3 domain;
 KW Guanine-nucleotide releasing factor; Repeat; Phosphorylation;
 KW 3D-structure.
 FT DOMAIN 1 119 CH.
 FT DOMAIN 194 373 DH.
 FT DOMAIN 402 504 PH.
 FT DOMAIN 516 564 PHORBOL-ESTER AND DAG BINDING.
 FT DOMAIN 617 660 SH3 1.
 FT DOMAIN 671 765 SH2 1.
 FT DOMAIN 782 842 SH2 2.
 FT CONFLICT 29 29 SH2.
 SQ SEQUENCE 845 AA; 98136 MW; 3666DCD1C5229DA CRC64;
 Query Match 15.8%; Score 93.5; DB 1; Length 845;
 Best Local Similarity 32.9%; Pred. No. 0.053;
 Matches 23; Conservative 14; Mismatches 20; Indels 13; Gaps 3;
 QY 26 ARAQEDYNAPDRFFIWKKGQOIYVYSKLVTEGAGAFVAGSVGDHDEMIGVFPSPN 85
 Db 787 AKARYDFCARDSRLSKSGDII-----KILNKGQGGWRRGRTYR-----IGFSPN 835
 QY 86 LVFEQRYOE 95
 Db 836 YVEED--YSE 843
 RESULT 11
 VAV3_MOUSE
 ID VAV3_MOUSE STANDARD; PRT; 847 AA.
 AC Q9R0C8;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Vav-3 protein.
 GN VAV3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20179693; PubMed=10713454;
 RA Trenkle T., McClelland M., Adikofer K., Welsh J.;
 RT "Major transcript variants of VAV3, a new member of the VAV family of
 RT guanine nucleotide exchange factors.";
 RL Gene 245:139-149(2000).
 CC -1- FUNCTION: EXCHANGE FACTOR FOR GTP-BINDING PROTEINS RHOA, RHOG AND,
 CC TO A LESSER EXTENT, RAC-1, BINDS PHYSICALLY TO THE NUCLEOTIDE-FREE
 CC STATES OF THOSE GTPASES (BY SIMILARITY).

```
CC CC -|- ALTERNATIVE PRODUCTS:
CC CC Event-Alternative splicing; Named isoforms=2;
CC CC Name:Alpha;
CC CC IsoId-Q9R0C8-1; Sequence-Displayed;
CC CC Name:Beta;
CC CC IsoId-Q9R0C8-2; Sequence=Not Described;
CC CC -|- SIMILARITY: Contains 1 calponin-homology (CH) domain.
CC CC -|- SIMILARITY: Contains 1 DBL-homology (DH) domain.
CC CC -|- SIMILARITY: Contains 1 PH domain.
CC CC -|- SIMILARITY: Contains 1 zinc-dependent phospho-ester and DAG binding domain.
CC CC -|- SIMILARITY: Contains 1 SH2 domain.
CC CC -|- SIMILARITY: Contains 2 SH3 domains.
-----
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-----
CC CC EMBL; AF067816; AAF09171.1; -.
CC CC HSSP; P29355; ISEM.
CC CC MGD; MGI:1888518; Vav3.
CC CC InterPro; IPR001715; Calponin-like.
CC CC InterPro; IPR003247; CH_type.
CC CC InterPro; IPR002219; DAG_pe-bind.
CC CC InterPro; IPR001331; GDS_CDC24.
CC CC InterPro; IPR001849; PH_-_.
CC CC InterPro; IPR000219; Rhogef.
CC CC InterPro; IPR000980; SH2.
CC CC InterPro; IPR001452; SH3.
CC CC InterPro; IPR003096; SW2_calponin.
CC CC Pfam; PF00307; CH_1.
CC CC Pfam; PF00130; DAG_pe-bind; 1.
CC CC Pfam; PF00169; PH_1.
CC CC Pfam; PF00621; Rhogef; 1.
CC CC Pfam; PF00017; SH2; 1.
CC CC Pfam; PF00018; SH3; 1.
CC CC PRINTS; PR00401; SH2DOMAIN.
CC CC PRINTS; PR00452; SH3DOMAIN.
CC CC PRINTS; PR00688; SM2CALPONIN.
CC CC ProDom; PP001527; CH_type; 1.
CC CC ProDom; PD000093; SH2; 1.
CC CC ProDom; PD000066; SH3; 1.
CC CC SMART; SM00109; C1; 1.
CC CC SMART; SM00033; CH; 1.
CC CC SMART; SM00233; PH; 1.
CC CC SMART; SM00325; Rhogef; 1.
CC CC SMART; SM00252; SH2; 1.
CC CC SMART; SM00326; SH3; 2.
CC CC PROSITE; PS50021; CH; 1.
CC CC PROSITE; PS50479; DAG_pe BIND DOM 1; 1.
CC CC PROSITE; PS50081; DAG-pe_BIND_DOM_2; 1.
CC CC PROSITE; PS50010; DR_2; 1.
CC CC PROSITE; PS50741; DR_1; 1.
CC CC PROSITE; PS50003; PH DOMAIN; 1.
CC CC PROSITE; PS50001; SH2; 1.
CC CC PROSITE; PS50002; SH3; 2.
CC CC Phospho-ester binding; Zinc; SH2 domain; SH3 domain; Repeat;
CC CC Guanine-nucleotide releasing factor; Alternative splicing.
FT FT DOMAIN 1 119 DH.
FT FT DOMAIN 192 371 PH.
FT FT DOMAIN 400 502 PHORBO-ESTER AND DAG BINDING.
FT FT DOMAIN 514 562 SH3 1.
FT FT DOMAIN 592 660 SH2.
FT FT DOMAIN 672 766 SH3 2.
FT FT DOMAIN 788 847 SH3 2.
SQ SQ SEQUENCE 847 AA; 97946 MW; 9A6B63FDD9E60F8F CRC64;
```

```

Matches 22: Conservative 13; Mismatches 21; Indels 11; Gaps 2
QY      23  ISLRAGEDNAPDCRFNFVKKGGQIIVYSKLTUTENGAGAWMASSVYGDHODEMGICVGF 82
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db       790  LGIAIARYDFCARMRRELSTLKGWVIXTKM-----SANGWMRGEVNGR-----VGWF 838
QY      83  PSNIIVRE 89
      ||| |||
Db      839  PSTVYEE 845

RESULT 12
VAV_HUMAN
ID _VAV_HUMAN STANDARD; PRT; 845 AA.
AC P15498; Q15860;
DT 01-APR-1990 (Rel. 14, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Vav proto-oncogene.
GN VAV1 OR VAV.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_Taxid=9606;
RR [1]
RR SEQUENCE FROM N.A.
RA Denksinger D.J., Borges C.R., Shaw C.L., Cushman A.M., Kawahara R.S.;
RT "Transcriptional regulation of the vav proto-oncogene."
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 62-845 FROM N.A.
RX MEDLINE=90005432; PubMed=2477241.
RA Katrav S., Martin-Zanca D., Barbacid M.;
RT "vav, a novel human oncogene derived from a locus ubiquitously
RT expressed in hematopoietic cells."
RL EMBO J. 8:2283-2290(1989).
RN [3]
RP SEQUENCE OF 1-61 FROM N.A.
RX MEDLINE=91172176; PubMed=2005887;
RA Katrav S., Cleveland J.L., Heslop H.E., Pulido D.;
RT "Loss of the amino-terminal helix-loop-helix domain of the vav proto-
RT oncogene activates its transforming potential."
RL Mol. Cell. Biol. 11:1912-1920(1991).
RN [4]
RP SEQUENCE OF 299-837 FROM N.A.
RA Romero F.;
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 299-334 FROM N.A.
RX MEDLINE=96038895; PubMed=7478592;
RA Ramos-Morales F., Romero F., Schweighoffer F., Bismuth G., Camonis J.,
RA Tortolero M., Fischer S.;
RT "The proline-rich region of Vav binds to Grb2 and Grb3-3."
RL Oncogene 11:1665-1669(1995).
RN [6]
RP SIMILARITY TO CDC24 FAMILY.
RX MEDLINE=92228488; PubMed=1565462;
RA Adams J.M., Houston H., Allen J., Lints T., Harvey R.;
RT "The hematopoietically expressed vav proto-oncogene shares homology
RT with the dbl GDS-GTP exchange factor, the bcr gene and a yeast gene
RT (CDC24) involved in cytoskeletal organization."
RL Oncogene 7:611-618(1992).
RN [7]
RP FUNCTION: Couples tyrosine kinase signals with the activation of
RN the Rho/Rac GTPases, thus leading to cell differentiation and/or
RN proliferation.
RN [8]
RP SUBUNIT: Interacts with SLA (By similarity). Interacts with Grb2
RN and Grb3.
RN [9]
RP TISSUE SPECIFICITY: WIDELY EXPRESSED IN HEMATOPOIETIC CELLS BUT
RN NOT IN OTHER CELL TYPES.
RN [10]
RP PTM: Phosphorylated on tyrosine residues.
RN [11]
RP MISCELLANEOUS: 'Vav' stands for the sixth letter of the Hebrew
RN alphabet.
RN [12]
RP SIMILARITY: Contains 1 calponin-homology (CH) domain.

```

CC -1- SIMILARITY: Contains 1 DBL-homology (DH) domain.
 CC -1- SIMILARITY: Contains 1 PH domain.
 CC -1- SIMILARITY: Contains 1 zinc-dependent phorbol-ester and DAG
 binding domain.
 CC -1- SIMILARITY: Contains 1 SH2 domain.
 CC -1- SIMILARITY: Contains 2 SH3 domains.
 CC -1- CAUTION: Ref.2 sequence differs from that shown due to frameshifts
 in position 322 and 355.

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 DR EMBL, AF030227, AAC25011.1, JOINED.
 DR EMBL, AF030201, AAC25011.1, JOINED.
 DR EMBL, AF030202, AAC25011.1, JOINED.
 DR EMBL, AF030203, AAC25011.1, JOINED.
 DR EMBL, AF030204, AAC25011.1, JOINED.
 DR EMBL, AF030205, AAC25011.1, JOINED.
 DR EMBL, AF030206, AAC25011.1, JOINED.
 DR EMBL, AF030207, AAC25011.1, JOINED.
 DR EMBL, AF030208, AAC25011.1, JOINED.
 DR EMBL, AF030209, AAC25011.1, JOINED.
 DR EMBL, AF030210, AAC25011.1, JOINED.
 DR EMBL, AF030211, AAC25011.1, JOINED.
 DR EMBL, AF030212, AAC25011.1, JOINED.
 DR EMBL, AF030213, AAC25011.1, JOINED.
 DR EMBL, AF030214, AAC25011.1, JOINED.
 DR EMBL, AF030215, AAC25011.1, JOINED.
 DR EMBL, AF030216, AAC25011.1, JOINED.
 DR EMBL, AF030217, AAC25011.1, JOINED.
 DR EMBL, AF030218, AAC25011.1, JOINED.
 DR EMBL, AF030219, AAC25011.1, JOINED.
 DR EMBL, AF030220, AAC25011.1, JOINED.
 DR EMBL, AF030221, AAC25011.1, JOINED.
 DR EMBL, AF030222, AAC25011.1, JOINED.
 DR EMBL, AF030223, AAC25011.1, JOINED.
 DR EMBL, AF030224, AAC25011.1, JOINED.
 DR EMBL, AF030225, AAC25011.1, JOINED.
 DR EMBL, AF030226, AAC25011.1, JOINED.
 DR EMBL, X16316, CAA34383.1, ALT_FRAME.
 DR EMBL, M59834, AAA63267.1, -.
 DR EMBL, X81931, CAA58783.1, -.
 DR PIR, B39576, TVHUV.
 DR HSSP, P29354, IGR1.
 DR TRANSFAC, T00680, -.
 DR Genew, HGNC:12657, VAV1.
 DR MIM, 164875, -.
 DR GO, GO:0003700, F:transcription factor activity, TAS.
 DR GO, GO:0007048, P:oncogenesis, TAS.
 DR InterPro, IPR001715, Calponin-like.
 DR InterPro, IPR003247, CH_type.
 DR InterPro, IPR002219, DAG_PE-bind.
 DR InterPro, IPR001849, PH_CDC24.
 DR InterPro, IPR000219, RhogEF.
 DR InterPro, IPR000980, SH2.
 DR InterPro, IPR001452, SH3.
 DR InterPro, IPR003096, SM22_calponin.
 DR Pfam, PF00307, CH, 1.
 DR Pfam, PF00130, DAG_PE-bind, 1.
 DR Pfam, PF00169, PH, 1.
 DR Pfam, PF00621, RhogEF, 1.
 DR Pfam, PF00017, SH2, 1.
 DR Pfam, PF00018, SH3, 2.
 DR PRINTS, PR00401, SH2DOMAIN.
 DR PRINTS, PR00452, SH3DOMAIN.
 DR PRINTS, PR00888, SM22CALPONIN.
 DR Prodom, PD001527, CH_type, 1.

DR Prodom: PD000093, SH2, 1.
 DR Prodom: PD000066, SH3, 1.
 DR SMART, SM00109, C1, 1.
 DR SMART, SM00033, CH, 1.
 DR SMART, SM00233, PH, 1.
 DR SMART, SM00325, RhogEF, 1.
 DR SMART, SM00252, SH2, 1.
 DR SMART, SM00326, SH3, 2.
 DR PROSITE, PS50021, CH, 1.
 DR PROSITE, PS500479, DAG_PE_BIND_DOM_1, 1.
 DR PROSITE, PS50081, DAG_PE_BIND_DOM_2, 1.
 DR PROSITE, PS50010, DH_2, 1.
 DR PROSITE, PS00741, DH_1, 1.
 DR PROSITE, PS50003, PH_DOMAIN, 1.
 DR PROSITE, PS50001, SH2, 1.
 DR PROSITE, PS50002, SH3, 2.
 KW Proto-oncogene; Phorbol-ester binding; zinc; SH2 domain; SH3 domain;
 FT Guanine-nucleotide releasing factor; Repeac; Phosphorylation.
 FT DOMAIN 1 119
 FT DOMAIN 194 373
 FT DOMAIN 402 504
 FT DOMAIN 516 564
 FT DOMAIN 617 660
 FT DOMAIN 671 765
 FT DOMAIN 782 842
 FT CONFLICT 264 264 A -> P (IN REF. 2).
 FT CONFLICT 718 718 I -> TV (IN REF. 2).
 SQ SEQUENCE 845 AA; 98313 MW; AC3BC9736F2F138 CRC64;

 QY Query Match 15.5%; Score 91.5; DB 1; Length 845;
 Beat Local Similarity 32.9%; Pred. No. 0.085;
 Matches 23; Conservative 14; Mismatches 20; Indels 13; Gaps 3;

 Db 787 AKARYDFCARDRELSKEDII-----KILKKGGQGGWWRGEIYGR-----VGWFPAN 835
 QY 86 LVREQRYQOE 95
 Db 836 YVEED-YSE 843

 RESULT 13
 VAV3 HUMAN STANDARD; PRT; 847 AA.
 ID VAV3 HUMAN
 AC Q9UKF4; O95230; Q9T5X8;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 28-FEB-2003 (Rel. 40, Last sequence update)
 DE Vav-3 protein.
 GN VAV3.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RA MEDLINE=9445043; PubMed=10523675;
 RX Movilla N., Bustelo X.R.,
 RT "Biological and regulatory properties of Vav-3, a new member of the
 RT Vav family of oncoproteins";
 RL Mol. Cell. Biol. 19:7870-7885(1999).
 RP SEQUENCE FROM N.A.
 RC TISSUE=Breast, and Colon carcinoma;
 RX MEDLINE=98371222; PubMed=9705494;
 RA Tremble T., Welsh J., Jung B., Mathieu-daude F., McClelland M.,
 RT "Non-stoichiometric reduced complexity probes for cDNA arrays";
 RL Nucleic Acids Res. 26:3883-3891(1998).
 CC -1- FUNCTION: EXCHANGE FACTOR FOR GTP-BINDING PROTEINS RHOA, RHOG AND,
 CC TO A LESSER EXTENT, RAC-1. BINDS PHYSICALLY TO THE NUCLEOTIDE-FREE
 CC STATES OF THOSE GTPASES.
 CC -1- ALTERNATIVE PRODUCTS:

KW Guanine-nucleotide releasing factor; Repeat; Phosphorylation.
FT DOMAIN 1 119 CH.
FT DOMAIN 198 376 DH.
FT DOMAIN 405 512 PH.
FT DOMAIN 524 572 PHORBOL-ESTER AND DAG BINDING.
FT DOMAIN 586 652 SH3 1.
FT DOMAIN 673 767 SH2.
FT DOMAIN 816 877 SH3 2.
FT MOD_RES 142 142 PHOSPHORYLATION (BY EGFR).
FT MOD_RES 159 159 PHOSPHORYLATION (BY EGFR).
FT MOD_RES 172 172 PHOSPHORYLATION (BY EGFR).
SQ SEQUENCE 878 AA; 101256 MW; C8FF7681032146B4 CRC64;

Query Match 14.3%; Score 84.5; DB 1; Length 878;
Best Local Similarity 27.6%; Pred. No. 0.48; Mismatches 22; Indels 13; Gaps 3;
Matches 21; Conservative 20;

QY 20 VYT--ISLAPAOEDYNAPDCRFLNVKKGOIYVYSKLVTEGAGAFMAGSVYGDHODEM 76
Db 812 VFTPRVIGTAVARYNPAARDRELRLREGDVRIYSRIIGDQG---WVKG-----ETN 861
QY 77 GIVGFPSPNLVREQRV 92
Db 862 GRIGMFPSTYVEEGEI 877

Search completed: December 29, 2003, 16:04:15
Job time : 5.31373 secs

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OM protein - protein search, using sw model

Run on: December 29, 2003, 16:03:18 ; Search time 16.9468 seconds
(Without alignments)
1674.996 Million cell updates/sec

Title: US-10-019-455A-49

Perfect score: 591
Sequence: 1 HGMFMDKLSKKLCADECV.....RVYQATKEIPPTIDFCE 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_ornanelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rviro:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | * Query Match | Length | DB ID | Description |
|------------|-------|---------------|--------|-------|--------------------|
| 1 | 234.5 | 39.7 | 96 | 11 | Q9J109 mesocricetu |
| 2 | 215 | 36.4 | 268 | 11 | Q8B1E9 mus musculu |
| 3 | 215 | 36.4 | 1239 | 11 | Q8B1E4 mus musculu |
| 4 | 182 | 30.8 | 137 | 11 | Q921X3 mus musculu |
| 5 | 176.5 | 29.9 | 88 | 13 | Q90XK1 tetraodon n |
| 6 | 165.5 | 28.0 | 119 | 4 | Q96P55 mus musculu |
| 7 | 156.5 | 26.5 | 119 | 11 | Q91ZV0 mus musculu |
| 8 | 108 | 18.3 | 68 | 11 | Q8C899 mus musculu |
| 9 | 93.5 | 15.8 | 166 | 11 | Q8C899 mus musculu |
| 10 | 93.5 | 15.8 | 287 | 11 | Q8R076 mus musculu |
| 11 | 93.5 | 15.8 | 806 | 11 | Q8VUD4 mus musculu |
| 12 | 93.5 | 15.8 | 845 | 11 | Q8B1V7 mus musculu |
| 13 | 93.5 | 15.8 | 846 | 13 | Q8UUX6 mus musculu |
| 14 | 91.5 | 15.5 | 719 | 4 | Q96D37 mus musculu |
| 15 | 86.5 | 14.6 | 839 | 13 | Q8UUX5 mus musculu |
| 16 | 82 | 13.9 | 827 | 13 | Q8UWE6 mus musculu |

| | | | | | |
|----|------|------|------|----|--------------------|
| 17 | 78.5 | 13.3 | 365 | 11 | Q9CXH0 mus musculu |
| 18 | 78.5 | 13.3 | 636 | 10 | Q9FTZ8 oryza sativ |
| 19 | 78.5 | 13.3 | 1196 | 4 | Q9H0H2 mus musculu |
| 20 | 78.5 | 13.3 | 1196 | 4 | Q9H0H2 mus musculu |
| 21 | 77 | 13.0 | 413 | 1 | Q93709 mus musculu |
| 22 | 76 | 12.9 | 645 | 10 | Q9FUD7 mus musculu |
| 23 | 76 | 12.9 | 615 | 10 | Q94E30 mus musculu |
| 24 | 76 | 12.9 | 638 | 10 | Q9ATQ5 mus musculu |
| 25 | 76 | 12.9 | 643 | 10 | Q9FUD4 mus musculu |
| 26 | 76 | 12.9 | 1257 | 5 | Q9VMA8 mus musculu |
| 27 | 76 | 12.9 | 1430 | 5 | Q9VMA7 mus musculu |
| 28 | 75.5 | 12.8 | 259 | 10 | Q8RZ28 mus musculu |
| 29 | 75.5 | 12.8 | 635 | 10 | Q9FUD1 mus musculu |
| 30 | 75.5 | 12.8 | 1215 | 5 | Q77202 mus musculu |
| 31 | 74 | 12.5 | 994 | 5 | Q93375 mus musculu |
| 32 | 73.5 | 12.4 | 533 | 5 | Q9MY10 mus musculu |
| 33 | 73.5 | 12.4 | 847 | 4 | Q16584 mus musculu |
| 34 | 73 | 12.4 | 352 | 10 | Q94EK2 mus musculu |
| 35 | 73 | 12.4 | 352 | 10 | Q94EK5 mus musculu |
| 36 | 73 | 12.4 | 479 | 10 | Q43366 mus musculu |
| 37 | 73 | 12.4 | 479 | 10 | Q937V1 mus musculu |
| 38 | 73 | 12.4 | 641 | 10 | Q9ATQ6 mus musculu |
| 39 | 73 | 12.4 | 850 | 11 | Q9J115 mus musculu |
| 40 | 72.5 | 12.3 | 498 | 4 | Q9H803 mus musculu |
| 41 | 72.5 | 12.3 | 839 | 10 | Q94F88 mus musculu |
| 42 | 72.5 | 12.3 | 1154 | 4 | Q9P2P0 mus musculu |
| 43 | 72.5 | 12.3 | 1430 | 11 | Q8VHK2 mus musculu |
| 44 | 72.5 | 12.3 | 1431 | 4 | Q8WXD9 mus musculu |
| 45 | 72 | 12.2 | 630 | 10 | Q9ARM8 mus musculu |

ALIGNMENTS

RESULT 1

Q9J109 PRELIMINARY; PRT; 96 AA.
ID Q9J109
AC Q9J109;
DT 01-OCT-2000 (TREMUREL. 15, Created)
DT 01-OCT-2000 (TREMUREL. 15, Last sequence update)
DT 01-MAR-2003 (TREMUREL. 23, last annotation update)
DE Melanoma inhibitory activity protein (Fragment).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
CX NCBI_TaxId=10036;
RN [1]
RP SEQUENCE FROM N.A.
RA Guba M., Bosserhoff A.K., Steindauer M., Anthuber M., Buettner R.,
JA Jauch K.W.,
RT "Overexpression of MIA enhances extravasation and metastasis of A-mel3
RL melanoma cells.",
RL Submitted (May-2000) to the EMBL/GenBank/DBJ databases.
CC -1-SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DR EMBL; AF271694; AAF76220.1; -
DR HSSP; Q16674; 111.
DR InterPro; IPR001452; SH3.
DR Pfam; PF00018; SH3; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PSS0002; SH3; 1.
KW SH3 domain.
FT NON_TER
FT 1
FT 96
SQ SEQUENCE 96 AA; 10756 MW; E7B466C3B50505BFB CRC64;

Query Match 39.7%; Score 234.5; DB 11; Length 96;
Best Local Similarity 46.4%; Pred. No. 1.8e-18;
Matches 45; Conservative 21; Mismatches 26; Indels 5; Gaps 3;

QY 8 LSKKLCADBECCYTTSLAPAEQDYNAPPCRFINVKKGQIIVYSKLVTEAGG-AFWAG 66
Db 1 LADRLKADQECSPISMVAALQDYVAPPCRFITIRGQVYVYFSKL---KRGRLFWG 57

QY 67 SVYGDHODEMGI-VGYFPSNLVREQRVYQATKEIPT 102
 DB 58 SVQGDYVGDLAARIGYFPFSSIVREDQTLKXGKVDVMT 94

RESULT 2

Q8BJE9 ID Q8BJE9 PRELIMINARY; PRT; 268 AA.
 AC Q8BJE9;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Weakly similar to NPIP-like protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Eye;
 RX MEDLINE=2354683; PubMed=14246851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 DR EMBL: AK084344; BAC39164.1; -
 FT NON_TER 268 268
 SQ SEQUENCE 268 AA; 29722 MW; 67339C562F684402 CRC64;
 Query Match 36.4%; Score 215; DB 11; Length 268;
 Best Local Similarity 41.3%; Pred. No. 9.6e-16;
 Matches 45; Conservative 13; Mismatches 39; Indels 12; Gaps 4;
 QY 1 HGFMDKLSSKKLCADEECVYITSLARQEDYNAPDGRFINVKGGQIYVYSKLVTENGA 60
 DB 28 HGR---RFSDLKVCQDECSMLMYRGKALDFTGPDGRFVFKKGGDVVYVYKLA--GGS 82
 QY 61 GAFNAGSYVGDHODEMGI-VGYFPSNLVREQRVYQATKEIPTTIDIFPC 109
 DB 83 LELWAGSV--EHS----FGYFPKDLIVLHKYTEELHLPADETDFVC 124

RESULT 3

Q8BI84 ID Q8BI84 PRELIMINARY; PRT; 1239 AA.
 AC Q8BI84;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Weakly similar to NPIP-like protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Retina;
 RX MEDLINE=2354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 DR EMBL: AK044749; BAC32064.1; -
 FT NON_TER 1239 1239
 SQ SEQUENCE 1239 AA; 136350 MW; 6E16F9D42CECF05 CRC64;

Query Match 36.4%; Score 215; DB 11; Length 1239;
 Best Local Similarity 41.3%; Pred. No. 6.2e-15;
 Matches 45; Conservative 13; Mismatches 39; Indels 12; Gaps 4;

QY 1 HGFMDKLSSKKLCADEECVYITSLARQEDYNAPDGRFINVKGGQIYVYSKLVTENGA 60

DB 28 HGR---RFSDLKVCQDECSMLMYRGKALDFTGPDGRFVFKKGGDVVYVYKLA--GGS 82
 QY 61 GAFNAGSYVGDHODEMGI-VGYFPSNLVREQRVYQATKEIPTTIDIFPC 109
 DB 83 LELWAGSV--EHS----FGYFPKDLIVLHKYTEELHLPADETDFVC 124

RESULT 4

Q921X3 ID Q921X3 PRELIMINARY; PRT; 137 AA.
 AC Q921X3;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Similar to cartilage derived retinoic acid sensitive protein.
 GN CDRAP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strusberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC009815; AA09815.1; -
 DR MGD; MGI:109615; Cdrap.
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF00018; SH3; 1.
 DR SMART; SMO0326; SH3; 1.
 SQ SEQUENCE 137 AA; 15441 MW; 971415522E6FDS36 CRC64;

Query Match 30.8%; Score 182; DB 11; Length 137;
 Best Local Similarity 56.9%; Pred. No. 2e-12;
 Matches 37; Conservative 9; Mismatches 15; Indels 4; Gaps 2;

QY 5 MDKLSKKLCADEECVYITSLARQEDYNAPDGRFINVKGGQIYVYSKLVTENGA-AF 63
 DB 26 MKPLADWLKCADEECVYITSLARQEDYNAPDGRFINVKGGQIYVYSKLVTENGA--KGRGLF 82
 QY 64 WAGSV 68
 DB 83 WGSV 87

RESULT 5

Q90XF1 ID Q90XF1 PRELIMINARY; PRT; 88 AA.
 AC Q90XF1;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Melanoma inhibitory activity protein (Fragment).
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorphia; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 NX NCBI_TaxID=99883;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bosserhoff A.K.; Buettner R.;
 RT "Characterization of the MIA gene family."
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF390176; AA126991.1; -
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF00018; SH3; 1.
 DR SMART; SMO0326; SH3; 1.
 FT NON_TER 1 1
 SQ SEQUENCE 88 AA; 10080 MW; C355C1FE04DA22EA CRC64;

Query Match 29.9%; Score 176.5; DB 13; Length 88;
 Best Local Similarity 42.4%; Pred. No. 4.9e-12;

Matches 39; Conservative 16; Mismatches 26; Indels 11; Gaps 4;

QY 23 ISLARAQEDYNAPDCRFINKKQGOIYYVSKLVTENGAGA-FWAGSV---YGDHODEMG 77
 DB 3 IMARLQDYPRDCCFIPRGOQLIYYVAML---KGRSGQFWAGSVQDSYVGGQEAR-- 57
 QY 78 IVGPPSNLVREGRVYQEAATKEIPTTIDFFC 109
 DB 58 -IGHFPSSIVEETHPLMAAQTEVKTSMDFYC 88

RESULT 6

Q96PCS PRELIMINARY; PRT; 119 AA.

AC Q96PCS; 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE Melanoma inhibitory activity protein 2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Bosserhoff A.K., Buettner R.;
 RT "Characterization of the MIA gene family";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF390175; AAL26990.1; -
 DR InterPro; IPR001452; SH3.
 DR SMART; SM00326; SH3; 1.
 SQ SEQUENCE 119 AA; 13535 MW; AEF529762D880ACS CRC64;

Query Match 28.0%; Score 165.5; DB 4; Length 119;
 Best Local Similarity 36.3%; Pred. No. 1.2e-10;
 Matches 37; Conservative 14; Mismatches 42; Indels 9; Gaps 2;

QY 8 LSSKRLCADEECVYTIISLARAQEDYNAPDCRFINKKQGOIYYVSKLVTENGAGA-FWAGS 67
 DB 26 LADLKCCGDLCEALINRVSNARDYRGPCRYLFTKGEISVYVKLGER--EDLWAGS 83
 QY 68 VYGDHODEMGIVGYFPNSLVREGRVYQEAATKEIPTTIDFFC 109
 DB 84 KGKE-----FGYPRDAVQIEVFISEIQTSTKSDFLC 118

RESULT 7

Q91ZV0 PRELIMINARY; PRT; 119 AA.

AC Q91ZV0; 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE Melanoma inhibitory activity protein 2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Bosserhoff A.K., Buettner R.;
 RT "Characterization of the MIA gene family";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF390177; AAL26992.1; -
 DR InterPro; IPR001452; SH3.
 DR SMART; SM00326; SH3; 1.
 SQ SEQUENCE 119 AA; 13397 MW; 589F390C0B49D1C7 CRC64;

Query Match 26.5%; Score 156.5; DB 11; Length 119;
 Best Local Similarity 36.3%; Pred. No. 1.2e-09;
 Matches 37; Conservative 13; Mismatches 43; Indels 9; Gaps 2;

QY 8 LSSKRLCADEECVYTIISLARAQEDYNAPDCRFINKKQGOIYYVSKLVTENGAGA-FWAGS 67
 DB 26 LADLKCCGDLCEALINRVSNARDYRGPCRYLFTKGEISVYVKLGER--EDLWAGS 83

QY 68 VYGDHODEMGIVGYFPNSLVREGRVYQEAATKEIPTTIDFFC 109
 DB 84 KGKD-----FGYPRDAVQIEVFISEIQTSTKSDFLC 118

RESULT 8

Q8C899 PRELIMINARY; PRT; 68 AA.

AC Q8C899; 01-MAR-2003 (TReMBLrel. 23, Created)
 DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE Otoraplin.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 DR EMBL; AK047965; BAC33202.1; -
 SQ SEQUENCE 68 AA; 7431 MW; 3CB875527D3CBF7F CRC64;

Query Match 18.3%; Score 108; DB 11; Length 68;
 Best Local Similarity 48.9%; Pred. No. 0.00016;
 Matches 23; Conservative 6; Mismatches 8; Indels 10; Gaps 2;

QY 1 HGFMDKLSKRLCADEECVYTIISLARAQEDYNAPDCRFINKKQGOIYYVSKLVTENGAGA-FWAGS 67
 DB 19 HGVFMKLSKRLCADEECVYTIISLARAQEDYNAPDCRFINKKQGOIYYVSKLVTENGAGA-FWAGS 65

RESULT 9

Q08526 PRELIMINARY; PRT; 166 AA.

AC Q08526; 01-JUL-1997 (TReMBLrel. 04, Created)
 DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE Vav-T.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=97190224; PubMed=9038379;
 RA Okumura K., Kaneko Y., Nonoguchi K., Nishiyama H., Yokoi H.,
 RA Higuchi T., Itoh K., Yoshida O., Miki T., Fujita J.;
 RT "Expression of a novel isoform of Vav, Vav-T, containing a single
 Schrodinger 3 domain in murine testicular germ cells";
 RL Oncogene 14:713-720(1997).
 CC -1-SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 DR EMBL; DB3266; BAA18950.1; -
 DR HSSP; Q60631; IGBO.
 DR MGD; MGI:98923; VAV.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.

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DR PRINTS; PRO0452; SH3DOMAIN.
DR ProDom; PD000093; SH2; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS00001; SH2; 1.
DR PROSITE; PS50002; SH3; 1.
KW SH3 domain.
SQ SEQUENCE 166 AA; 19434 MW; 2C3AF1FF07A5018F CRC64;

Query Match 15.8%; Score 93.5; DB 11; Length 166;
Best Local Similarity 32.9%; Pred. No. 0.019; 20; Indels 13; Gaps 3;
Matches 23; Conservative 14; Mismatches 21; Indels 13; Gaps 3;

QY 26 ARAQEDYNAPDCRFINVKKGQOIYVYSKLVTEAGAGAFWAGSYVYGDHDEMGIVGYPFN 85
DB 108 AKARYDFCARDBRELKSGDII---KILNKKGGQGMWGEIYGR-----IGMFPN 156
QY 86 LVREQRYVQE 95
DB 157 YVEED--YSE 164

RESULT 10
Q8R076 PRELIMINARY; PRT; 287 AA.
ID Q8R076
AC Q8R076;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Hypothetical 32.7 kDa protein.
GN VAV3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC027242; AAH27242.1; -.
DR MGI; MGI:1888518; VAV3.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR Pfam; PF00017; SH2; 1.
DR ProDom; PD000093; SH2; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 2.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 2.
KW Hypothetical protein.
SQ SEQUENCE 287 AA; 32662 MW; BF2850B8F921F048 CRC64;

Query Match 15.8%; Score 93.5; DB 11; Length 287;
Best Local Similarity 32.8%; Pred. No. 0.037;
Matches 22; Conservative 13; Mismatches 21; Indels 11; Gaps 2;

QY 23 ISLARAQEDYNAPDCRFINVKKGQOIYVYSKLVTEAGAGAFWAGSYVYGDHDEMGIVGYP 82
DB 230 LGAIARVDFCARDBRELKSGDII---SANGMWGEVNGR-----YGMF 278
QY 83 PSNLVRE 89
DB 279 PSTYVEE 285

RESULT 11
Q8VDU4 PRELIMINARY; PRT; 806 AA.
ID Q8VDU4
AC Q8VDU4;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)

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DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Similar to vav oncogene.
GN VAV.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
DR EMBL; BC020487; AAH20487.1; -.
DR MGI; MGI:98923; Vav.
DR InterPro; IPR005613; AIP3.
DR InterPro; IPR001715; Calponin-like.
DR InterPro; IPR003247; CH type.
DR InterPro; IPR002219; DAG_Pe-bind.
DR InterPro; IPR001331; GDS_CDC24.
DR InterPro; IPR001849; PH.
DR InterPro; IPR000219; RhogEF.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR003096; SM22_calponin.
DR Pfam; PF03915; AIP3; 1.
DR Pfam; PF00307; CH; 1.
DR Pfam; PF00130; DAG_Pe-bind; 1.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00621; RhogEF; 1.
DR PRINTS; PRO0452; SH3DOMAIN.
DR PRINTS; PRO0888; SM22CALPONIN.
DR ProDom; PD001527; CH type; 1.
DR ProDom; PD000093; SH2; 1.
DR ProDom; PD000066; SH3; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00109; C1; 1.
DR SMART; SM00326; SH3; 2.
DR PROSITE; PS50021; CH; 1.
DR PROSITE; PS00479; DAG_Pe BIND DOM 1; 1.
DR PROSITE; PS50081; DAG_Pe BIND_DOM 2; 1.
DR PROSITE; PS00741; DH_1; 1.
DR PROSITE; PS50010; DH_2; 1.
DR PROSITE; PS50003; PH DOMAIN; 1.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 2.
SQ SEQUENCE 806 AA; 93868 MW; F4368CD13A62D695 CRC64;

Query Match 15.8%; Score 93.5; DB 11; Length 806;
Best Local Similarity 32.9%; Pred. No. 0.13;
Matches 23; Conservative 14; Mismatches 20; Indels 13; Gaps 3;

QY 26 ARAQEDYNAPDCRFINVKKGQOIYVYSKLVTEAGAGAFWAGSYVYGDHDEMGIVGYPFN 85
DB 748 AKARYDFCARDBRELKSGDII---KILNKKGGQGMWGEIYGR-----IGMFPN 796
QY 86 LVREQRYVQE 95
DB 797 YVEED--YSE 804

RESULT 12
Q8BTV7 PRELIMINARY; PRT; 845 AA.
ID Q8BTV7
AC Q8BTV7;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE VAV proto-oncogene.
OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466651;
RA The FANTOM Consortium.
RT "The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AK088586; BAC0436.1;
SQ SEQUENCE 845 AA; 98093 MW; 5DDE0D9311DFB6B CRC64;

Query Match 15.8%; Score 93.5; DB 11; Length 845;
Best Local Similarity 32.9%; Pred. No. 0.14;
Matches 23; Conservative 14; Mismatches 20; Indels 13; Gaps 3;

QY 26 ARAQEDYNAPDCRFINKKGGQIYYYSKLVTEAGAFAGSVYGDHDEMGIYGVF 85
DB 767 AKARDPFCARDSESLKSGDIT---KILNKKGGCGMWRGRIYGR-----IGWFP 835
QY 86 LVREGRVYQE 95
DB 836 YVEED--YSE 843

RESULT 13
Q8UUX6 PRELIMINARY; PRT; 846 AA.
ID Q8UUX6;
AC Q8UUX6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE GDP/GTP exchange factor VAV3.
GN VAV3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxId=90311;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=11805146;
RA Inaba K., Ishai M., Scharenberg A.M., Freshney N., Downward J.,
RA Kurosaki T.;
RT "Vav3 Modulates B Cell Receptor Responses by Regulating
RT Phosphoinositide 3-Kinase Activation.";
RL J. Exp. Med. 195:199-200 (2002).
CC -1- SIMILARITY: CONTAINS 2 SH3 DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
DR EMBL; AY046915; AAL06249.1;
DR InterPro; IPR001715; Calponin-like.
DR InterPro; IPR003247; CH type.
DR InterPro; IPR000219; DAG_PE-bind.
DR InterPro; IPR001331; GDS_CDC24.
DR InterPro; IPR001849; PH.
DR InterPro; IPR000219; RhGEF.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR003096; SM22-calponin.
DR Pfam; PF00307; CH; 1.
DR Pfam; PF00130; DAG_PE-bind; 1.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00621; RhGEF; 1.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 1.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR PRINTS; PR00888; SM22CALPONIN.
DR ProDom; PD001527; CH type; 1.
DR ProDom; PD000093; SH2; 1.

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DR ProDom; PD000066; SH3; 1.
DR SMART; SM00109; C1; 1.
DR SMART; SM00033; CH; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00325; RhGEF; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 2.
DR PROSITE; PS50021; CH; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS00741; DH 1; 1.
DR PROSITE; PS50010; DH 2; 1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 2.
DR SH3 domain.
SQ SEQUENCE 846 AA; 97815 MW; C47E949D873821B CRC64;

Query Match 15.8%; Score 93.5; DB 13; Length 846;
Best Local Similarity 34.3%; Pred. No. 0.14;
Matches 23; Conservative 12; Mismatches 21; Indels 11; Gaps 2;

QY 23 ISLABQEDYNAPDCRFINKKGGQIYYYSKLVTEAGAFAGSVYGDHDEMGIYGVF 82
DB 789 IGILARIYDFCARDMSLSLKGDVVKIYTKM---SANGMWRGEVNGR-----VGWF 837
QY 83 PSNLVRE 89
DB 838 PSTYVEE 844

RESULT 14
Q96D37 PRELIMINARY; PRT; 719 AA.
ID Q96D37;
AC Q96D37;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Tissue=Placenta;
RA Straussberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 2 SH3 DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
DR EMBL; BC013361; AAH13361.1;
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR001331; GDS_CDC24.
DR InterPro; IPR001849; PH.
DR InterPro; IPR000219; RhGEF.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR Pfam; PF00130; DAG_PE-bind; 1.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00621; RhGEF; 1.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 2.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR ProDom; PD000093; SH2; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00109; C1; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00325; RhGEF; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 2.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.

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[illegible]

Search completed: December 29, 2003, 16:06:27
Job time : 16.9468 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OK protein - protein search, using sw model

Run on: December 29, 2003, 16:03:18 ; Search time 21.5686 Seconds
(without alignments)
809.506 Million cell updates/sec

Title: US-10-019-455A-49

Sequence: 591 1 HGMFMKLSKKLCADECV.....RVQVATKEIPTDIDFCE 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

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- 2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
- 3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
- 4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
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- 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
- 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|----------------------|
| 1 | 591 | 100.0 | 110 | 22 | Rat MLP protein se |
| 2 | 591 | 100.0 | 128 | 22 | Mouse MLP protein se |
| 3 | 574 | 97.1 | 110 | 22 | Mouse MLP protein |
| 4 | 574 | 97.1 | 128 | 22 | Human MLP protein |
| 5 | 541 | 91.5 | 110 | 22 | Human growth regul |
| 6 | 541 | 91.5 | 128 | 22 | Human MIP protein |
| 7 | 541 | 91.5 | 128 | 22 | Human angiotensin |
| 8 | 541 | 91.5 | 128 | 23 | Human PRO9873 prot |
| 9 | 541 | 91.5 | 128 | 23 | Human PRO9873 prot |

| | | | | | | |
|----|-------|------|------|----|----------|-----------------------|
| 10 | 541 | 91.5 | 128 | 23 | AAU83627 | Human PRO protein, |
| 11 | 541 | 91.5 | 128 | 23 | AAU09871 | Novel human secret |
| 12 | 515 | 87.1 | 105 | 22 | AAH83672 | Human growth regul |
| 13 | 462 | 78.2 | 87 | 22 | AAH69129 | Rat MLP protein regul |
| 14 | 264.5 | 44.8 | 131 | 16 | AAH69811 | Melanoma inhibiti |
| 15 | 264.5 | 44.8 | 131 | 22 | AAH65614 | Human MIA protein |
| 16 | 262.5 | 44.4 | 137 | 22 | AAH65615 | Recombinant human |
| 17 | 244.5 | 41.4 | 130 | 16 | AAH69812 | Melanoma inhibiti |
| 18 | 215 | 36.4 | 125 | 23 | AAH82119 | Mouse TANGO 130 MI |
| 19 | 215 | 36.4 | 303 | 22 | AAU29304 | Human PRO polypept |
| 20 | 215 | 36.4 | 303 | 22 | AAH87608 | Human PRO19670. H |
| 21 | 215 | 36.4 | 303 | 23 | ABG95933 | Human secreted/tira |
| 22 | 215 | 36.4 | 303 | 23 | ABH84994 | Human angiogenesis |
| 23 | 215 | 36.4 | 303 | 23 | ABU71392 | Human PRO19670 pro |
| 24 | 215 | 36.4 | 303 | 24 | ABU71588 | Human secreted pol |
| 25 | 215 | 36.4 | 303 | 24 | ABU72034 | Novel human secret |
| 26 | 215 | 36.4 | 303 | 24 | ABU72191 | Human PRO polypept |
| 27 | 215 | 36.4 | 303 | 24 | ABU65849 | Human secreted/tira |
| 28 | 215 | 36.4 | 303 | 24 | ABU66182 | Novel human secret |
| 29 | 215 | 36.4 | 303 | 24 | ABU67686 | Human secreted/tira |
| 30 | 215 | 36.4 | 303 | 24 | ABU65544 | Human PRO polypept |
| 31 | 215 | 36.4 | 303 | 24 | ABU58680 | Human secreted/tira |
| 32 | 215 | 36.4 | 303 | 24 | ABU56216 | Human PRO polypept |
| 33 | 215 | 36.4 | 303 | 24 | ABU57211 | Human secreted/tira |
| 34 | 215 | 36.4 | 303 | 24 | ABU10790 | Human secreted/tira |
| 35 | 215 | 36.4 | 714 | 21 | AAV70209 | Murine TANGO 130 p |
| 36 | 215 | 36.4 | 714 | 21 | AAV70209 | Human TANGO 130 MI |
| 37 | 215 | 36.4 | 138 | 22 | AAH25834 | Human TANGO 130 pr |
| 38 | 208.5 | 35.3 | 125 | 23 | AAH82120 | Human TANGO 130 po |
| 39 | 207.5 | 35.1 | 125 | 23 | AAH82120 | Human TANGO 130 po |
| 40 | 207.5 | 35.1 | 410 | 23 | ABH82118 | Human TANGO 130 po |
| 41 | 207.5 | 35.1 | 410 | 23 | ABH82118 | Human TANGO 130 po |
| 42 | 207.5 | 35.1 | 1907 | 22 | AAH29319 | Human PRO polypept |
| 43 | 199 | 33.7 | 499 | 24 | ABU71407 | Human PRO20088 pro |
| 44 | 199 | 33.7 | 499 | 24 | ABU58684 | Human secreted/tira |
| 45 | 199 | 33.7 | 499 | 24 | ABU58684 | Human secreted/tira |

ALIGNMENTS

RESULT 1
ID AAB69131 standard; Protein; 110 AA.

AC AAB69131;

DT 23-APR-2001 (first entry)

DE Rat MLP protein sequence SEQ ID NO:49.

KW MLP: MIA; melanoma inhibitory activity; cancer; bone disease;

KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;

KW cardiant; gene therapy; secretory cell function regulator; promoter;

KW inhibitor.

OS Rattus sp.

PN WC0200102564-A1.

PD 11-JAN-2001.

PF 29-JUN-2000; 2000WO-JP04278.

PR 30-JUN-1999; 99JP-0186718.

PA (TAKE) TAKEDA CHEM IND LTD.

PI Itoh Y, Niishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;

DR WPI; 2001-159271/16.

DR N-PSDB; AAF59039.


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xx Safe, low-toxicity secretory cell function-regulatory protein and
PT encoded DNA, applicable as drugs, in diagnosis and development of
PT promoters and inhibitors for preventing or treating e.g. bone and joint
PT diseases -
xx
xx Claim 5; Page 107; 11pp; Japanese.
xx
xx The present invention describes novel MLP proteins and their encoding
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
CC activities, and can be used in gene therapy and as secretory cell
CC function regulators. The MLP proteins and DNAs can be used in drugs, in
CC the diagnosis and development of promoters and inhibitors for preventing
CC or treating bone and joint diseases as well as pathologic angiogenesis.
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
CC in the exemplification of the present invention.
CC
xx
xx Sequence 110 AA;
SQ
Query Match 100.0%; Score 591; DB 22; Length 110;
Best Local Similarity 100.0%; Pred. No. 2.6e-68;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY 1 HGMPFMDKLSKKLCADDECVYITSLARQEDYNAPDCRFINVKKGQQLVYYSKLVTENGA 60
Db 1 HGMPFMDKLSKKLCADDECVYITSLARQEDYNAPDCRFINVKKGQQLVYYSKLVTENGA 60
QY 61 GAFWAGSYVGDHQDEMGIVGYFPFNSLVREQRVYQCATKEIPTTDIDFCE 110
Db 61 GAFWAGSYVGDHQDEMGIVGYFPFNSLVREQRVYQCATKEIPTTDIDFCE 110
RESULT 2
AAB69130
ID AAB69130 standard; Protein; 128 AA.
AC AAB69130;
XX
DT 23-APR-2001 (first entry)
XX
DE Rat MLP protein sequence SEQ ID NO:47.
XX
XX MLP; MA; melanoma inhibitory activity; cancer; bone disease;
KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
KW cardiac; gene therapy; secretory cell function regulator; promoter;
XX inhibitor.
XX
OS Rattus sp.
XX
XX WO200102564-A1.
XX
XX 11-JAN-2001.
XX
XX 29-JUN-2000; 2000MO-JP04278.
XX
XX 30-JUN-1999; 99JP-0186718.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
PA
PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K,
PI Tanaka H;
XX
XX WPI; 2001-159271/16.
DR N-PSDB; AAF59098.
XX
PT Safe, low-toxicity secretory cell function-regulatory protein and
PT encoded DNA, applicable as drugs, in diagnosis and development of
PT promoters and inhibitors for preventing or treating e.g. bone and joint
PT diseases -
xx
xx Claim 6; Page 106; 11pp; Japanese.
xx
xx The present invention describes novel MLP proteins and their encoding

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| | |
|-----------|--|
| CC | DNA's. The MLP proteins and DNAs have antiinflammatory and cardiant |
| CC | activities, and can be used in gene therapy and as secretory cell |
| CC | function regulators. The MLP proteins and DNAs can be used in drugs, in |
| CC | the diagnosis and development of promoters and inhibitors for preventing |
| CC | or treating bone and joint diseases as well as pathologic angiogenesis. |
| CC | AAFS9063 to AAFS9099 and AAB69122 to AAB69132 represent sequences used |
| CC | in the exemplification of the present invention. |
| XX | |
| SQ | Sequence 128 AA: |
| | |
| | Query Match 100.0%; Score 591; DB 22; Length 128; |
| | Best Local Similarity 100.0%; Pred. No. 3, 2e-68; |
| | Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| Qy | 1 HGMFMDKLSSKKLCADCECVYTITSLAPAQEDYNAPDCRFINVKKGGQIIVYYSKLVTENGA 60 |
| Db | 19 HGMFMDKLSSKKLCADCECVYTITSLAPAQEDYNAPDCRFINVKKGGQIIVYYSKLVTENGA 78 |
| Qy | 61 GAFNAGSYGDDHGDENGIVGCFPSNLVREQRVYVGATKEIPTDIDPFCE 110 |
| Db | 79 GAFNAGSYGDDHGDENGIVGCFPSNLVREQRVYVGATKEIPTDIDPFCE 128 |
| | |
| | RESULT 3 |
| AAAB69127 | |
| ID | AAAB69127 standard; Protein; 110 AA. |
| XX | |
| AC | AAAB69127; |
| XX | |
| DT | 23-APR-2001 (first entry) |
| XX | |
| DE | Mouse MLP protein sequence SEQ ID NO:26. |
| XX | |
| XX | MLP; MIA; melanoma inhibitory activity; cancer; bone disease; |
| KM | joint disease; pathologic angiogenesis; diagnosis; antiinflammatory; |
| KM | cardiant; gene therapy; secretory cell function regulator; promoter; |
| KM | inhibitor. |
| XX | |
| OS | Mus musculus. |
| XX | |
| XX | WO200102564-A1. |
| PN | 11-JAN-2001. |
| XX | |
| PD | 29-JUN-2000; 2000WO-JP04278. |
| PF | |
| XX | 30-JUN-1999; 99JP-0186718. |
| PR | |
| XX | (TAKE) TAKEDA CHEM IND LTD. |
| PA | |
| PI | Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K; |
| PI | Tanaka H; |
| DR | WPI; 2001-159271/16. |
| DR | N-PSDB; AAFS9080. |
| PT | |
| PT | Safe, low-toxicity secretory cell function-regulatory protein and |
| PT | encoded DNA, applicable as drugs, in diagnosis and development of |
| PT | promoters and inhibitors for preventing or treating e.g. bone and joint |
| PT | diseases - |
| XX | |
| PS | |
| XX | Claim 3; Page 98-99; 11pp; Japanese. |
| CC | |
| CC | The present invention describes novel MLP proteins and their encoding |
| CC | DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant |
| CC | activities, and can be used in gene therapy and as secretory cell |
| CC | function regulators. The MLP proteins and DNAs can be used in drugs, in |
| CC | the diagnosis and development of promoters and inhibitors for preventing |
| CC | or treating bone and joint diseases as well as pathologic angiogenesis. |
| CC | AAFS9063 to AAFS9099 and AAB69122 to AAB69132 represent sequences used |
| CC | in the exemplification of the present invention. |
| XX | |
| SQ | Sequence 110 AA: |

Query Match 97.1%; Score 574; DB 22; Length 110;
 Best Local Similarity 96.4%; Pred. No. 4.2e-66;
 Matches 106; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 HGFMDKLSKKLCADEECVYTTISLAAQEDYNAPDCRFINVKGGQIYVYSKLVTENGA 60
 DB 1 HGFMDKLSKKLCADEECVYTTISLAAQEDYNAPDCRFIDVKKGGQIYVYSKLVTENGA 60

QY 61 GAFWAGSVYGDHODEMGIVGFPSPNLVREORVYQEAATKEIPTTIDIFFCE 110
 DB 61 GEFWAGSVYGDHODEMGIVGFPSPNLVREORVYQEAATKEIPTTIDIFFCE 110

RESULT 4
 AAB69125
 ID AAB69125 standard; Protein; 128 AA.
 AC AAB69125;
 DT 23-APR-2001 (first entry)
 DE Mouse MLP protein sequence SEQ ID NO:12.
 XX
 XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
 XX joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
 XX cardiant; gene therapy; secretory cell function regulator; promoter;
 XX inhibitor.
 XX Mus musculus.
 XX WO200102564-A1.
 XX PD 11-JAN-2001.
 XX PF 29-JUN-2000; 2000WO-JP04278.
 XX PR 30-JUN-1999; 99JP-0186718.
 XX (TAKE) TAKEDA CHEM IND LTD.
 XX PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
 XX Tanaka H;
 XX WPI: 2001-159271/16.
 XX DR N-PSDB; AAF59068.
 XX Safe, low-toxicity secretory cell function-regulatory protein and
 XX encoded DNA, applicable as drugs, in diagnosis and development of
 XX promoters and inhibitors for preventing or treating e.g. bone and joint
 XX diseases -
 XX Claim 4; Page 93-94; 111pp; Japanese.
 XX The present invention describes novel MLP proteins and their encoding
 XX DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
 XX activities, and can be used in gene therapy and as secretory cell
 XX function regulators. The MLP proteins and DNAs can be used in drugs, in
 XX the diagnosis and development of promoters and inhibitors for preventing
 XX or treating bone and joint diseases as well as pathologic angiogenesis.
 XX CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
 XX in the exemplification of the present invention.
 XX Sequence 128 AA;

Query Match 97.1%; Score 574; DB 22; Length 128;
 Best Local Similarity 96.4%; Pred. No. 5.1e-66;
 Matches 106; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 HGFMDKLSKKLCADEECVYTTISLAAQEDYNAPDCRFINVKGGQIYVYSKLVTENGA 60
 DB 19 HGFMDKLSKKLCADEECVYTTISLAAQEDYNAPDCRFIDVKKGGQIYVYSKLVTENGA 78

QY 61 GAFWAGSVYGDHODEMGIVGFPSPNLVREORVYQEAATKEIPTTIDIFFCE 110
 DB 79 GEFWAGSVYGDHODEMGIVGFPSPNLVREORVYQEAATKEIPTTIDIFFCE 128

RESULT 5
 AAB69126
 ID AAB69126 standard; Protein; 110 AA.
 AC AAB69126;
 DT 23-APR-2001 (first entry)
 DE Human MLP protein sequence SEQ ID NO:24.
 XX
 XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
 XX joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
 XX cardiant; gene therapy; secretory cell function regulator; promoter;
 XX inhibitor.
 XX Homo sapiens.
 XX WO200102564-A1.
 XX PD 11-JAN-2001.
 XX PF 29-JUN-2000; 2000WO-JP04278.
 XX PR 30-JUN-1999; 99JP-0186718.
 XX (TAKE) TAKEDA CHEM IND LTD.
 XX PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
 XX Tanaka H;
 XX WPI: 2001-159271/16.
 XX DR N-PSDB; AAF59079.
 XX Safe, low-toxicity secretory cell function-regulatory protein and
 XX encoded DNA, applicable as drugs, in diagnosis and development of
 XX promoters and inhibitors for preventing or treating e.g. bone and joint
 XX diseases -
 XX Claim 1; Page 97-98; 111pp; Japanese.
 XX The present invention describes novel MLP proteins and their encoding
 XX DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
 XX activities, and can be used in gene therapy and as secretory cell
 XX function regulators. The MLP proteins and DNAs can be used in drugs, in
 XX the diagnosis and development of promoters and inhibitors for preventing
 XX or treating bone and joint diseases as well as pathologic angiogenesis.
 XX CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
 XX in the exemplification of the present invention.
 XX Sequence 110 AA;

Query Match 91.5%; Score 541; DB 22; Length 110;
 Best Local Similarity 89.1%; Pred. No. 7.8e-62;
 Matches 98; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 HGFMDKLSKKLCADEECVYTTISLAAQEDYNAPDCRFINVKGGQIYVYSKLVTENGA 60
 DB 1 HGFMDKLSKKLCADEECVYTTISLAAQEDYNAPDCRFINVKGGQIYVYSKLVTENGA 60

QY 61 GAFWAGSVYGDHODEMGIVGFPSPNLVREORVYQEAATKEIPTTIDIFFCE 110
 DB 61 GEFWAGSVYGDHODEMGIVGFPSPNLVREORVYQEAATKEIPTTIDIFFCE 110

RESULT 6
 AAB62671
 ID AAB62671 standard; Protein; 128 AA.
 XX

AC AAB82671;
 XX 02-OCT-2001 (first entry)
 XX
 DE Human growth regulatory-like polypeptide.
 XX Growth regulatory-like polypeptide; human; cartilage; melanoma;
 KM neuroectodermal tumour; glioma; cancer; therapy; diagnosis.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..23
 FT /label= signal_peptide
 FT Protein 24..128
 FT /label= Mature Protein
 FT /note= "separately claimed in Claim 10"
 XX
 PN WO200155332-A2.
 XX
 PD 02-AUG-2001.
 XX
 PF 25-JAN-2001; 2001WO-US02455.
 XX
 PR 25-JAN-2000; 2000US-0491404.
 PR 02-MAY-2000; 2000US-0563786.
 XX
 PA (HYSEQ-) HYSEQ INC.
 XX
 PI Mize NK, Boyle BJ, Arterburn MC, Tang YT, Liu C;
 PI Dimaac RT;
 DR WPI: 2001-483233/52.
 DR N-PSDB; AAB26343.
 XX
 PT Isolated human growth regulatory-like polypeptide useful for treating
 PT e.g. Alzheimer's disease, cancer, autoimmune disorders,
 PT hyperproliferative disorders, coagulation disorders, and nervous system
 PT disorders -
 XX
 PS Claim 10; Page 116-117; 119pp; English.
 XX
 CC The present sequence is that of a novel human growth regulatory-like
 CC polypeptide (GRP). The amino acid sequence is predicted from a
 CC novel assembled cDNA (see AAB26343) based on Hyseq clone number
 CC 13372272. The protein has a mol. wt. of 14 kDa unglycosylated. GRP
 CC belongs to the same protein family as growth regulatory proteins,
 CC growth factors, human melanoma derived growth regulatory protein
 CC precursor (64% similarity and 45% identity over 111 amino acids)
 CC or melanoma inhibitory activity, cattle cartilage-derived
 CC retinoic acid sensitive protein (CD-RAP, 44% identity and 64%
 CC similarity over 126 amino acids) and other retinoic acid-sensitive
 CC proteins. GRP polypeptides and polynucleotides of the invention
 CC can be used in the prophylaxis, treatment (including gene therapy)
 CC and diagnosis of disorders and diseases caused by, or involving,
 CC cartilage development and maintenance, inhibition of melanoma cell
 CC growth and tumours, including neuroectodermal tumours such as
 CC gliomas. The polypeptides, which include the GRP mature protein,
 CC may also have nutritional uses, cytokine and cell proliferation
 CC or differentiation activity, stem cell growth factor activity,
 CC haematopoietic regulating activity, tissue growth activity,
 CC immunosuppressive or immunostimulant activity, activin/inhibin
 CC activity, chemotactic/chemokinetic activity, haemostatic and
 CC thrombolytic activity, use in cancer diagnosis and therapy,
 CC drug screening, receptor/ligand activity, antiinflammatory
 CC activity, and treatment of leukaemia, nervous system disorders,
 CC arthritis and inflammation.
 XX
 SQ Sequence 128 AA;

QY 1 HGMFMDKLSKKLCADEECVYTTISLAQEDYNAPDCRFINVKKGQIYVSKLVENG 60
 DB 19 HGIFMDRLASKKLCADCECVYTTISLAQEDYNAPDCRFINVKKGQIYVSKLVENG 78
 QY 61 GAFWAGSVYGDHODMGIVGFPNSLVREORVYQATKEIPTTIDIFFCE 110
 DB 79 GEFWAGSVYGDGQDEMGVGVFPNVLVREORVYQATKEVPTTIDIFFCE 128
 RESULT 7
 AAB69123
 ID AAB69123 standard; Protein, 128 AA.
 AC AAB69123;
 XX
 DT 23-APR-2001 (first entry)
 XX
 DE Human MLP protein sequence SEQ ID NO:6.
 XX
 KM MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
 KM joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
 KM cartiant; gene therapy; secretory cell function regulator; promoter;
 KM inhibitor.
 XX
 OS Homo sapiens.
 XX
 PN WO200102564-A1.
 XX
 PD 11-JAN-2001.
 XX
 PF 29-JUN-2000; 2000WO-JP04278.
 XX
 PR 30-JUN-1999; 99JP-0186718.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
 PI Tanaka H;
 XX
 DR WPI: 2001-159271/16.
 DR N-PSDB; AAF59065.
 XX
 PT Safe, low-toxicity secretory cell function-regulatory protein and
 PT encoded DNA, applicable as drugs, in diagnosis and development of
 PT promoters and inhibitors for preventing or treating e.g. bone and joint
 PT diseases -
 XX
 PS Claim 2; Page 91-92; 111pp; Japanese.
 XX
 CC The present invention describes novel MLP proteins and their encoding
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
 CC activities, and can be used in gene therapy and as secretory cell
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in
 CC the diagnosis and development of promoters and inhibitors for preventing
 CC or treating bone and joint diseases as well as pathologic angiogenesis.
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
 CC in the exemplification of the present invention.
 XX
 SQ Sequence 128 AA;

Query Match 91.5%; Score 541; DB 22; Length 128;
 Best Local Similarity 89.1%; Pred. No. 9.7e-62;
 Matches 98; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 61 GAFWAGSVYGDHODMGIVGFPNSLVREORVYQATKEIPTTIDIFFCE 110
 DB 79 GEFWAGSVYGDGQDEMGVGVFPNVLVREORVYQATKEVPTTIDIFFCE 128

RESULT 8
 ABB95602
 ID ABB95602 standard; Protein; 128 AA.
 XX
 AC ABB95602;
 XX
 DT 19-JUL-2002 (first entry)
 XX
 DE Human angiogenesis related protein PRO9873 SEQ ID NO: 360.
 XX
 KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
 KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
 KW cardiac; cytosolic; antiangiogenic; hypotensive; vulnery;
 KW antiarteriosclerotic.
 XX
 OS Homo sapiens.
 XX
 PN WO200208284-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 09-JUL-2001; 2001WO-US21735.
 XX
 PR 20-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 25-JUL-2000; 2000US-22064P.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 02-AUG-2000; 2000US-222695P.
 PR 17-AUG-2000; 2000US-0643657.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 07-SEP-2000; 2000WO-US23328.
 PR 15-SEP-2000; 2000US-230978P.
 PR 18-SEP-2000; 2000US-0664610.
 PR 24-OCT-2000; 2000US-242922P.
 PR 08-NOV-2000; 2000US-0709238.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000US-0747259.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 22-JAN-2001; 2001US-0767809.
 PR 28-FEB-2001; 2001US-0796498.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 09-MAR-2001; 2001US-0803706.
 PR 14-MAR-2001; 2001US-0808689.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 30-MAY-2001; 2001US-0870574.
 PR 30-MAY-2001; 2001WO-US17443.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 28-JUN-2001; 2001WO-US00000.
 XX
 PA (GETH) GENENTECH INC.
 PA (BAKE) BAKER K P.
 PA (FERR) FERRARA N.
 PA (GERB) GERBER H.
 PA (GERR) GERRITSEN M E.
 PA (GODD) GODDARD A.
 PA (GODD) GODDARD P J.
 PA (GURN) GURNEY A L.
 PA (HILL) HILLAN K J.
 PA (MARS) MARSTERS S A.
 PA (PANJ) PAN J.

PA (PAON) PAONI N F.
 PA (STEP) STEPHAN J F.
 PA (WATA) WATANABE C K.
 PA (WILL) WILLIAMS P M.
 PA (WOOD) WOOD W I.
 XX
 PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
 PI Goddard PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W.
 XX
 DR MPI; 2002-171999/22.
 DR N-PSDB; ABL95740.
 XX
 PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal -
 XX
 PS Claim 11; Fig 360; 567pp; English.
 XX
 CC The present invention provides the protein and coding sequences of human
 CC PRO proteins. These are useful for treating or diagnosing a
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac
 CC hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The present sequence is a PRO protein of the invention.
 XX
 SQ Sequence 128 AA;
 Query Match 91.5%; Score 541; DB 23; Length 128;
 Best Local Similarity 89.1%; Pred. No. 9,7e-62;
 Matches 98; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
 QY 1 HGFMNDLSSKKLCADSECYTITSLAAQEDNNAAPDPRFINVKKGOIYYSKLWENGA 60
 DB 19 HGIFMDRLASKKLCADSECYTITSLAAQEDNNAAPDPRFINVKKGOIYYSKLWENGA 78
 QY 61 GAFWAGSVYGDHDEMGIVGPPSNLYREQRYQEAATKEPTTDIDPFCE 110
 DB 79 GEFWAGSVYGDQDDEMGVGFPRNLVKEQRYQEAATKEVPTTDIDPFCE 128
 XX
 RESULT 9
 ABB84996
 ID ABB84996 standard; Protein; 128 AA.
 XX
 AC ABB84996;
 XX
 DT 16-MAY-2002 (first entry)
 XX
 DE Human PRO9873 protein sequence SEQ ID NO:360.
 XX
 KW Human; angiogenesis; cardiac; cytosolic; antiangiogenic; hypotensive;
 KW vulnery; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
 KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
 KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
 KW age-related macular degeneration; arterial restenosis; angina;
 KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
 KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
 KW wound healing; chromosome mapping; gene mapping.
 XX
 OS Homo sapiens.
 XX
 PN WO200200690-A2.
 XX
 PD 03-JAN-2002.
 XX
 PF 20-JUN-2001; 2001WO-US19692.
 XX
 PR 23-JUN-2000; 2000US-213637P.
 PR 20-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220624P.

PR 25-JUL-2000; 2000US-220664P.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 02-AUG-2000; 2000US-222695P.
 PR 17-AUG-2000; 2000US-0643657.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23522.
 PR 07-SEP-2000; 2000WO-US23078P.
 PR 18-SEP-2000; 2000US-0664610.
 PR 18-SEP-2000; 2000US-0665350.
 PR 24-OCT-2000; 2000US-242922P.
 PR 08-NOV-2000; 2000US-0709238.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000US-0747259.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 22-JAN-2001; 2001US-0767609.
 PR 28-FEB-2001; 2001US-0796498.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06566.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0808689.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0842208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001US-0866034.
 PR 25-MAY-2001; 2001US-0866034.
 PR 30-MAY-2001; 2001US-0870574.
 PR 30-MAY-2001; 2001WO-US17443.
 PR 01-JUN-2001; 2001WO-US17800.
 XX
 PA (GENTECH) GENENTECH INC.
 PI Baker KP, Ferrara N, Gerber H, Gertlisen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Masters SA, Pan J, Paoni NF,
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W,
 XX
 DR WPI; 2002-090516/12.
 DR N-PSDB; ABL88251.
 XX
 PT One hundred and eighty seven nucleic acids encoding PRO polypeptides.
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal.
 XX
 PS Claim 11; Fig 360; 565pp; English.
 PS
 CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
 CC ABB85003. The PRO proteins and polynucleotides have cardiac, cytosolic,
 CC antiangiogenic, hypotensive, vulnery and antiarteriosclerotic
 CC activities, and can be used in gene therapy. The PRO polynucleotides,
 CC proteins, agonists and antagonists are useful for treating or diagnosing
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal.
 CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular
 CC degeneration, atherosclerosis, hypertension, arterial restenosis,
 CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
 CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
 CC carcinoma) and wound healing. The PRO polynucleotides have applications
 CC in molecular biology, including use as hybridisation probes, and in
 CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
 CC probes used in the exemplification of the present invention.
 CC
 XX
 SQ Sequence 128 AA;

Query Match 91.5%; Score 541; DB 23; Length 128;
 Best Local Similarity 89.1%; Pred. No. 9,7e-62;
 Matches 99; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

CY 1 HGFPMKLSKSKLCADEECYTTISLAPQEDYNAPPCRFINVKKGQGIYVYSKLVYENGA 60
 DB 19 HGIFMRLASKKLCADEECYTTISLAPQEDYNAPPCRFINVKKGQGIYVYSKLVYENGA 78

QY 61 GAFMAGSYGDHODEMIGVYFPNSNLVREQRYOEAITEPTDIDFCE 110
 DB 79 GEFMAGSYGDGQODEMVGWYFPRNLVREQRYOEAITEVPTDIDFCE 128
 RESULT 10
 AAU83627
 ID AAU83627 standard; Protein; 128 AA.
 XX
 AC AAU83627;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Human PRO protein, Seq ID No 72.
 XX
 KM Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
 KM breast cancer; prostate tumour; rectal tumour; liver tumour;
 KM pericyte cell proliferation; chondrocyte cell proliferation;
 KM tumour necrosis factor-alpha.
 XX
 OS Homo sapiens.
 XX
 PN WO200208288-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 29-JUN-2001; 2001WO-US21066.
 XX
 PR 20-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220585P.
 PR 25-JUL-2000; 2000US-220605P.
 PR 25-JUL-2000; 2000US-220607P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 25-JUL-2000; 2000US-220638P.
 PR 25-JUL-2000; 2000US-220664P.
 PR 25-JUL-2000; 2000US-220666P.
 PR 26-JUL-2000; 2000US-220893P.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 15-SEP-2000; 2000US-000000P.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 28-NOV-2000; 2000US-253646P.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000US-0747259.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001WO-US17092.
 XX
 PA (GENTECH) GENENTECH INC.
 PI Baker KP, Desnoyers L, Gertlisen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX
 DR WPI; 2002-172001/22.
 DR N-PSDB; ABL83571.
 XX
 PT One hundred and twenty two nucleic acids encoding PRO polypeptides.
 PT useful for treating a PRO related disorder and for diagnosing tumours
 PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
 PT tumour or liver tumour.
 XX
 PS Claim 11; Figure 72; 359pp; English.
 PS
 CC The invention relates to one hundred and twenty two nucleic acids
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
 CC agonists and antagonists are useful for treating a PRO related disorder.
 CC The PRO polypeptides are useful for diagnosing tumours, especially lung
 CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. The PRO polypeptides are useful for stimulating the
 CC proliferation of, or gene expression, in pericyte cells, for stimulating

CC the proliferation or differentiation of chondrocyte cells, for
 CC stimulating the release of tumour necrosis factor-alpha from human blood,
 CC for stimulating or inhibiting the proliferation of normal human dermal
 CC fibroblast cells. The PRO polypeptide may also be used as molecular
 CC weight markers and for tissue typing. The PRO nucleic acids have
 CC applications in molecular biology, including use as hybridisation probes,
 CC and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
 CC protein sequences of the invention.

XX
 SQ Sequence 128 AA;

Query Match 91.5%; Score 541; DB 23; Length 128;
 Best Local Similarity 89.1%; Pred. No. 9.7e-62;
 Matches 98; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

OY 1 HGFMFMDKLSKKLCADEECVYTTISLARAQEDYNAPDCRFINVKKGQIYYYSKLVTENGA 60
 DB 19 HGIFMDRLASKKLCADDECVYTTISLASAQEDYNAPDCRFINVKKGQIYYYSKLVTENGA 78
 OY 61 GAFMAGSVYGDHODEMGIVGFPPSNLVREQRYOEAATKEIPTTIDIFFCE 110
 DB 79 GEFMAGSVYGDGODEMGVGFPPSNLVREQRYOEAATKEIPTTIDIFFCE 128

RESULT 11
 AAU09871

ID AAU09871 standard; Protein; 128 AA.

XX
 AC AAU09871;

DT 26-FEB-2002 (first entry)

XX
 DE Novel human secreted protein #12.

XX
 KM Secreted protein; cytosolic; immunosuppressive; vulnerrary; vaccine;
 KM antiinflammatory; neuroprotective; nephrotropic; cardiovascular;
 KM human; cancer; autoimmune disease; wound healing disorder; infection;
 KM haematopoietic disorder; inflammatory disorder; infertility;
 KM neurological disease; psychiatric disease; cardiovascular disease;
 KM respiratory disease; renal; gastrointestinal.

XX
 OS Homo sapiens.

XX
 PN WO200179454-A1.

XX
 PD 25-OCT-2001.

XX
 PF 11-APR-2001; 2001WO-US11797.

XX
 PR 13-APR-2000; 2000US-196603P.

XX
 PR 24-APR-2000; 2000US-199417P.

XX
 PA (SMK) SMITHKLINE BEECHAM CORP.

XX
 PA (SMK) SMITHKLINE BEECHAM PLC.

XX
 PI Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;

XX
 DR WPI; 2002-061975/08.

XX
 DR N-PSDB; AAS17583.

XX
 PT New secreted proteins or polypeptides, useful for treating e.g. cancer,
 PT autoimmune diseases, wound healing disorder; infections, haematopoietic
 PT disorders, inflammatory disorders, infertility, cancer

XX
 PS Claim 1; Page 73-74; 92pp; English.

XX
 CC The invention relates to an isolated novel secreted polypeptide (I) and
 CC polynucleotide (II). (I) and (II) are useful for treating cancer,
 CC autoimmune diseases, wound healing disorder, infections, haematopoietic
 CC disorders, inflammatory disorders, infertility, neurological and
 CC psychiatric diseases, cardiovascular diseases, respiratory diseases,
 CC renal diseases, or gastrointestinal diseases. These may also be used to
 CC treat diseases, abnormalities and disorders caused by abnormal

CC expression, production, function and/or metabolism of the genes, as
 CC vaccines for inducing immunological response in a mammal, and in
 CC screening methods for detecting the effect of added compounds on the
 CC production of mRNA and polypeptide in cells. The polypeptides can be used
 CC as immunogens to produce antibody immunospecific for the polypeptides,
 CC and to identify membrane-bound or soluble receptors. The polynucleotides
 CC may be used as diagnostic reagents, in chromosome localisation studies,
 CC and in tissue expression studies. The present sequence represents the
 CC amino acid sequence of novel human secreted protein #12.

XX
 SQ Sequence 128 AA;

Query Match 91.5%; Score 541; DB 23; Length 128;
 Best Local Similarity 89.1%; Pred. No. 9.7e-62;
 Matches 98; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

OY 1 HGFMFMDKLSKKLCADEECVYTTISLARAQEDYNAPDCRFINVKKGQIYYYSKLVTENGA 60
 DB 19 HGIFMDRLASKKLCADDECVYTTISLASAQEDYNAPDCRFINVKKGQIYYYSKLVTENGA 78
 OY 61 GAFMAGSVYGDHODEMGIVGFPPSNLVREQRYOEAATKEIPTTIDIFFCE 110
 DB 79 GEFMAGSVYGDGODEMGVGFPPSNLVREQRYOEAATKEIPTTIDIFFCE 128

RESULT 12

AAB82672
 ID AAB82672 standard; Protein; 105 AA.

XX
 AC AAB82672;

DT 02-OCT-2001 (first entry)

XX
 DE Human growth regulatory-like polypeptide (mature protein).

XX
 KM Growth regulatory-like polypeptide; human; cartilage; melanoma;
 KM neuroectodermal tumour; glioma; cancer; therapy; diagnosis.

XX
 OS Homo sapiens.

XX
 PN WO200155332-A2.

XX
 PD 02-AUG-2001.

XX
 PF 25-JAN-2001; 2001WO-US02455.

XX
 PR 25-JAN-2000; 2000US-0491404.

XX
 PR 02-MAY-2000; 2000US-0563786.

XX
 PA (HYSE-) HYSEQ INC.

XX
 PI Mize NK, Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C;

XX
 PI Dermanac RT;

XX
 DR WPI; 2001-483233/52.

XX
 DR N-PSDB; AAB26343.

XX
 PT Isolated human growth regulatory-like polypeptide useful for treating
 PT e.g. Alzheimer's disease, cancer, autoimmune disorders,
 PT hyperproliferative disorders, coagulation disorders, and nervous system
 PT disorders

XX
 PS Claim 10; Page 117; 119pp; English.

XX
 CC The present sequence is that of a novel human growth regulatory-like
 CC polypeptide (GRLP) mature protein. The sequence is predicted from
 CC a novel assembled cDNA (see AAB26343) based on Hyseq clone number
 CC 16372272. The protein has a mol.wt. of 14 kDa unglycosylated. GRLP
 CC belongs to the same protein family as growth regulatory proteins,
 CC growth factors, human melanoma derived growth regulatory proteins,
 CC precursor (64% similarity and 45% identity over 111 amino acids)
 CC or melanoma inhibitory activity, cattle cartilage-derived
 CC retinoic acid sensitive protein (CD-RAP, 44% identity and 64%

CC similarity over 126 amino acids) and other retinoic acid-sensitive
 CC proteins. GRP polypeptides and polynucleotides of the invention
 CC can be used in the prophylaxis, treatment (including gene therapy)
 CC and diagnosis of disorders and diseases caused by, or involving,
 CC cartilage development and maintenance, inhibition of melanoma cell
 CC growth and tumours, including neuroectodermal tumours such as
 CC gliomas. The polypeptides, which include the GRP mature protein,
 CC may also have nutritional uses, cytokine and cell proliferation
 CC or differentiation activity, stem cell growth factor activity,
 CC haematopoietic regulating activity, tissue growth activity,
 CC immunosuppressive or immunostimulant activity, activating/inhibin
 CC activity, chemotactic/chemokinetic activity, haemostatic and
 CC thrombolytic activity, use in cancer diagnosis and therapy,
 CC drug screening, receptor/ligand activity, antiinflammatory
 CC activity, and treatment of leukaemia, nervous system disorders,
 CC arthritis and inflammation.

XX Sequence 105 AA;

Query Match 87.1%; Score 515; DB 22; Length 105;
 Best Local Similarity 89.5%; Pred. No. 1.7e-58;
 Matches 94; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 6 DKLSSKLCADBECCYTTISLARAQEDYNAPDCRFINVKKGQIYVSKLVTENGAGAFWA 65
 DB 1 DRLASKKLCADDECCYTTISLASAQEDYNAPDCRFINVKKGQIYVSKLVKENGAGAFWA 60

QY 66 GSVYGDHODEMGIVGFPSNLVREQRYCEATKEIPTDIDFCE 110
 DB 61 GSVYGDGODEMGIVGFPSNLVREQRYCEATKEIPTDIDFCE 105

RESULT 13

AAB69129 ID AAB69129 standard; Protein: 87 AA.

AC AAB69129;

DT 23-APR-2001 (first entry)

DE Rat MUP protein sequence SEQ ID NO:39.

KM MUP; MIA; melanoma inhibitory activity; cancer; bone disease;

KM joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;

KM cardiant; gene therapy; secretory cell function regulator; promoter;

XX inhibitor.

OS Rattus sp.

XX WO200102564-A1.

PD 11-JAN-2001.

PF 25-JUN-2000; 2000WO-JP04278.

PR 30-JUN-1999; 99JP-0186718.

PA (TAKE) TAKEDA CHEM IND LTD.

PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K,

PI Tanaka H;

XX WPI; 2001-159271/16.

XX Safe, low-toxicity secretory cell function-regulatory protein and

XX encoded DNA, applicable as drugs, in diagnosis and development of

XX promoters and inhibitors for preventing or treating e.g. bone and joint

XX diseases -

CC activities, and can be used in gene therapy and as secretory cell
 CC function regulators. The MUP proteins and DNAs can be used in drugs, in
 CC the diagnosis and development of promoters and inhibitors for preventing
 CC or treating bone and joint diseases as well as pathologic angiogenesis.
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
 CC in the exemplification of the present invention.

XX Sequence 87 AA;

Query Match 78.2%; Score 462; DB 22; Length 87;
 Best Local Similarity 100.0%; Pred. No. 9.7e-52;
 Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DKLSSKLCADBECCYTTISLARAQEDYNAPDCRFINVKKGQIYVSKLVTENGAGAFWA 65
 DB 1 DKLSSKLCADDECCYTTISLARAQEDYNAPDCRFINVKKGQIYVSKLVKENGAGAFWA 60

QY 66 GSVYGDHODEMGIVGFPSNLVREQRY 92
 DB 61 GSVYGDHODEMGIVGFPSNLVREQRY 87

RESULT 14

AAB69811 ID AAB69811 standard; Protein: 131 AA.

AC AAB69811;

DT 25-MAR-2003 (updated)

DT 26-OCT-1995 (first entry)

DE Melanoma inhibiting protein (human).

KM Melanoma; inhibition; cancer; melanoma; glioblastoma; neuroblastoma;

KM small cell lung cancer; neuroectodermal tumours; immunosuppressant;

KM phytohaemagglutinin; lymphocyte; interleukin 2; IL-2; detection;

XX probe; fusion protein.

OS Homo sapiens.

PN WO9503328-A2.

PD 02-FEB-1995.

PF 19-JUL-1994; 94WO-EP02369.

PR 20-JUL-1993; 93DE-4324247.

PA (BOEF) BOEHRINGER MANNHEIM GMBH.

PI Bogdahn U, Buettner R, Kaluza B;

XX WPI; 1995-075191/10.

DR N-PSDB; AAQ84050, AAQ84051.

PT New melanoma inhibiting protein and related nucleic acid -

PT vectors, transformed cells, antibodies etc., useful for treating

PT tumours and as immunosuppressant e.g. by gene therapy

XX Claim 1; Page 54; 85pp; German.

XX This protein has melanoma-inhibiting activity and can be used to

XX treat cancer (melanoma, glioblastoma, neuroblastoma, small cell

XX lung cancer, neuroectodermal tumours) or as an immunosuppressant

XX (it inhibits IL-2 or phytohaemagglutinin induced proliferation of

XX peripheral blood lymphocytes). Antibodies raised against the

XX protein can be used to detect cell producing the protein and also

XX for protein purification. Probes derived from DNA encoding the

XX protein (AAQ84050, AAQ84051) can be used to detect sequences encoding

XX the protein or related proteins. The protein may be expressed as

XX a fusion protein (conjugated with dihydrofolate reductase (DHFR)).

XX (Updated on 25-MAR-2003 to correct PN field.)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2003, 16:09:08 ; Search time 15.098 Seconds
(without alignments)

1449,984 Million cell updates/sec

Title: US-10-019-455A-49

Sequence: 1 HGMFMDKLSKKLCADEECV.....RVQEAETKEIPTDIDFCE 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 724715 seqs, 199017464 residues

Total number of hits satisfying chosen parameters: 724715

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*

- 1: /cgn2_6/ptoddata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptoddata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptoddata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptoddata/2/pubpaa/US06_PUBCOMB.pep:*
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- 18: /cgn2_6/ptoddata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|------------------|
| 1 | 541 | 91.5 | 128 | 12 | US-10-216-163-72 |
| 2 | 541 | 91.5 | 128 | 12 | US-10-218-765-72 |
| 3 | 541 | 91.5 | 128 | 12 | US-10-219-063-72 |
| 4 | 541 | 91.5 | 128 | 12 | US-10-219-066-72 |
| 5 | 541 | 91.5 | 128 | 12 | US-10-219-067-72 |
| 6 | 541 | 91.5 | 128 | 12 | US-10-219-068-72 |
| 7 | 541 | 91.5 | 128 | 12 | US-10-219-069-72 |
| 8 | 541 | 91.5 | 128 | 12 | US-10-219-073-72 |
| 9 | 541 | 91.5 | 128 | 12 | US-10-219-475-72 |
| 10 | 541 | 91.5 | 128 | 12 | US-10-219-480-72 |
| 11 | 541 | 91.5 | 128 | 12 | US-10-219-483-72 |
| 12 | 541 | 91.5 | 128 | 12 | US-10-219-525-72 |
| 13 | 541 | 91.5 | 128 | 12 | US-10-219-526-72 |
| 14 | 541 | 91.5 | 128 | 12 | US-10-219-530-72 |
| 15 | 541 | 91.5 | 128 | 12 | US-10-219-531-72 |

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| 16 | 541 | 91.5 | 128 | 12 | US-10-219-532-72 | Sequence 72, Appl |
| 17 | 541 | 91.5 | 128 | 12 | US-10-219-533-72 | Sequence 72, Appl |
| 18 | 541 | 91.5 | 128 | 12 | US-10-223-081-360 | Sequence 360, Appl |
| 19 | 541 | 91.5 | 128 | 12 | US-10-230-437-72 | Sequence 72, Appl |
| 20 | 541 | 91.5 | 128 | 12 | US-10-232-228-72 | Sequence 72, Appl |
| 21 | 541 | 91.5 | 128 | 12 | US-10-223-082-360 | Sequence 360, Appl |
| 22 | 541 | 91.5 | 128 | 15 | US-10-227-884-72 | Sequence 72, Appl |
| 23 | 541 | 91.5 | 128 | 15 | US-10-230-163-72 | Sequence 72, Appl |
| 24 | 541 | 91.5 | 128 | 15 | US-10-230-338-72 | Sequence 72, Appl |
| 25 | 541 | 91.5 | 128 | 15 | US-10-218-631-72 | Sequence 72, Appl |
| 26 | 541 | 91.5 | 128 | 15 | US-10-230-414-72 | Sequence 72, Appl |
| 27 | 541 | 91.5 | 128 | 15 | US-10-216-159A-72 | Sequence 72, Appl |
| 28 | 541 | 91.5 | 128 | 15 | US-10-218-849-72 | Sequence 72, Appl |
| 29 | 541 | 91.5 | 128 | 15 | US-10-227-873-72 | Sequence 72, Appl |
| 30 | 541 | 91.5 | 128 | 15 | US-10-227-883-72 | Sequence 72, Appl |
| 31 | 541 | 91.5 | 128 | 15 | US-10-219-076-72 | Sequence 72, Appl |
| 32 | 541 | 91.5 | 128 | 15 | US-10-230-434-72 | Sequence 72, Appl |
| 33 | 541 | 91.5 | 128 | 15 | US-10-219-003-72 | Sequence 72, Appl |
| 34 | 541 | 91.5 | 128 | 15 | US-10-219-075-72 | Sequence 72, Appl |
| 35 | 541 | 91.5 | 128 | 15 | US-10-219-464-72 | Sequence 72, Appl |
| 36 | 541 | 91.5 | 128 | 15 | US-10-219-466-72 | Sequence 72, Appl |
| 37 | 541 | 91.5 | 128 | 15 | US-10-219-479-72 | Sequence 72, Appl |
| 38 | 541 | 91.5 | 128 | 15 | US-10-219-481-72 | Sequence 72, Appl |
| 39 | 541 | 91.5 | 128 | 15 | US-10-230-260-72 | Sequence 72, Appl |
| 40 | 541 | 91.5 | 128 | 15 | US-10-232-231-72 | Sequence 72, Appl |
| 41 | 541 | 91.5 | 128 | 15 | US-10-232-233-72 | Sequence 72, Appl |
| 42 | 541 | 91.5 | 128 | 15 | US-10-216-165-72 | Sequence 72, Appl |
| 43 | 541 | 91.5 | 128 | 15 | US-10-218-956-72 | Sequence 72, Appl |
| 44 | 541 | 91.5 | 128 | 15 | US-10-219-468-72 | Sequence 72, Appl |
| 45 | 541 | 91.5 | 128 | 15 | US-10-219-478-72 | Sequence 72, Appl |

ALIGNMENTS

RESULT 1
US-10-216-163-72
Sequence 72, Application US/10216163
Publication No. US20030149239A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gertlens, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gueney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
TITLE OF INVENTION: MOOD, WILLIAM I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530PIC3
CURRENT APPLICATION NUMBER: US/10/216,163
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656

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; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
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; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
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; US-10-216-163-72

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; Publication No. US20030187201A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Destoyers, Luc
; APPLICANT: Geriltsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: F5530P1C19
; CURRENT APPLICATION NUMBER: US/10/218,765
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; PRIOR APPLICATION NUMBER: 60/169835

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; Publication No. US20030187202A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Geriltsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C24
; CURRENT APPLICATION NUMBER: US/10/219,063
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
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; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
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; PRIOR APPLICATION NUMBER: 60/079294
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; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-063-72

Query Match          91.5%; Score 541; DB 12; Length 128;
Best Local Similarity 89.1%; Pred. No. 1.7e-59;
Matches 98; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

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QY 1 HGMFMDKLSKKLCADEECVYTTISLARAQEDYNAPDCRFINVKKGQOIYVYSKLVYENGA 60
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; Publication No. US20030187203A1
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; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guiney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Matarabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C27
; CURRENT APPLICATION NUMBER: US/10/219,066
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
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; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
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; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
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; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-066-72

Query Match 91.5%; Score 541; DB 12; Length 128;
Best Local Similarity 89.1%; Pred. No. 1.7e-59;
Matches 98; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 HGMFMDKLSKKLCADEECVYTTISLARAQEDYNAPDCRFINVKKGQOIYVYSKLVYENGA 60
DB 19 HGIEMDLRLASKKLCADEECVYTTISLARAQEDYNAPDCRFINVKKGQOIYVYSKLVYENGA 78
QY 61 GAFMAGSVYGDHDEMGIVGYFFPSNLVREQRYQEAATKEIPTTDDIDFCE 110
DB 79 GEFMAGSVYGDGQDEMVGIVGYFFPRNLVKEQRYQEAATKEVPTTDDIDFCE 128

US-10-219-067-72
; Sequence 72, Application US/10219067
; Publication No. US20030187204A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guiney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Matarabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C31
; CURRENT APPLICATION NUMBER: US/10/219,067
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-067-72

Query Match 91.5%; Score 541; DB 12; Length 128;
Best Local Similarity 89.1%; Pred. No. 1.7e-59;
Matches 98; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 HGMFMDKLSKKLCADEECVYTTISLARAQEDYNAPDCRFINVKKGQOIYVYSKLVYENGA 60
DB 19 HGIEMDLRLASKKLCADEECVYTTISLARAQEDYNAPDCRFINVKKGQOIYVYSKLVYENGA 78
QY 61 GAFMAGSVYGDHDEMGIVGYFFPSNLVREQRYQEAATKEIPTTDDIDFCE 110
DB 79 GEFMAGSVYGDGQDEMVGIVGYFFPRNLVKEQRYQEAATKEVPTTDDIDFCE 128

RESULT 6
US-10-219-068-72
; Sequence 72, Application US/10219068
; Publication No. US20030187205A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.

```
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530PIC31
CURRENT APPLICATION NUMBER: US/10/219,068
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 60/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 72
LENGTH: 128
TYPE: PRT
ORGANISM: Homo Sapien
US-10-219-068-72

Query Match      91.5%; Score 541; DB 12; Length 128;
Best Local Similarity 89.1%; Pred. No. 1.7e-59;
Matches 98; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 HGMFMKLSKSKLCADEECVYTTISLAAQEDYNAPDCRFINVKKGQOIYYSKLVYENGA 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 19 HGIMDLASKSLKLCADDECVYTTISLAAQEDYNAPDCRFINVKKGQOIYYSKLVYENGA 78
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 GAFNAGSVYGDHODEMGIYGFPSNLVREQRYVQEAATKEIPTDIDFCE 110
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 79 GEFNAGSVYGDQDDEMGVGVFPRLVKEQRYVQEAATKEVPTDIDFCE 128
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
US-10-219-069-72
Sequence 72, Application US/10219069
Publication No. US20030187206A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530PIC40
CURRENT APPLICATION NUMBER: US/10/219,069
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 60/119,480
PRIOR FILING DATE: 2002-04-09
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PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 72
LENGTH: 128
TYPE: PRT
ORGANISM: Homo Sapien
US-10-219-069-72

Query Match      91.5%; Score 541; DB 12; Length 128;
Best Local Similarity 89.1%; Pred. No. 1.7e-59;
Matches 98; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 HGMFMKLSKSKLCADEECVYTTISLAAQEDYNAPDCRFINVKKGQOIYYSKLVYENGA 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 19 HGIMDLASKSLKLCADDECVYTTISLAAQEDYNAPDCRFINVKKGQOIYYSKLVYENGA 78
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 GAFNAGSVYGDHODEMGIYGFPSNLVREQRYVQEAATKEIPTDIDFCE 110
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 79 GEFNAGSVYGDQDDEMGVGVFPRLVKEQRYVQEAATKEVPTDIDFCE 128
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
US-10-219-073-72
Sequence 72, Application US/10219073
Publication No. US20030187207A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530PIC52
CURRENT APPLICATION NUMBER: US/10/219,073
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: 60/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
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;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-10-219-475-72
Query Match
Best Local Similarity 91.5%; Score 541; DB 12; Length 128;
Matches 98; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 72
LENGTH: 128
TYPE: PRT
ORGANISM: Homo Sapien
US-10-219-073-72

Query Match
Best Local Similarity 91.5%; Score 541; DB 12; Length 128;
Matches 98; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 72
LENGTH: 128
TYPE: PRT
ORGANISM: Homo Sapien
US-10-219-073-72

RESULT 9
US-10-219-475-72
Sequence 72, Application US/10219475
Publication No. US20030187208A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Macanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530P1C49
CURRENT APPLICATION NUMBER: US/10/219,475
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 72
LENGTH: 128

;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-10-219-475-72

Query Match
Best Local Similarity 91.5%; Score 541; DB 12; Length 128;
Matches 98; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-10-219-480-72
Query Match
Best Local Similarity 89.1%; Pred. No. 1.7e-59;
Matches 98; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 72
LENGTH: 128
TYPE: PRT
ORGANISM: Homo Sapien
US-10-219-480-72

RESULT 10
US-10-219-480-72
Sequence 72, Application US/10219480
Publication No. US20030187209A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Macanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530P1C38
CURRENT APPLICATION NUMBER: US/10/219,480
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 72
LENGTH: 128
TYPE: PRT
ORGANISM: Homo Sapien
US-10-219-480-72

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C41
CURRENT APPLICATION NUMBER: US/10/219,526
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 72
LENGTH: 128
TYPE: PRT
ORGANISM: Homo Sapien
US-10-219-526-72

Query Match 91.5%; Score 541; DB 12; Length 128;
Best Local Similarity 89.1%; Pred. No. 1.7e-59;
Matches 98; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 HGFMFKLSKSKLCADEECVYTTISLARAQEDYNAPDCRFINVKKGQOIYVYSKLVENGA 60
DB 19 HGIFMDRLASKKLCADEECVYTTISLARAQEDYNAPDCRFINVKKGQOIYVYSKLVENGA 78
QY 61 GAFWAGSYVGDGDGEMGVGYFPRLVKEGRVYQEAATKEVPTTIDIFCE 110
DB 79 GEFWAGSYVGDGDGEMGVGYFPRLVKEGRVYQEAATKEVPTTIDIFCE 128

RESULT 14
US-10-219-530-72
Sequence 72, Application US/10219530
Publication No. US2003018721A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C54
CURRENT APPLICATION NUMBER: US/10/219,530
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 72
LENGTH: 128
TYPE: PRT
ORGANISM: Homo Sapien
US-10-219-530-72

Query Match 91.5%; Score 541; DB 12; Length 128;
Best Local Similarity 89.1%; Pred. No. 1.7e-59;
Matches 98; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 HGFMFKLSKSKLCADEECVYTTISLARAQEDYNAPDCRFINVKKGQOIYVYSKLVENGA 60
DB 19 HGIFMDRLASKKLCADEECVYTTISLARAQEDYNAPDCRFINVKKGQOIYVYSKLVENGA 78
QY 61 GAFWAGSYVGDGDGEMGVGYFPRLVKEGRVYQEAATKEVPTTIDIFCE 110
DB 79 GEFWAGSYVGDGDGEMGVGYFPRLVKEGRVYQEAATKEVPTTIDIFCE 128

RESULT 15
US-10-219-531-72
Sequence 72, Application US/10219531
Publication No. US2003018721A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C56
CURRENT APPLICATION NUMBER: US/10/219,531
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656

; PRIOR FILING DATE: 1998-03-26
 ; PRIOR APPLICATION NUMBER: 60/079728
 ; PRIOR FILING DATE: 1998-03-27
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 246
 ; SEQ ID NO 72
 ; LENGTH: 128
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-219-531-72

Query Match 91.5%; Score 541; DB 12; Length 128;
 Best Local Similarity 89.1%; Pred. No. 1.7e-59;
 Matches 98; Conservative 7; Mismatches 5; Indels 0; Caps 0;
 QY 1 HGMFMDKLSSKLCADCECVYTTISLARAQEDYNAPDCRFINVKKGQOIYVYSKLVTENGA 60
 Db 19 HGIMDRILASKKLCADCECVYTTISLASHQEDYNAPDCRFINVKKGQOIYVYSKLVTENGA 78
 QY 61 GAFWAGSYGDDHODEMGIVGYFPSNLVREORVYQEAATKEIPTDIDPFCE 110
 Db 79 GEFWAGSYGDDGQDEMGIVGYFPRNLVKEQRYVQEAATKEVPTDIDPFCE 128

Search completed: December 29, 2003, 16:26:16
 Job time : 15.098 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 29, 2003, 16:03:18 : Search time 8.0112 Seconds

(without alignments)
580.961 Million cell updates/sec

Title: US-10-019-455A-49

Sequence: 1 HGMFMDKLSKKLCADECV.....RYQDATEIFPTIDDFCE 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents AA:*

1: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*\n2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*\n3: /cgn2_6/prodata/2/1aa/6A_COMB.pep:*\n4: /cgn2_6/prodata/2/1aa/6B_COMB.pep:*\n5: /cgn2_6/prodata/2/1aa/6CTUS_COMB.pep:*\n6: /cgn2_6/prodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 264.5 | 44.8 | 131 | 1 | US-08-578-649-2 |
| 2 | 244.5 | 41.4 | 130 | 1 | US-08-578-648-5 |
| 3 | 93.5 | 13.8 | 844 | 1 | US-07-646-537B-2 |
| 4 | 84.5 | 14.3 | 54 | 3 | US-09-346-510B-21 |
| 5 | 82.5 | 14.0 | 1589 | 3 | US-09-356-952-4 |
| 6 | 76.5 | 12.9 | 48 | 3 | US-09-346-510B-24 |
| 7 | 74 | 12.5 | 694 | 1 | US-08-164-839-4 |
| 8 | 74 | 12.5 | 694 | 1 | US-08-583-799-4 |
| 9 | 74 | 12.5 | 695 | 1 | US-08-164-839-6 |
| 10 | 74 | 12.5 | 695 | 1 | US-08-583-799-6 |
| 11 | 69.5 | 11.8 | 58 | 4 | US-08-630-915A-110 |
| 12 | 69 | 11.7 | 322 | 4 | US-08-630-915A-198 |
| 13 | 67 | 11.3 | 462 | 4 | US-08-630-915A-198 |
| 14 | 66.5 | 11.3 | 687 | 1 | US-08-164-839-31 |
| 15 | 66.5 | 11.3 | 687 | 1 | US-08-164-839-31 |
| 16 | 66.5 | 11.3 | 687 | 1 | US-08-164-839-31 |
| 17 | 66.5 | 11.3 | 687 | 1 | US-08-583-799-31 |
| 18 | 66.5 | 11.3 | 688 | 1 | US-08-583-799-33 |
| 19 | 66.5 | 11.3 | 688 | 1 | US-08-164-839-70 |
| 20 | 66.5 | 11.3 | 688 | 1 | US-08-164-839-72 |
| 21 | 66.5 | 11.3 | 688 | 1 | US-08-583-799-70 |
| 22 | 66 | 11.2 | 280 | 1 | US-08-583-799-72 |
| 23 | 66 | 11.2 | 280 | 1 | US-08-434-255-8 |
| 24 | 66 | 11.2 | 280 | 1 | US-08-459-967-8 |
| 25 | 66 | 11.2 | 280 | 1 | US-08-460-327-8 |
| 26 | 66 | 11.2 | 280 | 1 | US-08-459-871-8 |
| 27 | 66 | 11.2 | 280 | 3 | US-09-024-532-2 |
| | | | 280 | 4 | US-09-104-623A-2 |

| | | | | | | |
|----|----|------|------|---|--------------------|--------------------|
| 28 | 66 | 11.2 | 280 | 4 | US-09-019-532-2 | Sequence 2, Appli |
| 29 | 66 | 11.2 | 280 | 4 | US-09-417-359A-2 | Sequence 2, Appli |
| 30 | 66 | 11.2 | 370 | 1 | US-08-434-255-6 | Sequence 6, Appli |
| 31 | 66 | 11.2 | 370 | 1 | US-08-459-967-6 | Sequence 6, Appli |
| 32 | 66 | 11.2 | 370 | 1 | US-08-460-327-6 | Sequence 6, Appli |
| 33 | 66 | 11.2 | 370 | 1 | US-08-460-327-6 | Sequence 6, Appli |
| 34 | 66 | 11.2 | 397 | 1 | US-08-434-255-2 | Sequence 2, Appli |
| 35 | 66 | 11.2 | 397 | 1 | US-08-434-255-4 | Sequence 2, Appli |
| 36 | 66 | 11.2 | 397 | 1 | US-08-459-967-2 | Sequence 2, Appli |
| 37 | 66 | 11.2 | 397 | 1 | US-08-459-967-2 | Sequence 2, Appli |
| 38 | 66 | 11.2 | 397 | 1 | US-08-460-327-2 | Sequence 2, Appli |
| 39 | 66 | 11.2 | 397 | 1 | US-08-460-327-4 | Sequence 2, Appli |
| 40 | 66 | 11.2 | 397 | 1 | US-08-460-327-4 | Sequence 2, Appli |
| 41 | 66 | 11.2 | 397 | 1 | US-08-459-871-4 | Sequence 4, Appli |
| 42 | 65 | 11.0 | 57 | 4 | US-08-630-915A-125 | Sequence 125, App |
| 43 | 65 | 11.0 | 57 | 4 | US-08-630-915A-136 | Sequence 136, App |
| 44 | 65 | 11.0 | 788 | 4 | US-08-630-915A-30 | Sequence 30, Appli |
| 45 | 65 | 11.0 | 1719 | 2 | US-08-459-568-4 | Sequence 4, Appli |

ALIGNMENTS

RESULT 1
US-08-578-649-2
Sequence 2, Application US/08578649

Patent No. 5770366

GENERAL INFORMATION:

APPLICANT: Ulrich Bogdan

APPLICANT: Reinhard Butner

APPLICANT: Brigitte Kaluza

TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felfe & Lynch

STREET: 805 Third Avenue

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch 1.44 MB storage diskette

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/578,649

FILING DATE: 29-July-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 43 24 247.2

FILING DATE: 20-July-1993

ATTORNEY/AGENT INFORMATION:

NAME: Andrew L. Tiajoleff

REGISTRATION NUMBER: 31,575

TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 131 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-578-649-2

Query Match 44.8% Score 264.5; DB 1; Length 131;
Best Local Similarity 46.3%; Pred. No. 9, 6e-27;
Matches 50; Conservative 23; Mismatches 30; Indels 5; Gaps 3;
5 MDLSSKKLCADECVTISLRAQEDYNAPCRFINVKKGGQIYYSKLVLENAG-AF 63

Db 27 MPKADSKLCADECSHPISMAVALQDYAPDCRFLTHRGQVYVFSKL---KGGRLF 83

Qy 64 WAGSVGDHODEMGI-VGYPPSNLVREQRYQSEATKEIPTTIDPFCE 110
Db 84 WGSVGGQYVDLAAIRGIFPSSIVREDQTLKPGKVDVKDKMDFYQC 131

RESULT 2

US-08-578-649-5
Sequence 5, Application US/08578649
Patent No. 570366

GENERAL INFORMATION:

APPLICANT: Ulrich Bogdan
APPLICANT: Reinhard Butner
APPLICANT: Brigitte Kaluza
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felte & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/578,649

FILING DATE: 29-July-1994

CLASSIFICATION: 435

Prior Application Data:

APPLICATION NUMBER: DE P 43 24 247.2

FILING DATE: 20-July-1993

ATTORNEY/AGENT INFORMATION:

NAME: Andrew L. Tiajolo

REGISTRATION NUMBER: 31,575

REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 130 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-578-649-5

Query Match

Best Local Similarity 46.3%; Score 244.5; DB 1; Length 130;

Matches 50; Conservative 20; Mismatches 33; Indels 5; Gaps 3;

Qy 5 MDKLSKKLCADEECVYTIISLARAQEDYNAPDCRFINVKKGOIYVSKLVTEAGAG-AF 63
Db 26 MPKADSKLCADECSHPISMAVALQDYAPDCRFLTHRGQVYVFSKL---KGGRLF 82
Qy 64 WAGSVGDHODEMGI-VGYPPSNLVREQRYQSEATKEIPTTIDPFCE 110
Db 84 WGSVGGQYVDLAAIRGIFPSSIVREDLNSKPGKVDVKDKMDFYQC 130

RESULT 3

US-07-646-537B-2

Sequence 2, Application US/07646537B

Patent No. 5348864

GENERAL INFORMATION:

APPLICANT: Barbacid, Mariano

TITLE OF INVENTION: Vav Proto-Oncogene Protein

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Bristol-Myers Squibb Company
STREET: P.O. Box 4000

CITY: Princeton

STATE: New Jersey

COUNTRY: U.S.A.

ZIP: 08543-4000

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/646,537B

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Gaul, Timothy J.

REGISTRATION NUMBER: 33,111

REFERENCE/DOCKET NUMBER: DC10

TELECOMMUNICATION INFORMATION:

TELEPHONE: (609) 921-5901

TELEFAX: (609) 921-4526

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 844 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-646-537B-2

Query Match

Best Local Similarity 15.8%; Score 93.5; DB 1; Length 844;

Matches 23; Conservative 14; Mismatches 20; Indels 13; Gaps 3;

Qy 26 ARAQEDYNAPDCRFINVKKGOIYVSKLVTEAGAGAFWAGSVGDHODEMGI-VGYPPSN 85
Db 786 AKARYDFCARJSESLKEGDII---KLNKKGGQGMWRGEIYGR-----IGWFPNSN 834
Qy 86 LVREQRYQSE 95
Db 835 YVEED--YSE 842

RESULT 4

US-09-346-510B-21

Sequence 21, Application US/09346510B

Patent No. 6281014

GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

APPLICANT: Wang, Yinxiang

TITLE OF INVENTION: SH3-Containing Protein, DNA and Uses Thereof

FILE REFERENCE: D6222CIP

CURRENT APPLICATION NUMBER: US/09/346,510B

PRIOR FILING DATE: 1999-07-01

PRIOR APPLICATION NUMBER: 08/871,732

PRIOR FILING DATE: 1997-06-09

NUMBER OF SEQ ID NOS: 32

SEQ ID NO 21

LENGTH: 54

TYPE: PRT

ORGANISM: unknown

FEATURE:

NAME/KEY: Domain

OTHER INFORMATION: amino acid sequence of Vav SH3 domain

US-09-346-510B-21

Query Match

Best Local Similarity 14.3%; Score 84.5; DB 3; Length 54;

Matches 20; Conservative 13; Mismatches 18; Indels 11; Gaps 2;

Qy 28 AQEDYNAPDCRFINVKKGOIYVSKLVTEAGAGAFWAGSVGDHODEMGI-VGYPPSNLV 87
Db 1 ARYDFCARJSESLKEGDII---KLNKKGGQGMWRGEIYGR-----IGWFPANV 49

QY 88 RE 89
DB 50 EE 51

RESULT 5

US-09-356-952-4
; Sequence 4, Application US/09356952
; Patent No. 6117663
; GENERAL INFORMATION:
; APPLICANT: Boriack-Sjodin, Ann
; APPLICANT: Margalit, S. M.
; APPLICANT: Bor-Segali, Dafna
; APPLICANT: Cole, Philip
; APPLICANT: Kuriyan, John
; TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE
; FILE REFERENCE: 600-1-228N
; CURRENT APPLICATION NUMBER: US/09/356,952
; CURRENT FILING DATE: 1999-07-19
; EARLIER APPLICATION NUMBER: 60/093,631
; EARLIER FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1589
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-356-952-4

Query Match 14.0%; Score 82.5; DB 3; Length 1589;
Best Local Similarity 28.1%; Pred. No. 0.2; Mismatches 35; Indels 11; Gaps 4;

QY 8 ISSKLCADCECVYITSLRAQEDYNAP-----DCRFNVKKGQOIYVYSKLVTEHGAGA 62
DB 45 ISSSPSTSELTIRPIGIYVAAYDENYPIKDKSSQLSSVGGERTIYLNK-----NSSG- 99

QY 63 FWAGSVYGDHDEMGIVGYPFNSLVREQR 91
DB 100 WWDGLVIDDSNGKVN-RGMFPCNFGRLR 127

RESULT 6

US-09-346-510B-24
; Sequence 24, Application US/09346510B
; Patent No. 6281014
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Wang, Yinxiang
; TITLE OF INVENTION: SH3-Containing Protein, DNA and Uses Thereof
; FILE REFERENCE: D6221CIP
; CURRENT APPLICATION NUMBER: US/09/346,510B
; CURRENT FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: 08/871,732
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 24
; LENGTH: 48
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; NAME/KEY: Domain
; LOCATION: 2...49
; OTHER INFORMATION: amino acid sequence of Yav SH3 domain at position 2
; OTHER INFORMATION: through position 49 of SEQ ID NO. 6281014 21
US-09-346-510B-24

Query Match 12.9%; Score 76.5; DB 3; Length 48;
Best Local Similarity 31.6%; Pred. No. 0.0084;
Matches 18; Conservative 12; Mismatches 16; Indels 11; Gaps 2;

QY 31 DYNAPOCRFINVKKGOIYVYSKLVTEHGAGAFWAGSVYGDHDEMGIVGYPFNSLV 87
DB 3 DFCARDRSELTKEGDII-----KILNKKGGQGMWRGEIYGR-----VGWFPAHYV 48

RESULT 7

US-08-164-839-4
; Sequence 4, Application US/08164839
; Patent No. 5514573
; GENERAL INFORMATION:
; APPLICANT: YASUEDA, HISASHI
; APPLICANT: NAKANISHI, KAZUO
; APPLICANT: MOTOKI, MASAO
; APPLICANT: NAGASE, KAZUO
; APPLICANT: MATSUI, HIROSHI
; TITLE OF INVENTION: GENE ENCODING TRANSGLUTAMINASE DERIVED FROM FISH
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: P. C. C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/164,839
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/004,729
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5514573man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-599-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)412-3000
TELEFAX: (703)413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 694 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-164-839-4

Query Match 12.5%; Score 74; DB 1; Length 694;
Best Local Similarity 26.2%; Pred. No. 0.79;
Matches 21; Conservative 21; Mismatches 28; Indels 10; Gaps 3;

QY 31 DYNAPOCRFINVKKGOIYVYSKLVTEHGAGA---FWAGSVYGDHDEMGIVGYPFNSLV 87
DB 392 EVNADTIYIVQDDGR-----RKTEDHASVGNISTKSVYGNHREDVTLHKYPEGSGQ 446

QY 88 REQRYQEAATKEI--PTTDI 105
DB 447 KEREYVKKAGRYTESNEI 466

RESULT 8

US-08-583-799-4
; Sequence 4, Application US/08583799
; Patent No. 5607849
; GENERAL INFORMATION:
; APPLICANT: YASUEDA, HISASHI

APPLICANT: NAKANISHI, KAZUO
APPLICANT: MOTOKI, MASAO
APPLICANT: NAGASE, KAZUO
APPLICANT: MATSUI, HIROSHI
TITLE OF INVENTION: GENE ENCODING TRANSGLUTAMINASE DERIVED
FROM FISH
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,799
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/004,729
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5607849man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-599-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)412-3000
TELEFAX: (703)413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 694 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-583-799-4

Query Match 12.5%; Score 74; DB 1; Length 694;
Best Local Similarity 26.2%; Pred. No. 0.79;
Matches 21; Conservative 21; Mismatches 28; Indels 10; Gaps 3;

QY 31 DYNAPDCEFINVKKGQOIYVYSKLVTEAGAG--FMAGSVYGDHDEMGIVGFPNSLV 87
DB 392 EVNADTIYIVKKGQOR-----RKITDHASVGNISTKSYGNHREDVTLHYKYPEGSO 446
QY 88 REQRVQATKEI--PTTDI 105
DB 447 KEREVYKKAQRVTEPSNEI 466
RESULT 9
US-08-164-839-6
Sequence 6, Application US/08164839
Patent No. 5514573
GENERAL INFORMATION:
APPLICANT: YASUEDA, HISASHI
APPLICANT: NAKANISHI, KAZUO
APPLICANT: MOTOKI, MASAO
APPLICANT: NAGASE, KAZUO
APPLICANT: MATSUI, HIROSHI
TITLE OF INVENTION: GENE ENCODING TRANSGLUTAMINASE DERIVED
FROM FISH
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor

CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/164,839
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/004,729
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5514573man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-599-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)412-3000
TELEFAX: (703)413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 695 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-164-839-6

Query Match 12.5%; Score 74; DB 1; Length 695;
Best Local Similarity 26.2%; Pred. No. 0.79;
Matches 21; Conservative 21; Mismatches 28; Indels 10; Gaps 3;

QY 31 DYNAPDCEFINVKKGQOIYVYSKLVTEAGAG--FMAGSVYGDHDEMGIVGFPNSLV 87
DB 393 EVNADTIYIVKKGQOR-----RKITDHASVGNISTKSYGNHREDVTLHYKYPEGSO 447
QY 88 REQRVQATKEI--PTTDI 105
DB 448 KEREVYKKAQRVTEPSNEI 467
RESULT 10
US-08-583-799-6
Sequence 6, Application US/08583799
Patent No. 5607849
GENERAL INFORMATION:
APPLICANT: YASUEDA, HISASHI
APPLICANT: NAKANISHI, KAZUO
APPLICANT: MOTOKI, MASAO
APPLICANT: NAGASE, KAZUO
APPLICANT: MATSUI, HIROSHI
TITLE OF INVENTION: GENE ENCODING TRANSGLUTAMINASE DERIVED
FROM FISH
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,799

FILING DATE: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/004,729
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: OBION, No. 5607849man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-599-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)412-3000
TELEFAX: (703)413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 695 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-583-799-6

Query Match 12.5%; Score 74; DB 1; Length 695;
Best Local Similarity 26.2%; Pred. No. 0.79;
Matches 21; Conservative 21; Mismatches 28; Indels 10; Gaps 3;

QY 31 DYNAPDRFINVKGGQIYYYSKLVTEENGAGA---FWAGSVYGDHODEMGIYGFPSNLY 87
DB 393 EVNADTTIWIYVQXGQR---RKITDHSVSGNISTKSVYGNHREDVTLHYKYPEGSG 447
QY 88 REGRVYOATKEI--PTTDI 105
DB 448 KEREVYKKAGRYTEPSNEI 467

RESULT 11
US-08-630-915A-210
Sequence 210, Application US/08630915A
GENERAL INFORMATION:
PATENT NO. 6309820
APPLICANT: SPARKS, Andrew B.
APPLICANT: HOFFMAN, No. 6309820h
APPLICANT: KAY, Brian K.
APPLICANT: FOWLES, Dana M.
APPLICANT: MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915A
FILING DATE: 03-APR-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Mastrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 210:

SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-630-915A-210

Query Match 11.8%; Score 69.5; DB 4; Length 58;
Best Local Similarity 31.4%; Pred. No. 0.09;
Matches 16; Conservative 11; Mismatches 13; Indels 11; Gaps 2;

QY 40 INVKKGGQIYYYSKLVTEENGAGAFWAGSVYGDHODEMGIYGFPSNLYREQ 90
DB 19 LSLIKTKYIVKICSD---GWTGSYNGQ-----VGWFPSSNYTEE 58

RESULT 12
US-08-630-915A-198
Sequence 198, Application US/08630915A
GENERAL INFORMATION:
PATENT NO. 6309820
APPLICANT: SPARKS, Andrew B.
APPLICANT: HOFFMAN, No. 6309820h
APPLICANT: KAY, Brian K.
APPLICANT: FOWLES, Dana M.
APPLICANT: MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915A
FILING DATE: 03-APR-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Mastrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 198:
SEQUENCE CHARACTERISTICS:
LENGTH: 322 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-630-915A-198

Query Match 11.7%; Score 69; DB 4; Length 322;
Best Local Similarity 30.2%; Pred. No. 1.2;
Matches 19; Conservative 11; Mismatches 19; Indels 14; Gaps 3;

QY 40 INVKKGGQIYYYSKLVTEENGAGAFWAGSVYGDHODEMGIYGFPSNLYREQRYOATKE 99
DB 72 LSLVKGSRVYMERK-----SDGWRGSGSYNGQ-----IGWFPSSNYTEE--VDEAVAE 117
QY 100 IPT 102

Db 118 SPS 120

RESULT 13

US-08-630-915A-38
Sequence 38, Application US/08630915A
Patent No. 6309820
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: HOFFMAN, NO. 6309820h
APPLICANT: KAY, Brian K.
APPLICANT: FOWLES, Dana M.
APPLICANT: MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
TITLE OF INVENTION: USING SAME
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630.915A
FILING DATE: 03-APR-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,972
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8664/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 462 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-630-915A-38

Query Match 11.3%; Score 67; DB 4; Length 462;

Best Local Similarity 31.6%; Pred. No. 3.6; Matches 24; Conservative 7; Mismatches 21; Indels 24; Gaps 3;

Db 407 DYTQNDDELAFNKGQIINVLNKEDPD-----WKKGEVNOQ-----VOLFFSNVVK-- 452

QY 31 DYNAPDGRFINVKKGGQIYYVSKLVYENGAGAFWAGSVYGDHDEMGIYGFPSNLVREQ 90
91 RVYQEAATKEIPTTID 106
453 -----LTTDM 458

RESULT 14

US-08-164-839-31
Sequence 31, Application US/08164839
Patent No. 5514573
GENERAL INFORMATION:
APPLICANT: YASUEDA, HISASHI
APPLICANT: NAKANISHI, KAZUO
APPLICANT: MOTOKI, MASAO
APPLICANT: NAGASE, KAZUO

APPLICANT: MATSUI, HIROSHI
TITLE OF INVENTION: GENE ENCODING TRANSGLUTAMINASE DERIVED
TITLE OF INVENTION: FROM FISH
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/164.839
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/004,729
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5514573man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-599-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 412-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:
LENGTH: 687 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-164-839-31

Query Match 11.3%; Score 66.5; DB 1; Length 687;
Best Local Similarity 25.0%; Pred. No. 7.4;
Matches 26; Conservative 19; Mismatches 46; Indels 13; Gaps 4;

QY 7 KLSKKLADSECVYTTSLAARQEDYNAPDGRFINVKKGGQIYYV-----SKL-VTE 57
Db 356 ELSDSEYCCGCPVTAIRKGNLSVKYDAP---FIFAEVNADIYMWAGPGGRKKIDVDQ 412

QY 58 NGAGA-FWAGSVYGDHDEMGIYGFPSNLVREQRYQEAATKEI 100
413 SGVGKNISTKSLYGDYREDVTLHYKPEGSKKEKREYQKAGHRI 456

RESULT 15

US-08-164-839-33
Sequence 33, Application US/08164839
Patent No. 5514573
GENERAL INFORMATION:
APPLICANT: YASUEDA, HISASHI
APPLICANT: NAKANISHI, KAZUO
APPLICANT: MOTOKI, MASAO
APPLICANT: NAGASE, KAZUO
APPLICANT: MATSUI, HIROSHI
TITLE OF INVENTION: GENE ENCODING TRANSGLUTAMINASE DERIVED
TITLE OF INVENTION: FROM FISH
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.

ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/164,839
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/004,729
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5514573man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-599-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)412-3000
TELEFAX: (703)413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 687 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-164-839-33

Query Match 11.3%; Score 66.5; DB 1; Length 687;
Best Local Similarity 25.0%; Pred. No. 7.4;
Matches 26; Conservative 19; Mismatches 46; Indels 13; Gaps 4;

QY 7 KLSKSLCADEECYTTISLRAQEDYNAPDQRFINVKKGQIYV-----SKL-VTE 57
Db 356 ELSDGEYCCGCPPTAIKGNLSVKYDAP--FIFAEVNAIDIIYMMAGPGGERKKIDVDQ 412

QY 58 NGAGA-FWAGSVYGDHODEMGIQVPPSNLVRQRYQEAETKEI 100
Db 413 SGVGNISTSKSLYGDYREDVTLHKYPEGSKKEREVYQKAGHRI 456

Search completed: December 29, 2003, 16:11:52
Job time : 9.0112 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_pzn model

Run on: December 29, 2003, 16:11:59 ; Search time 1810.69 Seconds

(without alignments)
2485.278 Million cell updates/sec

Title: US-10-019-455a-49

Perfect score: 591 1 HGMFMDXLSKKLCADEECV.....RVYQATKEIPTTDIFCE 110

Sequence:

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0 %
Maximum Match 100 %

Listing first 45 summaries

Command line parameters:
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-O=/cgnr_1/USPTO.spool/US10019455/runat_29122003_160347_240/app_query_fasta_1.1770
-DB=genemb1 -QFMT=fastap -SUFFIX=rgs -MIMATCH=0.1 -LOOFCU=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=2losum62 -TRANS=human40.cdi -LIST=45
-DOCLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO_MMAR -LARGOQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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1: gb_da:*
2: gb_intg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_dat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pac:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*

29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rtd:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_hcgo_hum:*
40: em_hcgo_mus:*
41: em_hcgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 591 | 100.0 | 330 | 6 | BD010836 |
| 2 | 591 | 100.0 | 330 | 6 | BD093137 |
| 3 | 591 | 100.0 | 384 | 6 | BD010835 |
| 4 | 591 | 100.0 | 384 | 6 | BD093136 |
| 5 | 574 | 97.1 | 330 | 6 | BD010817 |
| 6 | 574 | 97.1 | 330 | 6 | BD093118 |
| 7 | 574 | 97.1 | 384 | 6 | BD010805 |
| 8 | 574 | 97.1 | 384 | 6 | BD093106 |
| 9 | 574 | 97.1 | 929 | 10 | AF243504 |
| 10 | 574 | 97.1 | 947 | 6 | BD010821 |
| 11 | 574 | 97.1 | 947 | 6 | BD093122 |
| 12 | 574 | 97.1 | 958 | 10 | MMU243939 |
| 13 | 574 | 97.1 | 1054 | 10 | AF233333 |
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| 16 | 541 | 91.5 | 384 | 6 | BD010802 |
| 17 | 541 | 91.5 | 384 | 6 | BD093103 |
| 18 | 541 | 91.5 | 521 | 6 | AX358818 |
| 19 | 541 | 91.5 | 521 | 6 | AX362311 |
| 20 | 541 | 91.5 | 521 | 6 | AX454774 |
| 21 | 541 | 91.5 | 521 | 6 | AX491252 |
| 22 | 541 | 91.5 | 846 | 9 | AF233361 |
| 23 | 541 | 91.5 | 865 | 9 | AF243505 |
| 24 | 541 | 91.5 | 923 | 6 | BD010820 |
| 25 | 541 | 91.5 | 923 | 6 | BD093121 |
| 26 | 541 | 91.5 | 1422 | 9 | HSAR242552 |
| 27 | 515 | 87.1 | 307 | 6 | BD010830 |
| 28 | 515 | 87.1 | 307 | 6 | BD093131 |
| 29 | 461.5 | 78.1 | 484 | 5 | AF233518 |
| 30 | 458 | 77.5 | 261 | 6 | BD010829 |
| 31 | 458 | 77.5 | 261 | 6 | BD093130 |
| 32 | 395 | 66.8 | 466 | 5 | AF233519 |
| 33 | 315.5 | 53.4 | 215581 | 2 | AC106161 |
| 34 | 279.5 | 47.3 | 144765 | 2 | BX510362 |
| 35 | 265.5 | 44.9 | 442 | 6 | AX331430 |
| 36 | 265.5 | 44.9 | 442 | 6 | AX331840 |
| 37 | 264.5 | 44.8 | 330 | 6 | A42959 |
| 38 | 264.5 | 44.8 | 330 | 6 | AX016802 |
| 39 | 264.5 | 44.8 | 396 | 9 | BT007044 |
| 40 | 264.5 | 44.8 | 396 | 12 | BT007775 |
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RESULT 1

ALIGNMENTS

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BD093137 Novel pol
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BD093136 Novel pol
BD010817 Novel pol
BD093118 Novel pol
BD010805 Novel pol
BD093106 Novel pol
AF243504 Mus muscu
BD010821 Novel pol
BD093122 Novel pol
BD093132 Novel pol
AF233333 Mus muscu
BD010816 Novel pol
BD093117 Novel pol
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BD010802 Novel pol
BD093103 Novel pol
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AX362311 Sequence
AX454774 Sequence
AX491252 Sequence
AF233361 Homo sapi
AF243505 Homo sapi
BD010820 Novel pol
BD093121 Novel pol
AJ242552 Homo sapi
BD010830 Novel pol
BD093131 Novel pol
AF233518 Gallus ga
BD010829 Novel pol
BD093130 Novel pol
AF233519 Rana care
AC106161 Rattus no
BX510362 Mus muscu
AX331430 Sequence
AX331840 Sequence
A42959 Sequence 18
AX016802 Sequence
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BT007775 Synthetic
A42942 Sequence 1
AX016785 Sequence
AX252508 Sequence
AX287209 Sequence
X75450 H. sapiens m

BD010836
LOCUS BD010836 330 bp DNA linear PAT 31-JAN-2002
DEFINITION Novel polypeptide and DNA thereof.
ACCESSION BD010836
VERSION BD010836.1 GI:18639209
KEYWORDS JP 2001069994-A/37.
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 330)
Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
Yoshimura, K. and Tanaka, H.
Novel polypeptide and DNA thereof
Patent: JP 2001069994-A 37 21-MAR-2001;
TAKEDA CHEMICAL INDUSTRIES LTD
COMMENT OS Rattus sp. (rat)
PN JP 2001069994-A/37
PD 21-MAR-2001
PF 29-JUN-2000 JP 2000195911
PR
PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI
SHINICHI MOGI,
YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC
A61P19/08,
PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC
G01N33/53//
PC C12P21/08, C12N15/00, A61K37/02, C12N5/00
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source 1..330
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/mol_type="genomic DNA"
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BASE COUNT 91 a 62 c 91 g 86 t
ORIGIN
Alignment Scores:
Pred. No.: 3,08e-63 Length: 330
Score: 591.00 Matches: 110
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
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QY 1 HisGlyMetPheMetAspLysLeuSerLysLysLeuCysAlaAspGluGluCysVal 20
Db 1 CATGGCATGTTATGATTAACCTTCTCTTAAGAGTTGTGCGAGATGAGAGTGTC 60
QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
Db 61 TATACCATTTCTCTGGCAAGACGACGAAAGACTCAATGCCCCGAGCTGATGTTCAATC 120
QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
Db 121 AATGTCAAGAAAGGCGACGATCTATGTTATTTCCAGCTGTAAACAGAAATGAGACT 180
QY 61 GlyAlaPheTyrAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
Db 181 GGGGCAATTCCTGGGCTGGCAGTGTATGTTGATGACCAACAGATGAGATGGGAATTTGGGT 240
QY 81 TyrPheProSerAsnLeuValArgGluGlnArgValTyrGlnGluAlaThrLysGluIle 100
Db 241 TATTTTCCCGACCACTGGTTAGAGCAACAGAGTGTACAGAGGCCACCAAGAGATT 300
QY 101 ProThrThrAspIleAspPhePheCysGlu 110

Db 301 CCAACCAAGCATATGACTTCTTCTGTGAA 330
RESULT 2
LOCUS BD093137 330 bp DNA linear PAT 27-AUG-2002
DEFINITION Novel polypeptide and its DNA.
ACCESSION BD093137
VERSION BD093137.1 GI:22638725
KEYWORDS WO 0102564-A/37.
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 330)
Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
Yoshimura, K. and Tanaka, H.
Novel polypeptide and its DNA
Patent: WO 0102564-A 37 11-JAN-2001;
TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO
OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,
HIDEYUKI TANAKA
COMMENT OS Rattus sp. (rat)
PN WO 0102564-A/37
PD 11-JAN-2001
PF 29-JUN-2000 WO 2000JP004278
PR 30-JUN-1999 JP 99P 186718
PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI
MOGI,
YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/12, C12N5/10, C12P21/02, C07K14/47, C07K16/18, A61K45/00, PC
A61K38/17,
PC A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/7088// (C12P21/
PC 02, C12R1:19)
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FH Key Location/Qualifiers
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source 1..330
/organism="Rattus sp."
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BASE COUNT 91 a 62 c 91 g 86 t
ORIGIN
Alignment Scores:
Pred. No.: 3,08e-63 Length: 330
Score: 591.00 Matches: 110
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
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QY 1 HisGlyMetPheMetAspLysLeuSerLysLysLeuCysAlaAspGluGluCysVal 20
Db 1 CATGGCATGTTATGATTAACCTTCTCTTAAGAGTTGTGCGAGATGAGAGTGTC 60
QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
Db 61 TATACCATTTCTCTGGCAAGACGACGAAAGACTCAATGCCCCGAGCTGATGTTCAATC 120
QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
Db 121 AATGTCAAGAAAGGCGACGATCTATGTTATTTCCAGCTGTAAACAGAAATGAGACT 180
QY 61 GlyAlaPheTyrAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
Db 181 GGGGCAATTCCTGGGCTGGCAGTGTATGTTGATGACCAACAGATGAGATGGGAATTTGGGT 240
QY 81 TyrPheProSerAsnLeuValArgGluGlnArgValTyrGlnGluAlaThrLysGluIle 100

| | | | |
|--|---|---|--------|
| Db | 241 | TATTCCCGAGCACTTGTTAGAGAGCAACAGTGTACGAGAGCCACCAAGAGATT | 300 |
| Qy | 101 | ProThrThrAspIleAspPheCysGlu | 110 |
| Db | 301 | CCAACCGAGATATGACTTCTTGTTGTA | 330 |
| RESULT 3 | | | |
| BD010835 | | | |
| LOCUS | BD010835 | 384 bp | DNA |
| DEFINITION | Novel polypeptide and DNA thereof. | | linear |
| ACCESSION | BD010835 | | |
| VERSION | BD010835.1 | GI:18639208 | |
| KEYWORDS | JP 2001069994-A/36. | | |
| SOURCE | Rattus sp. | | |
| ORGANISM | Rattus sp. | | |
| | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. | | |
| REFERENCE | 1 (bases 1 to 384) | | |
| AUTHORS | Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y., Yoshimura,K. and Tanaka,H. | | |
| TITLE | Novel polypeptide and DNA thereof | | |
| JOURNAL | Patent: JP 2001069994-A 36 21-MAR-2001; | | |
| COMMENT | TAKEDA CHEMICAL INDUSTRIES LTD | | |
| | OS Rattus sp. (rat) | | |
| | PN JP 2001069994-A/36 | | |
| | PD 21-MAR-2001 | | |
| | PF 29-JUN-2000 JP 2000195911 | | |
| | PR | | |
| | PI YASUKI ITO,KAZUNORI NISHI,KAZUHIRO OGI,SHOICHI OKUBO, PI SHIMICHI MOGI. | | |
| | PI YUKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA | | |
| | PC C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P9/00,A61P19/02, PC A61P19/08, | | |
| | PC C07K14/47,C07K16/18,C12N1/21,C12N5/10,G01N33/15,G01N33/50, PC G01N33/53// | | |
| | PC C12P21/08,C12N15/00,A61K37/02,C12N5/00 | | |
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| FT | /organism='Rattus sp. (rat)' | | |
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| BASE COUNT | 98 a 72 c 109 g 105 t | | |
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| Pred. No.: | 3,61e-63 | Length: | 384 |
| Score: | 591.00 | Matches: | 110 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 6 | Gaps: | 0 |
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| Db | 55 | CATGGCAAGTGTATGATTAACCTTCTTCTAAGAAGTGTGTGAGAGAGAGATGTGTC | 114 |
| Qy | 21 | TyTThrIleSerLeuAlaArgAlaGlnGluAspIyrAenAlaPcoAspCysArgPheIle | 40 |
| Db | 115 | TATACCATTTCTCTCGCAAGACACAGAAACACACACACACACACACACACACACAC | 174 |
| Qy | 41 | AsnValIysIysGlyGlnGlnIleTyValIyrSerIysLeuValIrhGluAsnGlyAla | 60 |
| Db | 175 | AATGCACGAAGAAGGACAGACATCATGTATTTCACCAAGCTGTGAACGAAATATGAGCT | 234 |
| Qy | 61 | GlyAlaPheMetPheAlaGlySerValIyrGlyAspHisGlnAspGluMetGlyIleValGly | 80 |

| DB | 225 | GGGGATTCTGGGCTGGAGTGTATTATGTGTACCCAGTAGTGAATGTGGGT | 294 |
|--|--|---|-----------------|
| QY | 81 | TYRPLEPQSEAAshnleuValArgGluGlnArgValIYrgingluAlaThnlyeGluIle | 100 |
| DB | 295 | TATTTCCCAACCACTTGTGTAGAGACCAAGAGTGTACAGAGGACCAACAGAGATT | 354 |
| QY | 101 | ProThrThraaplleaSphePhcCysGlu | 110 |
| DB | 355 | CCAACCGAGATGTGACTTCTCTGTGAA | 384 |
| RESULT 4 | BD093136 | | |
| LOCUS | BD093136 | 384 bp | DNA |
| DEFINITION | Novel polypeptide and its DNA. | | linear |
| ACCESSION | BD093136 | | PAT 27-AUG-2002 |
| VERSION | BD093136.1 | GI:22638724 | |
| KEYWORDS | WO 0102564-A/36. | | |
| SOURCE | Rattus sp. | | |
| ORGANISM | Rattus sp. | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. | | |
| AUTHORS | Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y., Yoshimura, K. and Tanaka, H. | | |
| TITLE | Novel polypeptide and its DNA | | |
| JOURNAL | Patent: WO 0102564-A 36 11-JAN-2001; TAKEDA CHEMICAL INDUSTRIES LTD, YASUKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA | | |
| COMMENT | OS Rattus sp. (rat) PN WO 0102564-A/36 PD 11-JAN-2001 PF 29-JUN-2000 WO 2000JP004278 PR 30-JUN-1999 JP 99P 186718 PI YASUKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI | | |
| FEATURES | PI MOGI, PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA PC C12N15/12, C12N5/10, C12P21/02, C07K14/47, C07K16/18, A61K45/00, PC A61K38/17, PC A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/7088// (C12P21/02, C12P21/19) PC 02, C12R1:19) CC FH Key Location/Qualifiers. source 1..384 Location/Qualifiers /organism="Rattus sp." /mol_type="genomic DNA" /db_xref="taxon:10118" | | |
| BASE COUNT | 98 a | 109 g | 105 t |
| ORIGIN | | | |
| Alignment Scores: | | | |
| Pred. No.: | 3,61e-63 | Length: | 384 |
| Score: | 591.00 | Matches: | 110 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 6 | Gaps: | 0 |
| US-10-019-455A-49 (1-110) x BD093136 (1-384) | | | |
| QY | 1 | HisGlyIyeIrePheVetAapLySLeuSeSerLyLySLeuCybaLaapGJugluCyVal | 20 |
| DB | 55 | CATGGCAATGTTATGATTAACCTTCTCTTACAGAGTTGTGTGAGATGAGAGTGTCT | 114 |
| QY | 21 | TYrThrlIeSerleuAlaArgAlaGlnGluAspTYrAsnAlaPProaapCysArgPheIle | 40 |
| DB | 115 | TATACCATTTCTCTGGCAAGACACAGAAAGACTACATACCCCGAGCTGTAGGTTTCATC | 174 |
| QY | 41 | AsnValLySylsgIyngInIleIYrValIYrSerLySLeuValThnrgIaenGluYala | 60 |

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Db      175 AATGCAAGAAAGGCGACAGATCTATTATTCACAGCTGTGACAGAAATGGAGCT 234
Qy      61 GYLAAPHETPALAGIServAlTYrGIYAspHisgluAsergluMetGlyIleValGly 80
Db      235 GGGGCAATCTGGGCTGGCAGCTTTATGTGACCCAGCATGAGATGGGAATTGGGCT 294
Qy      81 TYrPheProSerAsnLeuValArggluGlnArgValTYrGlnGluAlaThrIysGluIle 100
Db      235 TATTTCCCGACGACTTGGTTAGAGACACAGAGTGATCCAGAGGCGACCAAGAGACTT 354
Qy      101 ProThrThrAspIleAspPheCysGlu 110
Db      355 CCAACCGAGATATGACTTCTTGTGAA 384

RESULT 5
LOCUS   BD010817          330 bp      DNA          linear      PAT 31-JAN-2002
DEFINITION Novel polypeptide and DNA thereof.
ACCESSION BD010817
VERSION   BD010817.1 GI:18639190
KEYWORDS JP 2001069994-A/18.
SOURCE   Mus sp.
ORGANISM Mus sp.
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
          Yoshimura, K. and Tanaka, H.
          Novel polypeptide and DNA thereof
          Patent: JP 2001069994-A 18 21-PAR-2001;
          TAKEEDA CHEMICAL INDUSTRIES LTD
COMMENT  OS Mus sp. (mouse)
          PN JP 2001069994-A/18
          PD 21-MAR-2001
          PF 29-JUN-2000 JP 2000195911
          PR
          PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI
          SHINICHI MOGI,
          PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
          PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/02, PC
          A61P19/08,
          PC C07K16/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC
          G01N33/53//
          CC C12P21/08, C12N15/00, A61K37/02, C12N5/00
          FH Key Location/Qualifiers
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          FT /organism="Mus sp. (mouse)".
          FT Location/Qualifiers
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          FE /organism="Mus sp."
          FE /mol_type="genomic DNA"
          FE /db_xref="taxon:10095"

BASE COUNT 91 a 60 c 92 g 87 t
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Alignment Scores:
Pred. No.: 3,68e-61 Length: 330
Score: 574.00 Matches: 106
Percent Similarity: 99.09% Conservative: 3
Best Local Similarity: 96.36% Mismatches: 1
Query Match: 97.12% Indels: 0
DB: Gaps: 0
US-10-019-455a-49 (1-110) x BD010817 (1-330)

Qy      1 HisGlyMetPheMetAspIlySLeuSerSeryIlySLeuCyAlaAspGluGluCysVal 20
Db      1 CATGCGTATTATGATATAAAGCTTTCTTCTAGAGAGTTGTGCGGATGAGAGAGTGTGC 60
Qy      21 TYrThrIleSerLeuAlaArgAlaGlnGluAspTYrAsnAlaProAspCysArgPheIle 40

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Db      61 TATACTATTCTCTGCAAGACACAGAGATTACATGCCCGAGCTGTAGTTTCATC 120
Qy      41 AsnValIlyLeuGlyGlnGlnIleTYrValTYrSerIleLeuValThrGluAsnGlyAla 60
Db      121 GATGTACAGAAAGAGGAGCAGATCTATGTTTACTCCAACTGGTAAACAGAAACGAGCT 180
Qy      61 GYLAAPHETPALAGIServAlTYrGIYAspHisgluAsergluMetGlyIleValGly 80
Db      181 GAGAGATTGGGCTGGCAGCTTTTATGTGACCCAGCATGAGATGGGAATTGAGCT 240
Qy      81 TYrPheProSerAsnLeuValArggluGlnArgValTYrGlnGluAlaThrIysGluIle 100
Db      241 TATTTCCCGACGACTTGGTGAGAGAGACCGGTGTATACAGAGGCGACCAAGAGATC 300
Qy      101 ProThrThrAspIleAspPheCysGlu 110
Db      301 CCAACCGAGATATGACTTCTTGTGAA 330

RESULT 6
LOCUS   BD093118          330 bp      DNA          linear      PAT 27-AUG-2002
DEFINITION Novel polypeptide and its DNA.
ACCESSION BD093118
VERSION   BD093118.1 GI:22638706
KEYWORDS WO 0102564-A/18.
SOURCE   Mus sp.
ORGANISM Mus sp.
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
          Yoshimura, K. and Tanaka, H.
          Novel polypeptide and its DNA
          Patent: WO 0102564-A 18 11-PAN-2001;
          TAKEEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO
          OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,
          HIDEYUKI TANAKA
COMMENT  OS Mus sp. (mouse)
          PN WO 0102564-A/18
          PD 11-JAN-2001
          PF 29-JUN-2000 WO 2000JP004278
          PR 30-JUN-1999 JP 99P 186718
          PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI
          HIDEYUKI TANAKA
          OS Mus sp. (mouse)
          PN WO 0102564-A/18
          PD 11-JAN-2001
          PF 29-JUN-2000 WO 2000JP004278
          PR 30-JUN-1999 JP 99P 186718
          PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI
          HIDEYUKI TANAKA
          PI MOGI,
          PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
          PC C12N15/12, C12N5/10, C12P21/02, C07K16/47, C07K16/18, A61K45/00, PC
          A61K38/17,
          PC A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/7088// (C12P21/
          PC 02, C12R1:19)
          CC 02, C12R1:19)
          FH Key Location/Qualifiers
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          FT /organism="Mus sp."
          FT /mol_type="genomic DNA"
          FT /db_xref="taxon:10095"

BASE COUNT 91 a 60 c 92 g 87 t
ORIGIN
Alignment Scores:
Pred. No.: 3,68e-61 Length: 330
Score: 574.00 Matches: 106
Percent Similarity: 99.09% Conservative: 3
Best Local Similarity: 96.36% Mismatches: 1
Query Match: 97.12% Indels: 0
DB: Gaps: 0
US-10-019-455a-49 (1-110) x BD093118 (1-330)

Qy      1 HisGlyMetPheMetAspIlySLeuSerSeryIlySLeuCyAlaAspGluGluCysVal 20
Db      1 CATGCGTATTATGATATAAAGCTTTCTTCTAGAGAGTTGTGCGGATGAGAGAGTGTGC 60

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QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
DB 61 TATACCTATTCTCTGGCAGACAGCACAGAAATTACATGCCAGACTGTAGTTTCATC 120
QY 41 AsnValIleLysGlyGlnIleTyrValIleTyrSerLysLeuValIleThrGluAsnGlyAla 60
DB 121 GATGCAAGAAAGGCGAGCAGATCTATGTTTACTCCAAAGCTGTACAGAAAGCGAGCT 180
QY 61 GlyAlaPheTrpAlaGlySerValIleTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
DB 181 GGAGAGTTTGGCTGGCAGCTGTATGTCACACAGATGAGATGGGATTTGAGT 240
QY 81 TyrPheProSerAsnLeuValArgGluGlnArgValIleTyrGlnGluAlaThrLysGluIle 100
DB 241 TATTTCCCGACCAACTGTGTAGAGAGAGCGTGTATACAGAGGCCACCAAGAGATC 300
QY 101 ProThrThrAspIleAspPhePheCysGlu 110
DB 301 CCAACACAGATATTGACTTCTCTGTGAA 330

RESULT 7
BD010805 384 bp DNA linear PAT 31-JAN-2002
LOCUS BD010805
DEFINITION Novel polypeptide and DNA thereof.
ACCESSION BD010805.1 GI:18639178
VERSION JP 2001069994-A/6.
KEYWORDS Mus sp.
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 384)
Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
Yoshimura, K. and Tanaka, H.
Novel polypeptide and DNA thereof
Patent: JP 2001069994-A 6 21-MAR-2001;
TAKEDA CHEMICAL INDUSTRIES LTD
COMMENT OS Mus sp. (mouse)
PN JP 2001069994-A/6
PD 21-MAR-2001
PF 29-JUN-2000 JP 2000195911
PR

REFERENCE
AUTHORS ITO, Y., NISHI, K., OGI, K., OKUBO, S., MOGI, S., NOGUCHI, Y.,
TITLE Novel polypeptide and DNA thereof
JOURNAL Patent: JP 2001069994-A 6 21-MAR-2001;
TAKEDA CHEMICAL INDUSTRIES LTD
COMMENT OS Mus sp. (mouse)
PN JP 2001069994-A/6
PD 21-MAR-2001
PF 29-JUN-2000 JP 2000195911
PR

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BASE COUNT 98 a 68 c 111 g 107 t
ORIGIN
Alignment Scores:
Pred. No.: 4,32e-61 Length: 384
Score: 574.00 Matches: 106
Percent Similarity: 99.09% Conservative: 3
Best Local Similarity: 96.36% Mismatches: 1
Query Match: 97.12% Indels: 0
Gaps: 0
DB: 6
US-10-019-455a-49 (1-110) x BD010805 (1-384)

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QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
DB 115 TATACCTATTCTCTGGCAGACAGCACAGAAATTACATGCCAGACTGTAGTTTCATC 174
QY 41 AsnValIleLysGlyGlnIleTyrValIleTyrSerLysLeuValIleThrGluAsnGlyAla 60
DB 175 GATGCAAGAAAGGCGAGCAGATCTATGTTTACTCCAAAGCTGTACAGAAAGCGAGCT 234
QY 61 GlyAlaPheTrpAlaGlySerValIleTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
DB 235 GGAGAGTTTGGCTGGCAGCTGTATGTCACACAGATGAGATGGGATTTGAGT 294
QY 81 TyrPheProSerAsnLeuValArgGluGlnArgValIleTyrGlnGluAlaThrLysGluIle 100
DB 295 TATTTCCCGACCAACTGTGTAGAGAGCGCTGTATACAGAGGCCACCAAGAGATC 354
QY 101 ProThrThrAspIleAspPhePheCysGlu 110
DB 355 CCAACACAGATATTGACTTCTCTGTGAA 384

RESULT 8
BD093106 384 bp DNA linear PAT 27-AUG-2002
LOCUS BD093106
DEFINITION Novel polypeptide and its DNA.
ACCESSION BD093106.1 GI:22638694
VERSION WO 0102564-A/6.
KEYWORDS Mus sp.
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 384)
Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
Yoshimura, K. and Tanaka, H.
Novel polypeptide and its DNA
Patent: WO 0102564-A 6 11-JAN-2001;
TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO
OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,
HIDEYUKI TANAKA
COMMENT OS Mus sp. (mouse)
PN WO 0102564-A/6
PD 11-JAN-2001
PF 29-JUN-2000 WO 2000JP004278
PR 30-JUN-1999 JP 99P 186718
PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI
MOGI,
YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/12, C12N5/10, C12P21/02, C07K14/47, C07K16/18, A61K45/00, PC
A61K38/17
PC A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/0086, C12P21/
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CC
FH Key Location/Qualifiers.
FEATURES
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BASE COUNT 98 a 68 c 111 g 107 t
ORIGIN
Alignment Scores:
Pred. No.: 4,32e-61 Length: 384
Score: 574.00 Matches: 106
Percent Similarity: 99.09% Conservative: 3
Best Local Similarity: 96.36% Mismatches: 1
Query Match: 97.12% Indels: 0
Gaps: 0
DB: 6

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US-10-019-455a-49 (1-110) x BD093106 (1-384)

QY 1 HisGlyMetPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGlnGluCysVal 20
 Db 55 CATGGTGATTTATGATTAACCTTCTCTTAAGAAGTGTGTGGCGATGAGAGTGTGTC 114

QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
 Db 115 TATACATATTCTCTGGCAAGACACAGAAAGATTCAATGCCCGACGCTGATGCTCATC 174

QY 41 AsnValLysLysGlnGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
 Db 175 GATGTCAGAAAGGGGACGACATCTATGTTTCTCCAGCTGTAAACGAAACGAGACT 234

QY 61 GlyAlaPheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
 Db 235 GGAGAGTTTGGGCTGGCAGTGTATTATGTCGACACACAGATGATGGAAATTGTAGT 294

QY 81 TyrPheProSerAsnLeuValArgGlnArgValTyrGlnGluAlaThrLysGluIle 100
 Db 295 TATTTCCCGACCACTGGTGAAGGACGCGGTATACACAGAGGCCACCAAGGAGATC 354

QY 101 ProThrThrAspIleAspPhePheCysGlu 110
 Db 355 CCACACGCGATATTGACTTTCTGTGAA 384

RESULT 9
 AF243504 929 bp mRNA linear ROD 26-DEC-2000
 LOCUS AF243504 Mus musculus fibrocyte-derived protein (Fdp) mRNA, complete cds.
 DEFINITION AF243504
 VERSION AF243504.1 GI:11991841
 KEYWORDS
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 929)
 Cohen-Salmon, M., Frenz, D., Liu, W., Verpy, E., Voegelings, S. and Petit, C.
 Fdp, a new fibrocyte-derived protein related to MfA/CD-RAP, has an in vitro effect on the early differentiation of the inner ear mesenchyme
 J. Biol. Chem. 275 (51), 40036-40041 (2000)

REFERENCE
 JOURNAL MEDLINE
 PUBMED 10998416
 AUTHORS Cohen-Salmon, M., Frenz, D., Verpy, E., Voegelings, S. and Petit, C.
 TITLE Direct Submission
 JOURNAL Submitted (09-MAR-2000) Biotechnologies, Institut Pasteur, 25 rue du Dr. Roux, Paris 75015, France

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BASE COUNT 260 a 156 c 220 g 293 t
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Alignment Scores:
 Pred. No.: 1,1e-60 Length: 929
 Score: 574.00 Matches: 106
 Percent Similarity: 99.09% Conservative: 3
 Best Local Similarity: 96.36% Mismatches: 1
 Query Match: 97.12% Indels: 0
 DB: 10 Gaps: 0

US-10-019-455a-49 (1-110) x AF243504 (1-929)

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QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
 Db 123 TATACATATTCTCTGGCAAGACACAGAAAGATTCAATGCCCGACGCTGATGCTCATC 182

QY 41 AsnValLysLysGlnGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
 Db 183 GATGTCAGAAAGGGGACGACATCTATGTTTCTCCAGCTGTAAACGAAACGAGACT 242

QY 61 GlyAlaPheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
 Db 243 GGAGAGTTTGGGCTGGCAGTGTATTATGTCGACACACAGATGATGGAAATTGTAGT 302

QY 81 TyrPheProSerAsnLeuValArgGlnArgValTyrGlnGluAlaThrLysGluIle 100
 Db 303 TATTTCCCGACCACTGGTGAAGGACGCGGTATACACAGAGGCCACCAAGGAGATC 362

QY 101 ProThrThrAspIleAspPhePheCysGlu 110
 Db 363 CCACACGCGATATTGACTTTCTGTGAA 392

RESULT 10
 BD010821 947 bp DNA linear PAT 31-JAN-2002
 LOCUS BD010821 Novel polypeptide and DNA thereof.
 DEFINITION BD010821
 ACCESSION BD010821 GI:18639194
 VERSION BD010821.1 GI:18639194
 KEYWORDS JP 2001069994-A/22.

SOURCE Mus sp.
 ORGANISM Mus sp.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 947)
 Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y., Yoshimura, K. and Tanaka, H.
 Novel polypeptide and DNA thereof
 Patent: JP 2001069994-A 22 21-MAR-2001;
 TAKEDA CHEMICAL INDUSTRIES LTD
 OS Mus sp. (mouse)
 PN JP 2001069994-A/22

REFERENCE
 JOURNAL
 PATENT
 AUTHORS Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y., Yoshimura, K. and Tanaka, H.
 TITLE Novel polypeptide and DNA thereof
 JOURNAL Patent: JP 2001069994-A 22 21-MAR-2001;
 TAKEDA CHEMICAL INDUSTRIES LTD
 COMMENT OS Mus sp. (mouse)
 PN JP 2001069994-A/22
 PD 21-MAR-2001
 PF 29-JUN-2000 JP 2000195911
 PR

PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI SHINICHI MOGI,
 PI YUKO NOGUCHI KOJI YOSHIMURA, HIDEYUKI TANAKA
 PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC A61P19/08,
 PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/45, G01N33/50, PC G01N33/53//
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BASE COUNT 279 a 158 c 221 g 289 t
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Alignment Scores:
Pred. No.: 1,12e-60 Length: 947
Score: 574.00 Matches: 106
Percent Similarity: 99.09% Conservative: 3
Best Local Similarity: 96.36% Mismatches: 1
Query Match: 97.12% Indels: 0
DB: 6 Gaps: 0

US-10-019-455a-49 (1-110) x BD010821 (1-947)

QY 1 HisGlyMetPheMetAspLysLeuSerLysLysLeuCyAAlaAspGluGluCyVal 20
Db 65 CATGGTGTATTATGAGTAACTTCTCTTAAGAAAGTTGTGTGGAGATGAGAGTGTGTC 124

QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
Db 125 TATACTATTCTCTGGCAAGAGCAGAGAAATTACATGCCAGACTGTAGTTTCATC 184

QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
Db 185 GATGTCAAGAAAGGAGCAGATCTATGTTACTCCAGCTGTAAACAGAAACGAGACT 244

QY 61 GlyAlaPheTyrAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
Db 245 GGAAGATTGGGTGGCGAGTGTATGTCGACCCAGAGATGAGATGGAAATTGTAGGT 304

QY 81 TyrPheProSerAsnLeuValArgGluGlnArgValTyrGlnGluAlaThrLysGluIle 100
Db 305 TATTCCCGCAACTGTGTGAAGAGCAGCGTGTATACCAAGAGGCCACCAAGAGATC 364

QY 101 ProThrThrAspIleAspPhePheCysGlu 110
Db 365 CCACCCAGGATATTGACTTCTGTGAA 394

RESULT 11
BD093122 947 bp DNA linear PAT 27-AUG-2002
LOCUS Novel polypeptide and its DNA.
DEFINITION BD093122
ACCESSION BD093122.1 GI:22638710
VERSION WO 0102564-A/22.
KEYWORDS Mus sp.
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 947)
Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y., Yoshimura, K. and Tanaka, H.
Novel polypeptide and its DNA
Patent: WO 0102564-A 22 11-JAN-2001;
TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
HIDEYUKI TANAKA
OS Mus sp. (mouse)
PN WO 0102564-A/22
PD 11-JAN-2001
PF 29-JUN-2000 WO 2000/P004278
PR 30-JUN-1999 JP 99P 186718
PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI MOGI,
YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/12, C12N5/10, C12P21/02, C07K14/47, C07K16/18, A61K45/00, PC
A61K38/17
PC A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/7088//C12P21/
CC 02, C12R1:19
FH Key Location/Qualifiers.
1. 947

BASE COUNT 279 a 158 c 221 g 289 t
ORIGIN

Alignment Scores:
Pred. No.: 1,12e-60 Length: 947
Score: 574.00 Matches: 106
Percent Similarity: 99.09% Conservative: 3
Best Local Similarity: 96.36% Mismatches: 1
Query Match: 97.12% Indels: 0
DB: 6 Gaps: 0

US-10-019-455a-49 (1-110) x BD093122 (1-947)

QY 1 HisGlyMetPheMetAspLysLeuSerLysLysLeuCyAAlaAspGluGluCyVal 20
Db 65 CATGGTGTATTATGAGTAACTTCTCTTAAGAAAGTTGTGTGGAGATGAGAGTGTGTC 124

QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
Db 125 TATACTATTCTCTGGCAAGAGCAGAGAAATTACATGCCAGACTGTAGTTTCATC 184

QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
Db 185 GATGTCAAGAAAGGAGCAGATCTATGTTACTCCAGCTGTAAACAGAAACGAGACT 244

QY 61 GlyAlaPheTyrAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
Db 245 GGAAGATTGGGTGGCGAGTGTATGTCGACCCAGAGATGAGATGGAAATTGTAGGT 304

QY 81 TyrPheProSerAsnLeuValArgGluGlnArgValTyrGlnGluAlaThrLysGluIle 100
Db 305 TATTCCCGCAACTGTGTGAAGAGCAGCGTGTATACCAAGAGGCCACCAAGAGATC 364

QY 101 ProThrThrAspIleAspPhePheCysGlu 110
Db 365 CCACCCAGGATATTGACTTCTGTGAA 394

RESULT 12
MMU243939 958 bp mRNA linear ROD 29-JAN-2001
LOCUS MMU243939
DEFINITION Mus musculus mRNA for melanoma inhibitory activity-like protein (Mial gene).
ACCESSION AJ243939
VERSION AJ243939.1 GI:12619174
KEYWORDS melanoma inhibitory activity-like protein; Mial gene.
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 958)
Rendtorff, N.D., Frodin, M., Attie-Bitach, T., Vekemans, M. and Tommerup, N.
Identification and characterization of an inner ear-expressed human melanoma inhibitory activity (MIA)-like gene (MIAL) with a frequent polymorphism that abolishes translation
Genomics 71 (1), 40-52 (2001)
JOURNAL MEDLINE
PUBMED 11161796
REFERENCE 2 (bases 1 to 958)
TITLES
AUTHORS
JOURNAL
COMMENT Submitted (20-JUL-1999) Rendtorff N.D., Department of Medical Genetics, Institute of Medical Biochemistry and Genetics, Blegdamsvej 3, 2200 Copenhagen N, DENMARK
Related sequence: AJ245552.
FEATURES
1. 958
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"

AUTHORS Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
Yoshimura, K. and Tanaka, H.
TITLE Novel polypeptide and DNA thereof
JOURNAL Patent: JP 200106994-A 17 21-MAR-2001;
TAKEDA CHEMICAL INDUSTRIES LTD
COMMENT OS Homo sapiens (human)
PN JP 200106994-A/17
PD 21-MAR-2001
PF 29-JUN-2000 JP 2000195911

PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI
SHINICHI MOGI,
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC
A61P19/08,
PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC
G01N33/53//
PC C12P21/08, C12N15/00, A61K37/02, C12N5/00
CC
FH Key Location/Qualifiers
FT source 1. 330
Location/Qualifiers
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source 1. 330
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 91 a 60 c 91 g 88 t
ORIGIN

Alignment Scores:

Pred. No.: 3.97e-57 Length: 330
Score: 541.00 Matches: 98
Percent Similarity: 95.45% Conservative: 7
Best Local Similarity: 89.09% Mismatches: 5
Query Match: 91.54% Indels: 0
DB: 6 Gaps: 0

US-10-019-455a-49 (1-110) x BD010816 (1-330)

QY 1 HisgIyMeCPheMeAspLyLeuSerSerLySylsLeuCyAlaAspGluGluCysVal 20
DB 1 CATGGAATATTATTCAGACCGCTAGCTCCAAAGAGCTCTGTGAGATGATGATGCTC 60
QY 21 TyrThrIleSerLeuAlaArgAlaGlnGlnAspTyrAsnAlaProAspCysArgPheIle 40
DB 61 TATATCTATTCTCTGGCTAGTGGCTCAAGAGATTATATGCCCCGAGCTGATGATTCATT 120
QY 41 AsnValLySylsGlnGlnIleTyrValTyrSerLySylsLeuValThrGluAsnGlyAla 60
DB 121 AACGTTAAAAAGGCGACAGATCTATGTGATCTCAAGAGCTGTGTTAAAAAGAAATGAGCT 180
QY 61 GlyAlaPheTrrPAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
DB 181 GGAGATTTTGGCTGGCAGTGTATTATGCTATGCGCAGACGAGATGGAGTGTGCGCT 240
QY 81 TyrPheProSerAsnLeuValArgGlnGlnArgValTyrGlnGlnAlaThrLySylsIle 100
DB 241 TATTTCCCGAGAACTTGTCAAGAAACAGCGTGTATGACGAGAACTTACCAAGAGAGTT 300
QY 101 ProThrThrAspIleAspPhePheCysGlu 110
DB 301 CCCACACGAGATTTGACTTCTTCTGCGAG 330

RESULT 15
BD093117 330 bp DNA linear PAT 27-AUG-2002
LOCUS BD093117
DEFINITION Novel polypeptide and its DNA.
ACCESSION BD093117
VERSION BD093117.1 GI:22638705
KEYWORDS WO 0102564-A/17.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 330)
AUTHORS Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
Yoshimura, K. and Tanaka, H.
TITLE Novel polypeptide and its DNA
JOURNAL Patent: WO 0102564-A 17 11-JAN-2001;
TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO
OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,
HIDEYUKI TANAKA
COMMENT OS Homo sapiens (human)
PN WO 0102564-A/17
PD 11-JAN-2001
PF 29-JUN-2000 WO 2000JP004278
PR 30-JUN-1999 JP 99P 186718
PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI

PI MOGI,
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/12, C12N5/10, C12P21/02, C07K14/47, C07K16/18, A61K45/00, PC
A61K38/17,
PC A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/7086//C12P21/
PC 02, C12N1:19)
CC
FH Key Location/Qualifiers
FEATURES
source 1. 330
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 91 a 60 c 91 g 88 t
ORIGIN

Alignment Scores:

Pred. No.: 3.97e-57 Length: 330
Score: 541.00 Matches: 98
Percent Similarity: 95.45% Conservative: 7
Best Local Similarity: 89.09% Mismatches: 5
Query Match: 91.54% Indels: 0
DB: 6 Gaps: 0

US-10-019-455a-49 (1-110) x BD093117 (1-330)

QY 1 HisgIyMeCPheMeAspLyLeuSerSerLySylsLeuCyAlaAspGluGluCysVal 20
DB 1 CATGGAATATTATTCAGACCGCTAGCTCCAAAGAGCTCTGTGAGATGATGATGCTC 60
QY 21 TyrThrIleSerLeuAlaArgAlaGlnGlnAspTyrAsnAlaProAspCysArgPheIle 40
DB 61 TATATCTATTCTCTGGCTAGTGGCTCAAGAGATTATATGCCCCGAGCTGATGATTCATT 120
QY 41 AsnValLySylsGlnGlnIleTyrValTyrSerLySylsLeuValThrGluAsnGlyAla 60
DB 121 AACGTTAAAAAGGCGACAGATCTATGTGATCTCAAGAGCTGTGTTAAAAAGAAATGAGCT 180
QY 61 GlyAlaPheTrrPAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
DB 181 GGAGATTTTGGCTGGCAGTGTATTATGCTATGCGCAGACGAGATGGAGTGTGCGCT 240
QY 81 TyrPheProSerAsnLeuValArgGlnGlnArgValTyrGlnGlnAlaThrLySylsIle 100
DB 241 TATTTCCCGAGAACTTGTCAAGAAACAGCGTGTATGACGAGAACTTACCAAGAGAGTT 300
QY 101 ProThrThrAspIleAspPhePheCysGlu 110
DB 301 CCCACACGAGATTTGACTTCTTCTGCGAG 330

Search completed: December 29, 2003, 19:57:24
Job time : 1812.69 secs

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 29, 2003, 16:23:14 ; Search time 1136.05 Seconds

(without alignments)
2349.180 Million cell updates/sec

SUMMARIES

29: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Title: US-10-019-455A-49
Perfect score: 1 HGMFMDKLSKKLCADECEV.....RVQEAATKEPTTIDDFCE 110
Sequence: 1 HGMFMDKLSKKLCADECEV.....RVQEAATKEPTTIDDFCE 110

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 22781392 segs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seg length: 0
Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters: -DEV=xlh
-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO/spool/US10019455/runat_29122003_160347_254/app_query.fasta_1.1770
-DB=EST -QFMT=fastap -SUFIX=1rst -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNIT=bits -START=1 -END=-1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10019455@cgn.1.1.6063 @runat_29122003_160347_254 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPELLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database:

EST.*
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2: em_esthum.*
3: em_estlin.*
4: em_estmu.*
5: em_estrov.*
6: em_estrpl.*
7: em_estro.*
8: em_hic.*
9: gb_est1.*
10: gb_est2.*
11: gb_hic.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: em_gss_hum.*
18: em_gss_inv.*
19: em_gss_pln.*
20: em_gss_vit.*
21: em_gss_fun.*
22: em_gss_mam.*
23: em_gss_mus.*
24: em_gss_pro.*
25: em_gss_rtd.*
26: em_gss_phg.*
27: em_gss_vrl.*
28: gb_gssi.*

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 574 | 97.1 | 398 | 13 | BQ570035 |
| 2 | 574 | 97.1 | 488 | 13 | BQ564607 |
| 3 | 574 | 97.1 | 514 | 13 | BQ568498 |
| 4 | 574 | 97.1 | 534 | 13 | BQ564134 |
| 5 | 574 | 97.1 | 560 | 13 | BQ569741 |
| 6 | 574 | 97.1 | 608 | 13 | BQ568494 |
| 7 | 574 | 97.1 | 630 | 13 | BQ568471 |
| 8 | 574 | 97.1 | 684 | 13 | BQ563768 |
| 9 | 574 | 97.1 | 696 | 13 | BQ611549 |
| 10 | 569 | 96.3 | 474 | 13 | BQ565137 |
| 11 | 548 | 92.7 | 409 | 13 | BQ566932 |
| 12 | 542 | 91.7 | 490 | 13 | BQ565411 |
| 13 | 525 | 88.8 | 604 | 13 | BQ567343 |
| 14 | 483 | 81.7 | 365 | 13 | B7232622 |
| 15 | 441 | 74.6 | 527 | 10 | BE236443 |
| 16 | 427 | 72.3 | 485 | 13 | BQ565179 |
| 17 | 413.5 | 70.0 | 795 | 13 | BQ748241 |
| 18 | 362.5 | 61.3 | 533 | 9 | AL925854 |
| 19 | 357 | 60.4 | 588 | 13 | BQ566776 |
| 20 | 348 | 58.9 | 280 | 13 | BQ568785 |
| 21 | 292.5 | 49.5 | 3240 | 11 | AK047965 |
| 22 | 279.5 | 47.3 | 677 | 13 | BQ563227 |
| 23 | 265.5 | 44.9 | 442 | 9 | AA282143 |
| 24 | 265.5 | 44.9 | 633 | 14 | CD360404 |
| 25 | 265.5 | 44.9 | 929 | 13 | BQ195892 |
| 26 | 264.5 | 44.8 | 473 | 14 | CA433401 |
| 27 | 264.5 | 44.8 | 480 | 12 | BM1715936 |
| 28 | 264.5 | 44.8 | 492 | 12 | BM565478 |
| 29 | 264.5 | 44.8 | 507 | 12 | BM674250 |
| 30 | 264.5 | 44.8 | 515 | 13 | BQ592734 |
| 31 | 264.5 | 44.8 | 522 | 13 | BQ681978 |
| 32 | 264.5 | 44.8 | 522 | 13 | BQ157778 |
| 33 | 264.5 | 44.8 | 529 | 13 | BQ194561 |
| 34 | 264.5 | 44.8 | 609 | 12 | BM791767 |
| 35 | 264.5 | 44.8 | 890 | 12 | BQ766328 |
| 36 | 264.5 | 44.6 | 1140 | 12 | BQ765502 |
| 37 | 263.5 | 44.6 | 437 | 9 | AV592759 |
| 38 | 263.5 | 44.6 | 453 | 9 | AA627297 |
| 39 | 263.5 | 44.6 | 517 | 10 | BE665724 |
| 40 | 263.5 | 44.6 | 544 | 13 | BQ208982 |
| 41 | 263.5 | 44.6 | 594 | 14 | CA509768 |
| 42 | 260.5 | 44.1 | 381 | 9 | A1620915 |
| 43 | 260.5 | 44.1 | 430 | 10 | BF439750 |
| 44 | 260.5 | 44.1 | 678 | 10 | BB647928 |
| 45 | 260 | 44.0 | 349 | 9 | AM023324 |

ALIGNMENTS

RESULT 1
LOCUS BQ570035 398 bp mRNA linear EST 19-JUN-2002
DEFINITION g1143b10.y1 Mouse Organ of Corti cDNA pbluescript Mus musculus cDNA
ACCESSION BQ570035
VERSION BQ570035.1 GI:21473352
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 398)

Tue Dec 30 10:20:53 2003

us-10-019-455a-49.rst

Page 1

AUTHORS Kachar, B.
TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
JOURNAL Unpublished
COMMENT Contact: Kachar, B.
 Structural Cell Biology
 National Institute of Deafness and other Communication Disorders
 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
 Tel: 301-402-1599
 Fax: 301-402-1765
 Email: kachar@nidcd.nih.gov
 Plate: 143 row: b column: 10
 Seq primer: M13RPI reverse primer (ABI).
 Location/Qualifiers

FEATURES
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 /mol_type="mRNA"
 /strain="BALB/c"
 /db_xref="taxon:10090"
 /clone="g1143b10"
 /sex="male and female"
 /dev_stage="post natal day 5 to 13"
 /note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR GigaPack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and Phage H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with GigaPack III Gold and, upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAAACGCTATGACC) and 25x strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster

City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in Genbank and have known function; 23% have hits in Genbank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 105 a 69 c 116 g 108 t

ORIGIN

Alignment Scores:

| Pred. No.: | Length: | Matches: | Mismatches: | Indels: | Gaps: |
|------------------------|----------|----------|-------------|---------|-------|
| Score: | 1,19e-71 | 398 | 106 | 3 | 0 |
| Percent Similarity: | 574.00 | | | | |
| Best Local Similarity: | 99.09% | | | | |
| Query Match: | 96.36% | | | | |
| DB: | 97.12% | | | | |

US-10-019-455a-49 (1-110) x B0570035 (1-398)

QY 1 HisGlyMetCpHeMetAspLyLeuSerSerLyLeuCyAlaAspGluGluCyVal 20
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Db 67 CATGCTGATTTATGATTAACCTTCTTAAAGAGTTGTGCGATGAGAGTGTGTC 126
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QY 21 TTTThrIleSerLeuAlaArgAlaGluAspTyrAsnAlaProAspCysArgPheIle 40
 |||||:::
Db 127 TATACTATTTCTCTGGAGAGACAGAGAGATTACATGCCACAGACTGTAGCTTCAATC 186
 |||||:::
QY 41 AsnValIleSgLyGluGlnIleTyrValTyrSerLyLeuValThrGluGlnGlyAla 60
 |||||:::
Db 187 GATGTCAAGAAAGGACGACGATCTATGTTTATCCAGTGTGTAACAGAAACGAGGCT 246
 |||||:::
QY 61 GlyAlaPheTyrAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
 |||||:::
Db 247 GGAAGATTTGGCTGGCAGAGTGTATGAGACACACAGATGAGATGGAAATTGTAGGT 306
 |||||:::
QY 81 TyrPheProSerLeuLeuValArgGluGlnArgValTyrGlnGluAlaThrLyGluIle 100
 |||||:::
Db 307 TATTTCCCGACCACTTGGAAGGACGCGGTATACCGAGAGGCCACAGAGATC 366
 |||||:::
QY 101 ProThrThrAspIleAspPhePheCysGlu 110
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Db 367 CCACACGAGATTTACTTCTTCTGTGAA 396
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RESULT 2
LOCUS B0564607 488 bp mRNA linear EST 19-JUN-2002
DEFINITION g119h02.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA
 g119h02.5', mRNA sequence.

ACCESSION B0564607
VERSION B0564607.1 GI:21467924
KEYWORDS EST.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 488)

REFERENCE Kachar, B.
AUTHORS Kachar, B.
TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
JOURNAL Unpublished
COMMENT Contact: Kachar, B.
 Structural Cell Biology
 National Institute of Deafness and other Communication Disorders
 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
 Tel: 301-402-1599
 Fax: 301-402-1765
 Email: kachar@nidcd.nih.gov
 Plate: 19 row: h column: 02
 Seq primer: M13RPI reverse primer (ABI).
 Location/Qualifiers

FEATURES
 source 1..488
 /organism="Mus musculus"
 /mol_type="mRNA"

(catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR GigaPack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMuV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and Phase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been pre-digested with EcoR I and Xho I. The phagemid was packaged with GigaPack III Gold and, upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's EXASist interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concerta (TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAAACGGTATGACC) and 25th strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 147 a 85 c 143 g 139 t
ORIGIN

Alignment Scores:

Pred. No.: 1 73e-71 Length: 514
Score: 574.00 Matches: 106
Percent Similarity: 99.09% Conservative: 3
Best Local Similarity: 96.36% Mismatches: 1
Query Match: 97.12% Indels: 0
DB: 13 Gaps: 0

US-10-019-455a-49 (1-110) x BQ568498 (1-514)

QY 1 HisGlyMetPheMetAspLysLeuSerLysLysLeuCYsAlaAspGluGluCYsVal 20
DB 59 CATGCTGATATTATGATTAATCTTCTTAAGAGCTGTGTGCGATGAGAGATGCTC 118
QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
DB 119 TATACCTATTCTCTGGCAAGACACAGAGATTCATATGCCCGACTGTAGTTATC 178
QY 41 AsnValLysLysGlyGlnGlnIleLeuValTyrSerLysLeuValThrGluAsnGlyAla 60
DB 179 GATGTCAAGAAAGGCGACAGATCTATGTTACTCAAGCTGCTAAACAGAAACGAGCT 238
QY 61 G1AlaPheTyrAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
DB 239 GGAGAGCTTTGGCGCTGGCAGTGTTATGCTGACCCACGATGAGATGGAAATTGTAGCT 298

QY 81 TyrPheProSerAsnLeuValArgGluGluArgValTyrGlnGluIleThrLysGluIle 100
DB 299 TATTCCCGACCACTGTGGAAAGACACAGCTGATACAGAGGCGCACCAAGAGATC 358
QY 101 ProThrAspIleAspPhePheCysGlu 110
DB 359 CCAACACGAGATATGACTTCTCTGAA 388
RESULT 4
LOCUS BQ564134
DEFINITION g11d01.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA
ACCESSION BQ564134
VERSION BQ564134.1 GI:21467451
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 534)
REFERENCE
AUTHORS Kachar,B.
TITLE Est analysis of gene expression in the mouse Organ of Corti at the onset of hearing
JOURNAL Unpublished
COMMENT Contact: Kachar,B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: Kachar@nidcd.nih.gov
Plate: 11 row: d column: 01
Seq primer: M13P1 reverse primer (AB1).
FEATURES
Location/Qualifiers
1..534
/organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
/db_xref="taxon:10090"
/clone="g11d01"
/sex="male and female"
/dev_stage="Post natal day 5 to 13"
/note="Organ: Organ of Corti. Vector: pBluescript. The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5-72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR GigaPack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMuV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and Phase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden)

and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XL1 Blue MRF⁺ cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExSist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 µl of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAAACGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 155 a 87 c 148 g 144 t
ORIGIN

Alignment Scores:
Pred. No.: 1,838-71 Length: 534
Score: 574.00 Matches: 106
Percent Similarity: 99.09% Conservative: 3
Best Local Similarity: 96.36% Mismatches: 1
Query Match: 97.12% Indels: 0
Gaps: 13

US-10-019-455A-49 (1-110) x BQ564134 (1-534)

QY 1 HisGlyMetPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysVal 20
DB 57 CATGGTGTATTATGATTAACCTTCTCTAAGAAAGTTGTGTGGAGAGAGAGATGCTC 116
QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
DB 117 TATACTATTCTCTGCAAGACAGACAGAAATTACATGCCCACTGTAGTTGATC 176
QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
DB 177 GATGTCAGAAAGGCGACAGATCTATGTTACTCCAGCTGGTACAGAAACGAGACT 236
QY 61 GlyAlaPheTTPAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
DB 237 GGAAGCTTTGGCGCGAGCTTTATGCTACACCAAGAGAGAGATGGT 296
QY 81 TyrPheProSerAsnLeuValArgGluGlnArgValTyrGlnGlnIleThrLysGluIle 100
DB 297 TATTTCCTCCACCACTTGTGAAGAGACGCTGTATACCAAGAGAGGCGACCAAGACATC 356
QY 101 ProThrThrAspPhePhePheCysGlu 110
DB 357 CCAACCAAGATTTGACTTCTCTGTGA 386

RESULT 5
BQ569741 560 bp mRNA linear EST 19-JUN-2002
LOCUS BQ569741
DEFINITION g1135f01.y1 Mouse Organ of Corti cDNA Bluescript Mus musculus cDNA
clone g1135f01 5', mRNA sequence.
ACCESSION BQ569741
VERSION BQ569741.1 GI:21473058
KEYWORDS EST.

SOURCE

ORGANISM

Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 560)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
Unpublished
Contact: Kachar, B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: kachar@nidcd.nih.gov
Plate: 135 row: f column: 01
Seq primer: M13RPI reverse primer (ABI).
Location/Qualifiers

FEATURES

source

1..560
/organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
/db_xref="taxon:10090"
/clone="g1135f01"
/sex="male and female"
/dev_stage="Post natal day 5 to 13"
/clone_lib="Mouse Organ of Corti cDNA Bluescript"
/note="Organ: Organ of Corti; Vector: Bluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (p) day 5; 72 from p6; 60 from p7; 46 from p8; 18 from p9; 20 from p10; 14 from p12 and 24 from p13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was clipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro FastTrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-ZAP XR vector kit (catalog # 237211, Stratagene) and Uni-ZAP XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 µg RNA was reverse transcribed using a hybrid of 3'g0(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of 119ase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XL1 Blue MRF⁺ cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExSist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 µl of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAAACGCTATGACC) and 25%

strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 160 a 92 c 154 g 153 t 1 others

ALIGNMENT SCORES:

Pred. No.: 1,97e-71 Length: 560
Score: 574.00 Matches: 106
Percent Similarity: 99.09% Conservative: 3
Best Local Similarity: 96.36% Mismatches: 1
Query Match: 97.12% Indels: 0
DB: 13 Gaps: 0

US-10-019-455A-49 (1-110) x B0569741 (1-560)

QY 1 HisGlyMetPheMetAspLysLeuSerLysLysLeuCysAlaAspGluGluCysVal 20
DB 60 CATGCGTATTTATGATTAATCTTCTTAAGAGTTGTGTGGGATGAGGAGTGTGTC 119
QY 21 TTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 40
DB 120 TATACATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 179
QY 41 AenValLysLysGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 60
DB 180 GATGTAAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 239
QY 61 GAlaAlaPheTyrPheLysLysLysLysLysLysLysLysLysLysLysLysLys 80
DB 240 GGGAGATTTTGGGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 299
QY 81 TTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 100
DB 300 TATTTTCCCGAGCACTTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 359
QY 101 TTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 110
DB 360 CCACACGAGGATTTACTTCTTCTGAA 389

RESULT 6
B0564944 608 bp mRNA linear EST 19-JUN-2002
LOCUS B0564944
DEFINITION g127909.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA
clone g127909 5', mRNA sequence.

ACCESSION B0564944
VERSION B0564944.1 GI:21468261
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 608)
AUTHORS Kachar, B.
TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing

JOURNAL Unpublished
COMMENT Contact: Kachar, B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/449 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: kachar@nidcd.nih.gov
Plate: 27 row: 9 column: 09

FEATURES

Seq primer: M13RPL reverse primer (AB1).
Location/Qualifiers
1..608
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/mol_type="mRNA"
/strain="BALB/c"
/db_xref="taxon:10090"
/clone="g127909"
/sex="male and female"
/dev_stage="Post natal day 5 to 13"
/clone_lib="Mouse Organ of Corti cDNA pBluescript"
/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away. Ectria vasculature and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR GigaPack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug RNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with GigaPack III Gold and upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExSist Intertence resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAAACAGCTATGAC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT

169 a 107 c 166 g 166 t

ALIGNMENT SCORES:

Pred. No.: 2.22e-71 Length: 608
Score: 574.00 Matches: 106

Percent Similarity: 99.09% Conservative: 3
 Best Local Similarity: 96.36% Mismatches: 1
 Query Match: 97.12% Indels: 0
 Gaps: 0

US-10-019-455a-49 (1-110) x BQ568471 (1-608)

QY 1 HisGlyMetPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysVal 20
 DB CATGGTGTATTTATGATTAACCTTCTCTTAAGAAGTTGTGTGGCATGAGAGATGTCTC 126
 QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProaspCysArgPheIle 40
 DB TATACTATTCTCTGGCAAGACACAGAGATTAATGCCCCAGACTGAGTTTCATC 186
 QY 41 AsnValIleLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
 DB GATGTCAGAAAGGACAGACAGATCTATGTTTACTCCAAAGCTGGTACAGAAACGGAGCT 246
 QY 61 GlyAlaPheTyrAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
 DB GGAAGAGTTTGGCTGGCAGCTTTATGCTGACCAACAGATGAGATGGGATTTGTAGCT 306
 QY 81 TyrPheProSerAsnLeuValArgGluGlnArgValTyrGlnGluAlaThrLysGluIle 100
 DB TATTTCCCAACCACTTGCTGAGACAGACGCTGATATACAGAGCCACCAAGAGATGC 366
 QY 101 ProThrThrAspIleAspPheCysGlu 110
 DB 367 CCAACCAAGGATATTGACTTCTCTGTGAA 396

RESULT 7
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 LOCUS 91108904.y1 Mouse Organ of Corti cDNA Bluescript Mus musculus cDNA
 DEFINITION clone g1108904 5', mRNA sequence.
 ACCESSION BQ568471
 VERSION BQ568471.1 GI:21471788
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Kachar, B.
 EST analysis of gene expression in the mouse Organ of Corti at the
 onset of hearing
 Unpublished
 Contact: Kachar, B.
 Structural Cell Biology
 National Institute of Deafness and other Communication Disorders
 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
 Tel: 301-402-1599
 Fax: 301-402-1765
 Email: kachar@nidcd.nih.gov
 Plate: 108 row: 9 column: 04
 Seq primer: M13RPI reverse primer (ABT).
 Location/Qualifiers
 1. 630
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="BALB/c"
 /db_xref="taxon:10090"
 /clone="g1108904"
 /sex="male and female"
 /dev_stage="Post natal day 5 to 13"
 /note="Organ: Organ of Corti; Vector: Bluescript; The
 OC as follows: 102 samples from post-natal (P) day 5; 72
 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
 14 from P12 and 24 from P13. After killing animals by
 cervical dislocation followed by decapitation, the bulla

JOURNAL
 COMMENT
 FEATURES
 SOURCE

US-10-019-455a-49 (1-110) x BQ568471 (1-630)

QY 1 HisGlyMetPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysVal 20
 DB CATGGTGTATTTATGATTAACCTTCTCTTAAGAAGTTGTGTGGCATGAGAGATGTCTC 126
 QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProaspCysArgPheIle 40
 DB TATACTATTCTCTGGCAAGACACAGAGATTAATGCCCCAGACTGAGTTTCATC 186
 QY 41 AsnValIleLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
 DB GATGTCAGAAAGGACAGACAGATCTATGTTTACTCCAAAGCTGGTACAGAAACGGAGCT 246
 QY 61 GlyAlaPheTyrAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
 DB GGAAGAGTTTGGCTGGCAGCTTTATGCTGACCAACAGATGAGATGGGATTTGTAGCT 306
 QY 81 TyrPheProSerAsnLeuValArgGluGlnArgValTyrGlnGluAlaThrLysGluIle 100
 DB TATTTCCCAACCACTTGCTGAGACAGACGCTGATATACAGAGCCACCAAGAGATGC 366
 QY 101 ProThrThrAspIleAspPheCysGlu 110
 DB 367 CCAACCAAGGATATTGACTTCTCTGTGAA 396

BASE COUNT 178 a 111 c 167 g 174 t

Alignment Scores:

Score: 2,34e-71 Length: 630
 Percent Similarity: 99.09% Mismatches: 106
 Best Local Similarity: 96.36% Mismatches: 1
 Query Match: 97.12% Indels: 0
 DB: 13 Gaps: 0

US-10-019-455a-49 (1-110) x BQ568471 (1-630)

QY 1 HisGlyMetPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysVal 20
 DB CATGGTGTATTTATGATTAACCTTCTCTTAAGAAGTTGTGTGGCATGAGAGATGTCTC 126
 QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProaspCysArgPheIle 40
 DB TATACTATTCTCTGGCAAGACACAGAGATTAATGCCCCAGACTGAGTTTCATC 186
 QY 41 AsnValIleLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
 DB GATGTCAGAAAGGACAGACAGATCTATGTTTACTCCAAAGCTGGTACAGAAACGGAGCT 246
 QY 61 GlyAlaPheTyrAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
 DB GGAAGAGTTTGGCTGGCAGCTTTATGCTGACCAACAGATGAGATGGGATTTGTAGCT 306
 QY 81 TyrPheProSerAsnLeuValArgGluGlnArgValTyrGlnGluAlaThrLysGluIle 100
 DB TATTTCCCAACCACTTGCTGAGACAGACGCTGATATACAGAGCCACCAAGAGATGC 366
 QY 101 ProThrThrAspIleAspPheCysGlu 110
 DB 367 CCAACCAAGGATATTGACTTCTCTGTGAA 396

was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus.

Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR GigaPack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly, 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with GigaPack III Gold and, upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExSist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96 (TW) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAAACGCTTATAC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on M7 Retard thermal cyclers (MW Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified.

```

Db      187 GATGTCAAGAAAGGCGAGAGATGATGTTTACTCCAGCTGTAAAGAAAGGAGCT 246
Qy      61 G1yAlaPheTpa1AG1SeValTyrg1AspHisGlnAspGluMeTg1y1LeValGly 80
Db      247 GGAGAGTTTGGGCTGGCAGTGTATGATGACCAAGAGATGAGATGGGAATTTAGAT 306
Qy      81 TyrrPheProSerAsnLeuValArgGluGlnArgValTyrg1GlnAlaThrLysGluIle 100
Db      307 TATTTTCCCGAAGCACTTGTAAGAGAGCGGTGTATACCAAGAGGCCACCAAGAGATC 366
Qy      101 ProThrThraSp1LeaSpPhePheCysGlu 110
Db      367 CCACCAAGGATATTGACTTCTTCTGTGA 396

RESULT 8
B0563768      684 bp      mRNA      linear      EST 19-JUN-2002
LOCUS      g106c09.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA
DEFINITION
ACCESSION      B0563768
VERSION      B0563768.1 GI:21466749
KEYWORDS
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 684)
AUTHORS      Kachar,B.
TITLE      EST analysis of gene expression in the mouse Organ of Corti at the
JOURNAL      onset of hearing
COMMENT      Unpublished
Contact: Kachar,B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: kachar@nidcd.nih.gov
Plate: 06 row: C column: 09
Seq primer: M13Rpl reverse primer (AB1).
FEATURES
Source
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/strain="BALB/c"
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/sex="male and female"
/notes="Organ: Organ of Corti; Vector: pBluescript; The
organ of Corti (OC) was fine dissected from a total of 386
OC as follows: 102 samples from post-natal (p) day 5, 72
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
14 from P12 and 24 from P13. After killing animals by
cervical dislocation followed by decapitation, the bulla
was removed and opened in Leibowitz medium. The bony
capsule of the cochlea was clipped away, stria vascularis
and spiral ligament were removed and the sensory
epithelium was carefully dissected out of the modiolus.
Total RNA was extracted using the micro Fasttrack kit
(catalog # K1593-02; Invitrogen, Carlsbad, CA), according
to manufacturer's instructions. Reverse transcription and
library construction were carried out with the Uni-Zap XR
vector kit (catalog # 237211, Stratagene) and Uni-Zap XR
GigaPack III Gold Cloning kit (catalog # 237612), both
from Stratagene (La Jolla, CA, USA), according to
manufacturer's instructions. Briefly: 1.5 ug mRNA was
reverse transcribed using a hybrid oligo(dT) linker-primer
that contains an Xho I site. First strand synthesis was
primed with the linker-primer and transcribed using
Moloney murine leukemia virus reverse transcriptase
(MMLV-RT) and 5-methyl dCTP. The second strand was

```

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synthesized with DNA polymerase and RNase H. Complementary
DNA was blunt ended with Pfu DNA polymerase, ligated with
EcoR I adapters in the presence of ligase and digested
with Xho I. The cDNA was sequentially size fractionated
over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden)
and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA)
columns to enrich for cDNAs greater than 400bp and 1000 bp
, respectively. The cDNA was then directionally ligated to
the Uni-Zap XR vector, which had been predigested with
EcoR I and Xho I. The phagemid was packaged with GigaPack
III Gold and, upon titration on XLI Blue MRF+ cells, the
yield of the phage library was estimated to be 11,100,000
recombinants. Stratagene's ExAssist Interference
resistance helper phage (catalogue # 211203) was adopted
to rescue plasmid DNA from the phages. Upon plating of the
rescued library, individual cDNA clones were selected and
grown in 96-well, 2 ml growth plate. Plasmid DNA was
purified from 200 ul of saturated culture with the
Concert96(TM) plasmid purification kit (Invitrogen,
Carlsbad, CA) as instructed by the manufacturer. ESTs from
the 5' end of the cDNA clones were generated with the
universal M13 reverse primer (CAGGAAACAGTATGAC) and 25x
strength BigDye terminator sequencing chemistry (Applied
Biosystems, Foster City, CA). Sequencing reactions were
performed on MJ Tetrad thermal cyclers (MJ Research,
Watham, MA) and analyzed on 3700 automated capillary
sequencers using POP5 polymer (Applied Biosystems, Foster
City, CA). The frequency distribution of the library is
as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10;
1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of
genes are present in GenBank and have known function; 23%
have hits in GenBank, but do not have assigned function;
12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT      194 a      120 c      178 g      192 t
ORIGIN

Alignment Scores:
Pred. No.:      2,63e-71      Length:      684
Score:      574.00      Matches:      106
Percent Similarity: 99.09%      Conservative: 3
Best Local Similarity: 96.36%      Mismatches: 1
Query Match: 97.12%      Indels: 0
DB: 13      Gaps: 0

US-10-019-455A-49 (1-110) x B0563768 (1-684)
Qy      1 HisGlyMetPheMetAspLysLeuSerSerLysLeuCysAlaAspGluGluCysVal 20
Db      67 CATGTGTATTATGATGAATAAATTCTTCTTAAGAGTGTGTGGGATGAGAGTGTGTC 126
Qy      21 TyrrHisSerLeuAlaArgAlaGlnGlnAspTyrrAsnAlaProAspCysAspPheIle 40
Db      127 TATCTATTCTTCTGGCAAGACACAGAGATTTACATGCCAGCTGTAGTTATC 186
Qy      41 AsnValLysGlyGlnGlnIleTyrrValTyrrSerLysLeuValThrGluAsnGlyAla 60
Db      187 GATGTCAAGAAAGGCGAGAGATGATGTTTACTCCAGCTGTAAAGAAAGGAGCT 246
Qy      61 G1yAlaPheTpa1AG1SeValTyrg1AspHisGlnAspGluMeTg1y1LeValGly 80
Db      247 GGAGAGTTTGGGCTGGCAGTGTATGATGACCAAGAGATGAGATGGGAATTTAGAT 306
Qy      81 TyrrPheProSerAsnLeuValArgGluGlnArgValTyrg1GlnAlaThrLysGluIle 100
Db      307 TATTTTCCCGAAGCACTTGTAAGAGAGCGGTGTATACCAAGAGGCCACCAAGAGATC 366
Qy      101 ProThrThraSp1LeaSpPhePheCysGlu 110
Db      367 CCACCAAGGATATTGACTTCTTCTGTGA 396

RESULT 9
B0611549      696 bp      mRNA      linear      EST 31-AUG-2001
LOCUS

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/lab_host="SOLR"
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head"
/note="Site_1: XhoI; Site_2: SctI. cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'.
GAGAGAGAGAGAGATCCCAAGAGCTCTTTTTTTTTTTTTTT 3'], cDNA was
prepared by using triazole thermo-activated reverse

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/organism="Mus musculus"
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/mol_type="mRNA"
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/strain="BALB/c"
/db xref="taxon:10090"
/clone="g142g03"
/sex="male and female"
/dev_stage="Post natal day 5 to 13"
/clone_id="Mouse Organ of Corti cDNA pBluescript"
/organ="Organ: Organ of Corti; Vector: pBluescript; The
organ of Corti (OC) was fine dissected from a total of 386
OC as follows: 102 samples from post-natal (p) day 5; 72
from p6; 60 from p7; 46 from p8; 18 from p9; 20 from p10;
14 from p12 and 24 from p13. After killing animals by
cervical dislocation followed by decapitation, the bulla
was removed and opened in Leibowitz medium. The bony
capsule of the cochlea was chipped away, sera vascularis
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GigaPack III Gold Cloning kit (catalog # 237612), both
from Stratagene (La Jolla, CA, USA), according to
manufacturer's instructions. Briefly: 1.5 ug mRNA was
reverse transcribed using a hybrid oligo(dT) linker-primer
that contains an Xho I site. First strand synthesis was
primed with the linker- primer and transcribed using
Moloney murine leukemia virus reverse transcriptase
(MMLV-RT) and 5-methyl dCTP. The second strand was
synthesized with DNA polymerase and RNase H. Complementary
DNA was blunt ended with Pfu DNA polymerase, ligated with
EcoR I adapters in the presence of ligase and digested
with Xho I. The cDNA was sequentially size fractionated
over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden)
and Clontech Chroma Spin-1000 (Clontech, CA) and 1000 bp
columns to enrich for cDNAs greater than 400bp and, cDNA
, respectively. The cDNA was then directionally ligated to
the Uni-Zap XR vector, which had been predigested with
EcoR I and Xho I. The phagemid was packaged with GigaPack
III Gold and, upon titration on XL1 Blue MRF' cells, the
yield of the phage library was estimated to be 11,100,000
recombinants. Stratagene's EXASist interference
resistance helper phage (catalogue # 211203) was adopted
to rescue plasmid DNA from the phages. Upon plating of the
rescued library, individual cDNA clones were selected and
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the 5' end of the cDNA clones were generated with the
universal M13 reverse primer (CAGGAAACGCTATGACC) and 25%
strength BigDye terminator sequencing chemistry (Applied
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performed on MJ Tetrad thermal cyclers (MJ Research,
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genes are present in Genbank and have known function; 23%
have hits in Genbank, but do not have assigned function;
12% are uncharacterized ESTs and 20% are unidentified."

```

BASE COUNT 145 a 78 c 131 g 120 t

ORIGIN

Alignment Scores:

Pred. No.: 7,98e-71 Length: 474
Score: 569.00 Matches: 105
Percent Similarity: 98.18% Conservative: 3
Best Local Similarity: 95.45% Mismatches: 2
Query Match: 96.28% Indels: 0
DB: 13 Gaps: 0

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US-10-019-455A-49 (1-110) x B0565637 (1-474)
Qy 1 H3GlymetPheMetAspLeuSerSerIysLeuCysAlaAspGluGlyCysVal 20
Db 68 CATGATGATTTATATGATTAATCTTCTTATATAGTTGTGTGGATGAGAGATGCTTC 127
Qy 21 TTTTATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 40
Db 128 TATATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 187
Qy 41 AenValIysLysGlyGlnGlnIleTyrValIysSerIysLeuValThrGlnsGlyAla 60
Db 188 GATGCAAGAAAGGGCAGACAGATCATGTTTACTTCAAGCTGTATACAGAAACGAGACT 247
Qy 61 GAlaApeTtPALagIysSerValTyrGlyAspHisGlnAspGluMerGlyIleValGly 80
Db 248 GGAGAGTTTGGCGCGAGGTTTATGTTACCAACGATGAGATGGAAATTTAGT 307
Qy 81 TTTTProSerAsnLeuValArgGluGlnArgValTyrGlnGlnAlaThrLysGluIle 100
Db 308 TATTTCCCGCACTTGTGTAAGAGCGAGCTGTATACGAGAGCCACCAAGAGATC 367
Qy 101 ProThrAspIleAspPhePheCysGlu 110
Db 368 CCAACCAAGATATTGACTTCTTCTGTA 397

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RESULT 11

B0566932

LOCUS

DEFINITION

g173g09.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA

clone g173g09 5', mRNA sequence.

ACCESSION

B0566932

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

Kachar, B.

TITLE

EST analysis of gene expression in the mouse Organ of Corti at the

onset of hearing

UNPUBLISHED

CONTACT: Kachar, B.

Structural Cell Biology

National Institute of Deafness and other Communication Disorders

50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA

Tel: 301-402-1599

Fax: 301-402-1765

Email: kachar@nidcd.nih.gov

Plate: 73 row: 9 column: 09

Seq primer: M13RPI reverse primer (ABI).

Location/Qualifiers

1..409

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/mol_type="mRNA"

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/db_xref="taxon:10090"

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/sex="male and female"

/dev_stage="Post natal day 5 to 13"

/clone_id="Mouse Organ of Corti cDNA pBluescript"

/organ="Organ: Organ of Corti; Vector: pBluescript; The

organ of Corti (OC) was fine dissected from a total of 386

OC as follows: 102 samples from post-natal (p) day 5; 72

from p6; 60 from p7; 46 from p8; 18 from p9; 20 from p10;

14 from p12 and 24 from p13. After killing animals by

cervical dislocation followed by decapitation, the bulla

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capsule of the cochlea was chipped away, sera vascularis

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BASE COUNT 102 a 75 c 121 g 111 t
ORIGIN

Alignment Scores:
Pred. No.: 6,45e-68 Length: 409
Score: 548.00 Matches: 104
Percent Similarity: 97.27% Conservative: 3
Best Local Similarity: 94.55% Mismatches: 2
Query Match: 92.72% Indels: 1
DB: 13 Gaps: 0

US-10-019-455a-49 (1-110) x BQ566932 (1-409)

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DB 81 CATTGCGATTTATGATTAACCTTTCTTTAAGAGGTGTGCTTGATAGAGAGTGTGT 140
QY 20 ITTThrIleSerLeuAlaArgAlaGlnGluAspTYrAsnAlaProAspCYsArgPheI 40
DB 141 CTTATCTATTTCTCTGCGAAGAGCACAGGAATTAACAATGCCAGACTGTAGCTTAT 200
QY 40 eAsnValLysLysGlyGlnGlnIleTYrValLysSerLysLeuValITrGluAenGlyAl 60
DB 201 CGATGTCAAGAAAGGCGACAGATCTATGTTACTCCAAAGCTGTAACAGAAACGAGAC 260
QY 60 aGlyAlaPheTTPAlaGlySerValTYrGlyAspHisGlnAspGIuMetGlyIleValGI 80
DB 261 TGAAGAGTTTGGGCGAGTGTATTAGTGTAACCAAGAGATGAGATGGGAAATTGTAGG 320

QY 80 YTYrPheProSerAsnLeuValArgGlnGluArgValTYrGlnGluAlaThrLysGluI 100
DB 321 TTTATTTCCAGCACTGTGTGAAGAGCAGCGCTGTATACAGAGGCCCAAGAGAT 380
QY 100 ePTrOTrHThAspIleAspPhePheCYs 109
DB 381 CCCAACCAAGCGCTATTGACTTCTTCTGT 408

RESULT 12

BQ565411

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Unpublished
Contact: Kachar, B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: kachar@nidcd.nih.gov
Plate: 37 row: b column: 12
Seq primer: M13RPI reverse primer (ABI).
Location/Qualifiers
1..490
/organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
/db_xref="taxon:10090"
/cclone="g137b12"
/sex="male and female"
/dev_stage="Post natal day 5 to 13"
/clone_lib="Mouse Organ of Corti cDNA Bluescript"
/note="Organ: Organ of Corti; Vector: pBluescript. The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (p) day 5, 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR GigaPack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden)

and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with GigaPack III Gold and, upon titration on XL1 Blue MRF⁺ cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAAACGCTATGACC) and 25x strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 191 a 77 c 109 g 112 t
ORIGIN

Alignment Scores:
Pred. No.: 6,05e-67 Length: 490
Score: 542.00 Matches: 100
Percent Similarity: 98.18% Conservatives: 8
Best Local Similarity: 90.91% Mismatches: 2
Query Match: 91.71% Indels: 0
DB: 13 Gaps: 0

US-10-019-455a-49 (1-110) x B0565411 (1-490)

QY 1 HSGLMetPheMetAspLysLeuSerSerLysLeuCysAlaAspGluGluCysVal 20
DB 141 CATGGGATTTTATGATTAACCTTCTTAAAAATGTCGCCGATTAAGAGCTGTC 200
QY 21 TTTTThleSerLeuAlaArgAlaGingluAspTyrAsnAlaProAspCysArgPheIle 40
DB 201 TTTACTATTCTCTGGCAAGACACAGGAAATTAATGCCCAACTGATAGTTTCATC 260
QY 41 AenValLysLysGluGingluInleTyrValTyrSerLysLeuValThrGluAsnGluVala 60
DB 261 GATGTCAAAAAGGGGACGAAATCTATGTTACTCCAGCTGGTAACAAAAAACGACT 320
QY 61 GAlaAlaPheTyrAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
DB 321 GGAAGCTTTTGGCGCTGCTTTATGGGACCAACGATGAATGGGATTTAGCT 380
QY 81 TYPheProSerAsnLeuValArgGluGlnArgValTyrGlnGluAlaThrLysGluIle 100
DB 381 TATTTTCCCAACACTGTTGTGAAGGAGCGCTGTATATCCAGAGGCCACCAAGAGATTC 440
QY 101 ProThrThrAspIleAspPheCysGlu 110
DB 441 CCACACACGATATGACTTCTTCGGGAA 470

RESULT 13
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LOCUS g188d08.y1 Mouse Organ of Corti cDNA pluescript Mus musculus cDNA
DEFINITION clone g188d08 5', mRNA sequence.
ACCESSION B0567343
VERSION B0567343.1 GI:21470660
KEYWORDS EST.

SOURCE
ORGANISM Mus musculus (house mouse)
MUS musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Kachar, B.
TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
JOURNAL Unpublished
COMMENT Contact: Kachar, B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: kachar@nid.nih.gov
Plate: 88 row: d column: 08
Seq primer: M13RP1 reverse primer (ABI).
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/mol_type="mRNA"
/strain="BAU3/c"
/db_xref="taxon:10090"
/clone="g188d08"
/sex="male and female"
/dev_stage="post natal day 5 to 13"
/clone_lib="Mouse Organ of Corti cDNA pluescript".
/note="Organ: Organ of Corti; Vector: pluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR GigaPack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with GigaPack III Gold and, upon titration on XL1 Blue MRF⁺ cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAAACGCTATGACC) and 25x

strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Thermal Cycler (MJ Research, Waltham, MA) and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 178 a 108 c 152 g 166 t
ORIGIN

Alignment Scores:

Pred. No.: 2,21e-64 Length: 604
Score: 525.00 Matches: 97
Percent Similarity: 99.00% Conservative: 2
Best Local Similarity: 97.00% Mismatches: 1
Query Match: 88.83% Indels: 0
DB: 13 Gaps: 0

US-10-019-455a-49 (1-110) x B0567343 (1-604)

QY 11 LysLysLeuCyAlaAaSpGluGluCysValTTrThrIleSerLeuAlaArgAlaGlnGlu 30
DB 1 AAGAGAGTGTGTGGGATGAGAGAGTGTGTATATCTTCTGCGACAGACAGAGAA 60
QY 31 AspTyrAsnAlaProAspCysArgPheIleAsnValLysGlnGlnIleTyrVal 50
DB 61 GATACACATGCCCGACCTAGATTCATCATGTCAGAAAGGAGGAGATCTATGTT 120
QY 51 TySerLysLeuValTTrGluAerGlyAlaPheTTrpAlaGlySerValTyrGly 70
DB 121 TACCCCAAGCTGGTGAACAGAAACGAGCTGAGAGTGGCTGGCTGGCTGTTATGTT 180
QY 71 AspHISGlnAspGluMetGlyIleValGlyTyrPheProSerAsnLeuValArgGluGln 90
DB 181 GACACACAGAGTATGATGGAGATTTGATTTTCCCGACACTTGGTGAAGAGAGAG 240
QY 91 ArgValTyrGlnGlnAlaThrLysGluIleProThrAspIleAspPhePheCysGlu 110
DB 241 CGTGTATACAGAGAGGCGACCAAGAGATCCCAACGAGATTTTACTTCTCTGAA 300

RESULT 14

BY232622

LOCUS BY232622 RIKEN full-length enriched, adult inner ear Mus musculus

DEFINITION cDNA clone F930026J20 5', mRNA sequence.

ACCESSION BY232622

VERSION BY232622.1 GI:26413732

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE

AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 365)
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nishikido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schorbach, C., Gotohori, T., Baldarelli, R., Hill, D. P., Buit, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Bratt, D., Brusic, V., Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Fraser, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Guernicich, S., Hirokawa, N., Jackson, I. C., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lemhar, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G., Petrovsky, N., Pilai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sanderlin, A., Schneider, C., Sempere, C. A., Setou

TITLE

JOURNAL MEDLINE

PUBMED

COMMENT

M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Vardaro, R., Wagner, L., Whlstedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wyshew-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Akakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsr.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Aizawa, K., Akimura, T., Akakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watabiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission
Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Kirk W. Beisel (Boys Town National Research Hospital 555 North 30th Street Omaha, NE 68131 USA) whose assistance we gratefully acknowledge. Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.
Location/Qualifiers
1..365
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="F930026J20"
/tissue.type="inner ear"
/dev stage="adult"
/clone.lib="RIKEN full-length enriched, adult inner ear"

FEATURES

source

BASE COUNT 97 a 60 c 110 g 98 t

ORIGIN

Alignment Scores:

Pred. No.: 1.06e-58 Length: 365
Score: 483.00 Matches: 91
Percent Similarity: 97.92% Conservative: 3
Best Local Similarity: 94.79% Mismatches: 2
Query Match: 81.73% Indels: 0
DB: 13 Gaps: 0

US-10-019-455a-49 (1-110) x BY232622 (1-365)

QY 1 HisGlyMetPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysVal 20
 Db CATGCTGATATTATGAGTAACCTTTCTCTAAGAAAGTTGTGTGGATGACGAGCTGTCT 137
 QY 21 TyrThrIleSerLeuAlaArgAlaGlnGlnAspTyrAsnAlaProAspCysArgPheIle 40
 Db TATCTATTCTCTGGCAGACAGACAGAGATTAATGCTCCAGCTGATGATTCATC 197
 QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
 Db GATGTCAGAAAGAGGACACAGATCTATGTTCTCCAGCTGTAACGAAAGAGAGCT 257
 QY 61 GlyAlaPheTyrPalaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
 Db GGAGAGTTTGGGGCTGGCAGCTGTTATGTTATGATGATGATGATGATGATGATGAT 197
 QY 81 TyrPheProSerAsnLeuValArgGlnGlnArgValTyrGlnGluAla 96
 Db TATTTCCCAACCACTTGTGAGAGAGAGAGCTGATGATGATGATGATGATGATGAT 365

RESULT 15
 BE236443 527 bp mRNA linear EST 25-APR-2001
 LOCUS 144645 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.
 DEFINITION BE236443
 ACCESSION BE236443
 VERSION BE236443.1 GI:9021161
 KEYWORDS EST.

SOURCE
 Bos taurus (cow)

ORGANISM
 Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 Bovidae; Bovinae; Bos.

REFERENCE
 AUTHORS
 1 (bases 1 to 527)
 Smith, I.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
 Casas, E., Wray, J.E., White, J., Cho, J., Fahnenkrug, S.C., Bennett,
 G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
 Pereira, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
 Keele, J.W.

TITLE
 Sequence evaluation of four pooled-tissue normalized bovine cDNA
 libraries and construction of a gene index for cattle

JOURNAL
 MEDLINE
 PUBMED
 21180013
 11282978

COMMENT
 Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and all trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -minscore 18
 and -mismatch 12 options.

PCR Primers
 FORWARD: AGGAACAGCTATGACCAT
 BACKWARD: GTTTCAGTACGACGACG
 Plate: 54 row: C column: 18
 Seq primer: ATTTCAGTACGACCTATAG.

FEATURES
 source
 1..527
 Location/Qualifiers

/organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /clone_id="MARC 4BOV"

/note="Vector: PCMV SPORT6; Site 1: NotI; Site 2: SalI;
 Library made from pooled tissue from day 20 and day 40
 embryos."

BASE COUNT 173 a 94 c 126 g 134 t

ORIGIN
 Alignment Scores: 1.83e-52 Length: 527
 Pred. No.:

Score: 441.00
 Percent Similarity: 82.888
 Best Local Similarity: 76.584
 Query Match: 74.624
 DB: 10
 Gaps: 2

US-10-019-455a-49 (1-110) x BE236443 (1-527)

QY 1 HisGlyMetPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysVal 20
 Db CATGCTGATATTATGAGTAACCTTTCTCTAAGAAAGTTGTGTGGATGACGAGCTGTCT 148
 QY 21 TyrThrIleSerLeuAlaArgAlaGlnGlnAspTyrAsnAlaProAspCysArgPheIle 40
 Db TATCTATTCTCTGGCAGACAGACAGAGATTAATGCTCCAGCTGATGATTCATC 208
 QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
 Db AACGTAAAAAAGAGACAGTGTATGTTTCTCCAAAGCTG----- 250
 QY 61 GlyAlaPheTyrPalaGlySerValTyrGlyAspHis-----GlnAspGluMetGlyIleVal 79
 Db -----GTTATGGCAATCACTGACGATGAAATGGAAACCGTG 289
 QY 80 GlyTyrPheProSerAsnLeuValArgGlnGlnArgValTyrGlnGluAlaThrLysGlu 99
 Db GGTATTTTCCAGCAACTTGGTCCAGAAACAATGTATACCAAGAACCCACAGAGA 349
 QY 100 IleProThrThrAspIleAspPheCysGlu 110
 Db GTTCTACACGAGATATGATCTTTTCTGCGAG 382

Search completed: December 29, 2003, 22:00:54
 Job time: 1140.05 secs

score greater than or equal to the score of the result being printed,

OS Rattus sp.
yy

8
9
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7
8
9
0

PN WO200102564-A1.
 XX
 PD 11-JAN-2001.
 XX
 PF 29-JUN-2000; 2000WO-JP04278.
 XX
 PR 30-JUN-1999; 99JP-0186718.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Itch Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K,
 PI Tanaka H;
 XX
 DR WPI: 2001-159271/16.
 DR P-FSDB; AAB69131.
 XX
 PT Safe, low-toxicity secretory cell function-regulatory protein and
 PT encoded DNA, applicable as drugs, in diagnosis and development of
 PT promoters and inhibitors for preventing or treating e.g. bone and joint
 PT diseases -
 XX
 PS Claim 12; Page 107; 11pp; Japanese.
 XX
 CC The present invention describes novel MLP proteins and their encoding
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
 CC activities, and can be used in gene therapy and as secretory cell
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in
 CC the diagnosis and development of promoters and inhibitors for preventing
 CC or treating bone and joint diseases as well as pathologic angiogenesis.
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
 CC in the exemplification of the present invention.
 XX
 SQ Sequence 330 BP; 91 A; 62 C; 91 G; 86 T; 0 other;
 XX
 Alignment Scores:
 Pred. No.: 3,71e-77 Length: 330
 Score: 591.00 Matches: 110
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0
 US-10-019-455a-49 (1-110) x AAF59099 (1-330)

QY 1 HisGlyMetPheMetAspLysLeuSerSerLysLeuCysAlaAspGluGluCysVal 20
 DB 1 CATGCGATGTTTATGATAAATCTTCTTAAGAAAGTTGTGACATGAGAGTGCTGC 60
 QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
 DB 61 TATACCATTTCTCTGGCAAGACGACAGAACTTAAAGTCCCGGACTGTGGTTCATC 120
 QY 41 AsnValLysLysGlnGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
 DB 121 AATGTCAAGAAAGGCGACGATCTATGTTTATTCACACTGGTAAACAAAATGGAGCT 180
 QY 61 GlyAlaPheTyrPheLysSerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
 DB 181 GGGGCAATTCGGGCTGGCAGATGTTTATGTGACCAACAGATGAGATGGGAATTGGGT 240
 QY 81 TyrPheProSerAsnLeuValArgGluGlnArgValTyrGlnGluAlaThrLysGluIle 100
 DB 241 TATTTCCCAAGCAACTGTGTAGAGCAACGAGTGTACAGAGGCCCAAGAGGATT 300
 QY 101 ProThrThrAspLysPhePheCysGlu 110
 DB 301 CCAACCAAGGATTTGACTTCTCTGTGA 330

RESULT 2
 AAF59098
 ID AAF59098 standard; DNA; 384 BP.
 XX
 AC AAF59098;

XX
 DT 23-APR-2001 (first entry)
 XX
 DE Rat MLP nucleotide sequence SEQ ID NO:46.
 XX
 KM MLP, MIA; melanoma inhibitory activity; cancer; bone disease;
 KM joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
 KM cardiant; gene therapy; secretory cell function regulator; promoter;
 KM inhibitor; ds.
 XX
 OS Rattus sp.
 XX
 PN WO200102564-A1.
 XX
 PD 11-JAN-2001.
 XX
 PF 29-JUN-2000; 2000WO-JP04278.
 XX
 PR 30-JUN-1999; 99JP-0186718.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Itch Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K,
 PI Tanaka H;
 XX
 DR WPI: 2001-159271/16.
 DR P-FSDB; AAB69130.
 XX
 PT Safe, low-toxicity secretory cell function-regulatory protein and
 PT encoded DNA, applicable as drugs, in diagnosis and development of
 PT promoters and inhibitors for preventing or treating e.g. bone and joint
 PT diseases -
 XX
 PS Claim 13; Page 105-106; 11pp; Japanese.
 XX
 CC The present invention describes novel MLP proteins and their encoding
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
 CC activities, and can be used in gene therapy and as secretory cell
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in
 CC the diagnosis and development of promoters and inhibitors for preventing
 CC or treating bone and joint diseases as well as pathologic angiogenesis.
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
 CC in the exemplification of the present invention.
 XX
 SQ Sequence 384 BP; 98 A; 72 C; 109 G; 105 T; 0 other;
 XX
 Alignment Scores:
 Pred. No.: 4,61e-77 Length: 384
 Score: 591.00 Matches: 110
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0
 US-10-019-455a-49 (1-110) x AAF59098 (1-384)

QY 1 HisGlyMetPheMetAspLysLeuSerSerLysLeuCysAlaAspGluGluCysVal 20
 DB 55 CATGCGATGTTTATGATAAATCTTCTTAAGAAAGTTGTGACATGAGAGTGCTC 114
 QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
 DB 115 TATACCATTTCTCTGGCAAGACGACAGAACTTAAAGTCCCGGACTGTAGTTCATC 174
 QY 41 AsnValLysLysGlnGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
 DB 175 AATGTCAAGAAAGGCGACGATCTATGTTTATTCACAGCTGGTAAACAAAATGGAGCT 234
 QY 61 GlyAlaPheTyrPheLysSerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
 DB 235 GGGGCAATTCGGGCTGGCAGATGTTTATGTGACCAACAGATGAGATGGGAATTGGGT 294
 QY 81 TyrPheProSerAsnLeuValArgGluGlnArgValTyrGlnGluAlaThrLysGluIle 100

DB 295 TATTTCCTCCAGACTTGGTTAGAGCAGACAGTGTACCGAGGCCACCAAGAGATT 354

QY 101 ProThrThrAspIleasPhePheCysGlu 110

DB 355 CCAACCAACGAGATTGACTTCTTCTGTGAA 384

RESULT 3

AFS9080

ID AAFS9080 standard; DNA; 330 BP.

XX AAFS9080;

AC

XX

DT 23-APR-2001 (first entry)

XX

DE Mouse MLP nucleotide sequence SEQ ID NO:25.

XX

KW MLP; MIA; melanoma inhibitory activity; cancer; bone disease;

KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;

KW cardiant; gene therapy; secretory cell function regulator; promoter;

KW inhibitor; ds.

XX

OS Mus musculus.

XX

PN WO200102564-A1.

XX

PD 11-JAN-2001.

XX

PF 29-JUN-2000; 2000WO-JP04278.

XX

PR 30-JUN-1999; 99JP-0186718.

XX

PA (TAKE) TAKEDA CHEM IND LTD.

XX

PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K,

PI Tanaka H;

XX

DR WPI: 2001-159271/16.

XX

DR P-PSDB; AAB69127.

XX

PT Safe, low-toxicity secretory cell function-regulatory protein and

PT encoded DNA, applicable as drugs, in diagnosis and development of

PT promoters and inhibitors for preventing or treating e.g. bone and joint

PT diseases -

XX

PS Claim 10; Page 98; 11pp; Japanese.

XX

XX The present invention describes novel MLP proteins and their encoding

CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant

CC activities, and can be used in gene therapy and as secretory cell

CC function regulators. The MLP proteins and DNAs can be used in drugs, in

CC the diagnosis and development of promoters and inhibitors for preventing

CC or treating bone and joint diseases as well as pathologic angiogenesis.

CC AAFS9063 to AAFS9099 and AAB69122 to AAB69132 represent sequences used

CC in the exemplification of the present invention.

XX

SQ Sequence 330 BP; 91 A; 60 C; 92 G; 87 T; 0 other;

Alignment Scores:

Pred. No.: 1.15e-74 Length: 330

Score: 574.00 Matches: 106

Percent Similarity: 99.094 Conservative: 3

Best Local Similarity: 96.368 Mismatches: 1

Query Match: 97.128 Indels: 0

DB: Gaps: 0

US-10-019-455a-49 (1-110) x AAFS9080 (1-330)

QY 1 HisGlyMetPheMetCAspIysLeuSerIysIleuGlyAlaAspGluGlyVal 20

DB 1 CATGGGTATTTATGATTAACCTTCTCTTAAGAGTTGTGCGGATGAGAGTGTGC 60

QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40

DB 61 TATCTATTTCCTGCGAGAGCAGAGAAAGATTCAATGCCCACTGTAGTTTCATC 120

QY 41 AsnValIysIysGlyGlnGlnIleTyrValTyrSerIysLeuValThrGluAsnGlyAla 60

DB 121 GATGTCAAGAAAGGCGACGACATCTATGTTACTCCAAAGCTGGTAAACAGAAACGAGCT 180

QY 61 GlyAlaPheTTPAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80

DB 181 GGAGAGTTTGGCTGGCAGAGTTTATGCTGACACACAGATGAGATGCGAATTGTAGT 240

QY 81 TyrPheProSerAsnLeuValArgGluGlnArgValTyrGlnGluAlaThrIleGluIle 100

DB 241 TATTTCCTCCAGCAACTTGGTGAACAGACAGCGTGTATACAGAGGCCACCAAGAGATC 300

QY 101 ProThrThrAspIleasPhePheCysGlu 110

DB 301 CCAACCAACGAGATTGACTTCTTGTGAA 330

RESULT 4

AFS9068

ID AAFS9068 standard; DNA; 384 BP.

XX AAFS9068;

AC

XX

DT 23-APR-2001 (first entry)

XX

DE Mouse MLP nucleotide sequence SEQ ID NO:10.

XX

KW MLP; MIA; melanoma inhibitory activity; cancer; bone disease;

KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;

KW cardiant; gene therapy; secretory cell function regulator; promoter;

KW inhibitor; ds.

XX

OS Mus musculus.

XX

PN WO200102564-A1.

XX

PD 11-JAN-2001.

XX

PF 29-JUN-2000; 2000WO-JP04278.

XX

PR 30-JUN-1999; 99JP-0186718.

XX

PA (TAKE) TAKEDA CHEM IND LTD.

XX

PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K,

PI Tanaka H;

XX

DR WPI: 2001-159271/16.

XX

DR P-PSDB; AAB69125.

XX

PT Safe, low-toxicity secretory cell function-regulatory protein and

PT encoded DNA, applicable as drugs, in diagnosis and development of

PT promoters and inhibitors for preventing or treating e.g. bone and joint

PT diseases -

XX

PS Claim 11; Page 93; 11pp; Japanese.

XX

XX The present invention describes novel MLP proteins and their encoding

CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant

CC activities, and can be used in gene therapy and as secretory cell

CC function regulators. The MLP proteins and DNAs can be used in drugs, in

CC the diagnosis and development of promoters and inhibitors for preventing

CC or treating bone and joint diseases as well as pathologic angiogenesis.

CC AAFS9063 to AAFS9099 and AAB69122 to AAB69132 represent sequences used

CC in the exemplification of the present invention.

XX

SQ Sequence 384 BP; 98 A; 68 C; 111 G; 107 T; 0 other;

Alignment Scores:

Pred. No.: 1.43e-74 Length: 384

Score: 574.00 Matches: 106

Percent Similarity: 99.09%
 Best Local Similarity: 96.36%
 Query Match: 97.12%
 DB: 22
 Gaps: 0

US-10-019-455a-49 (1-110) x AAF59068 (1-384)

QY 1 HisGlyMetPheMetAspLysLeuSerLysLysLeuCysAlaAspGluGluCysVal 20
 DB 55 CATGGTGATTTATGATTAACCTTCTCTAAGAGTGTGGGATGAGAGTGTGTC 114
 QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
 DB 115 TATACCTATTCTCTGGCAAGACACAGAGATTACAAAGCCCACTGTTGTTTCATC 174
 QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
 DB 175 GATGTCAGAAAGGAGGACAGATCTATGTTTACTCCAGCTGATACAGAAACGAGCT 234
 QY 61 GlyAlaPheThrPalaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
 DB 235 GGAGAGTTTGGCTGGCAGCTGTTATGTGACCCAGCATGAGATGGAAATGTAGGT 294
 QY 81 TyrPheProSerAsnLeuValArgGluGlnArgValTyrGlnGluAlaThrLysGluIle 100
 DB 295 TATTTCCCGCAACTTGCTGTAAGACAGCTGTATACAGAGGCCACCAAGAGATC 354
 QY 101 ProThrThrAspIleAspPhePheCysGlu 110
 DB 355 CCAACCAAGATATTGACTTCTCTGTGAA 384

RESULT 5
 ID AAF59084 standard; DNA; 947 BP.

XX AAF59084;
 XX 23-APR-2001 (first entry)
 XX Mouse MLP nucleotide sequence SEQ ID NO:30.
 KM MLP: MIA; melanoma inhibitory activity; cancer; bone disease;
 KM joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
 KM cardiac; gene therapy; secretory cell function regulator; promoter;
 KM inhibitor; ds.
 XX
 XX OS Mus musculus.
 XX PN W0200102564-A1.
 XX 11-JAN-2001.
 XX 29-JUN-2000; 2000MO-JP04278.
 XX 30-JUN-1999; 99JP-0186718.
 XX (TAKE) TAKEDA CHEM IND LTD.
 XX Itoh Y, Nishi K, Ogi K, Okubo S, Mogi S, Noguchi Y, Yoshimura K;
 PI Tanaka H;
 DR WPI; 2001-159271/16.

XX Safe, low-toxicity secretory cell function-regulatory protein and
 PT encoded DNA, applicable as drugs, in diagnosis and development of
 PT promoters and inhibitors for preventing or treating e.g. bone and joint
 PT diseases -
 XX Example 2; Page 100-101; 11pp; Japanese.
 XX The present invention describes novel MLP proteins and their encoding
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiac
 CC activities, and can be used in gene therapy and as secretory cell

CC function regulators. The MLP proteins and DNAs can be used in drugs, in
 CC the diagnosis and development of promoters and inhibitors for preventing
 CC or treating bone and joint diseases as well as pathologic angiogenesis.
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
 CC in the exemplification of the present invention.

XX Sequence 947 BP; 279 A; 158 C; 221 G; 289 T; 0 other;

Alignment Scores:

Pred. No.: 5,24e-74 Length: 947
 Score: 574.00 Matches: 106
 Percent Similarity: 99.09% Conservative: 3
 Best Local Similarity: 96.36% Mismatches: 1
 Query Match: 97.12% Indels: 0
 DB: 22 Gaps: 0

US-10-019-455a-49 (1-110) x AAF59084 (1-947)

QY 1 HisGlyMetPheMetAspLysLeuSerLysLysLeuCysAlaAspGluGluCysVal 20
 DB 65 CATGGTGATTTATGATTAACCTTCTCTAAGAGTGTGTGGGATGAGAGTGTGTC 124
 QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
 DB 125 TATACCTATTCTCTGGCAAGACACAGAGATTACAAAGCCCACTGTTGTTTCATC 184
 QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
 DB 185 GATGTCAGAAAGGAGGACAGATCTATGTTTACTCCAGCTGATACAGAAACGAGCT 244
 QY 61 GlyAlaPheThrPalaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
 DB 245 GGAGAGTTTGGCTGGCAGCTGTTATGTGACCAAGATGAGATGGAAATGTAGGT 304
 QY 81 TyrPheProSerAsnLeuValArgGluGlnArgValTyrGlnGluAlaThrLysGluIle 100
 DB 305 TATTTCCCGCAACTTGCTGTAAGACAGCTGTATACAGAGGCCACCAAGAGATC 364
 QY 101 ProThrThrAspIleAspPhePheCysGlu 110
 DB 365 CCAACCAAGATATTGACTTCTCTGTGAA 394

RESULT 6

ID AAF59079 standard; DNA; 330 BP.

XX AAF59079;
 XX 23-APR-2001 (first entry)
 XX Human MLP nucleotide sequence SEQ ID NO:23.
 DE
 XX
 KM MLP: MIA; melanoma inhibitory activity; cancer; bone disease;
 KM joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
 KM cardiac; gene therapy; secretory cell function regulator; promoter;
 KM inhibitor; ds.
 XX
 XX OS Homo sapiens.
 XX PN W0200102564-A1.
 XX 11-JAN-2001.
 XX 29-JUN-2000; 2000MO-JP04278.
 XX 30-JUN-1999; 99JP-0186718.
 XX (TAKE) TAKEDA CHEM IND LTD.
 XX Itoh Y, Nishi K, Ogi K, Okubo S, Mogi S, Noguchi Y, Yoshimura K;
 PI Tanaka H;
 DR WPI; 2001-159271/16.

DR P-PSDB; AAB69126.
 XX Safe, low-toxicity secretory cell function-regulatory protein and
 PT encoded DNA, applicable as drugs, in diagnosis and development of
 PT promoters and inhibitors for preventing or treating e.g. bone and joint
 PT diseases -
 XX
 PS Claim 8; Page 97; 111pp; Japanese.
 XX
 CC The present invention describes novel MLP proteins and their encoding
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
 CC activities, and can be used in gene therapy and as secretory cell
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in
 CC the diagnosis and development of promoters and inhibitors for preventing
 CC or treating bone and joint diseases as well as pathologic angiogenesis.
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
 CC in the exemplification of the present invention.
 XX
 SQ Sequence 330 BP; 91 A; 60 C; 91 G; 88 T; 0 other;
 Alignment Scores:
 Pred. No.: 7,93e-70 Length: 330
 Score: 541.00 Matches: 98
 Percent Similarity: 95.45% Conservative: 7
 Best Local Similarity: 89.09% Mismatches: 5
 Query Match: 91.54% Indels: 0
 DB: 22 Gaps: 0
 US-10-019-455a-49 (1-110) x AAF59079 (1-330)
 QY 1 HisGlyMetPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysVal 20
 Db 1 CATGGAAATTTATGAGACCGCTAGCTTCCAAAGAGCTCTGCGAGATGATGAGTGTCTC 60
 QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
 Db 61 TATACATTTCTCTGGCTAGTGTCTCAAGAAATTTAATGCCCCGAGCTGTATGATTCATT 120
 QY 41 AsnValLysLysGlnGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
 Db 121 AACGTTAAAAAGGCGACGAGATCTATGTCTCAAAAGCTGTGTAAGAAATGAGAGCT 180
 QY 61 GlyAlaPheThrAlaGlySerValTyrGlyAspPheIleAspGluMetGlyIleValGly 80
 Db 181 GGAGAAATTTTGGGCTGGCGAGTGTATTATGCTGATGCCAGGAGAGATGGAGTCTGTGGCT 240
 QY 81 TyrPheProSerAsnLeuValArgGluGlnArgValTyrGlnGluAlaThrLysGluIle 100
 Db 241 TATTTCCCGAGAACTTGCTCAAGAACGCTGTGTACCGAGAAAGCTAACCAGGAAGTT 300
 QY 101 ProThrThrAspIleAspPhePheCysGlu 110
 Db 301 CCCACCACGGAATATGACTTCTTCTGGGAG 330
 RESULT 7
 AAF59065
 ID AAF59065 standard; DNA; 384 BP.
 XX
 AC AAF59065;
 XX
 DT 23-APR-2001 (first entry)
 XX
 DE Human MLP nucleotide sequence SEQ ID NO:4.
 XX
 KW MLP; MTA; melanoma inhibitory activity; cancer; bone disease;
 KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
 KW cardiant; gene therapy; secretory cell function regulator; promoter;
 KW inhibitor; ds.
 XX
 OS Homo sapiens.
 XX
 XX WO200102564-A1.
 XX

PD 11-JAN-2001.
 XX
 XX 29-JUN-2000; 2000WO-JP04278.
 PF
 XX 30-JUN-1999; 99JP-0186718.
 FR
 XX (TAKE) TAKEDA CHEM IND LTD.
 PA
 XX Itoh Y, Nishi K, Ogi K, Okubo S, Mogi S, Noguchi Y, Yoshimura K;
 PI Tanaka H;
 DR WPI; 2001-159271/16.
 XX P-PSDB; AAB69123.
 DR
 XX Safe, low-toxicity secretory cell function-regulatory protein and
 PT encoded DNA, applicable as drugs, in diagnosis and development of
 PT promoters and inhibitors for preventing or treating e.g. bone and joint
 PT diseases -
 XX
 PS Example 1; Page 91; 111pp; Japanese.
 XX
 CC The present invention describes novel MLP proteins and their encoding
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
 CC activities, and can be used in gene therapy and as secretory cell
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in
 CC the diagnosis and development of promoters and inhibitors for preventing
 CC or treating bone and joint diseases as well as pathologic angiogenesis.
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
 CC in the exemplification of the present invention.
 XX
 SQ Sequence 384 BP; 99 A; 70 C; 106 G; 109 T; 0 other;
 Alignment Scores:
 Pred. No.: 9.86e-70 Length: 384
 Score: 541.00 Matches: 98
 Percent Similarity: 95.45% Conservative: 7
 Best Local Similarity: 89.09% Mismatches: 5
 Query Match: 91.54% Indels: 0
 DB: 22 Gaps: 0
 US-10-019-455a-49 (1-110) x AAF59065 (1-384)
 C 1 HisGlyMetPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysVal 20
 Db 55 CATGGAAATTTATGAGACCGCTAGCTTCCAAAGAGCTCTGCGAGATGATGAGTGTCTC 114
 QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
 Db 115 TATACATTTCTCTGGCTAGTGTCTCAAGAAATTTAATGCCCCGAGCTGTATGATTCATT 174
 QY 41 AsnValLysLysGlnGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
 Db 175 AACGTTAAAAAGGCGACGAGATCTATGTCTACTCAAGCTGTGTAAGAAATGAGAGCT 234
 QY 61 GlyAlaPheThrAlaGlySerValTyrGlyAspPheIleAspGluMetGlyIleValGly 80
 Db 235 GGAGAAATTTTGGGCTGGCGAGTGTATTATGCTGATGCCAGGAGAGATGGAGTCTGTGGCT 294
 QY 81 TyrPheProSerAsnLeuValArgGluGlnArgValTyrGlnGluAlaThrLysGluIle 100
 Db 295 TATTTCCCGAGAACTTGCTCAAGAACGCTGTGTACCGAGAAAGCTAACCAGGAAGTT 354
 QY 101 ProThrThrAspIleAspPhePheCysGlu 110
 Db 355 CCCACCACGGAATATGACTTCTTCTGGGAG 384
 RESULT 8
 AAS17583
 ID AAS17583 standard; cDNA; 387 BP.
 XX
 AC AAS17583;
 XX
 DT 26-FEB-2002 (first entry)
 XX

| XX | DE | DNA encoding novel secreted protein #12. |
|----|----|---|
| XX | XX | Secreted protein; cytostatic; immunosuppressive; vulnary; vaccine; |
| XX | KM | antiinflammatory; neuroprotective; nephrotoxic; cardiovascular; |
| XX | KM | human; cancer; autoimmune disease; wound healing disorder; infection; |
| XX | KM | hematopoietic disorder; inflammatory disorder; infertility; |
| XX | KM | neurological disease; psychiatric disease; cardiovascular disease; |
| XX | KM | respiratory disease; renal; gastrointestinal; ss. |
| XX | OS | Homio sapiens. |
| XX | XX | |
| XX | XX | Key |
| XX | XX | Location/Qualifiers |
| XX | XX | CD8 |
| XX | XX | 1..387 |
| XX | XX | /*tag= a |
| XX | XX | /product= "Human secreted protein" |
| XX | XX | WO200179454-A1. |
| XX | XX | 25-OCT-2001. |
| XX | XX | 11-APR-2001; 2001WO-US11797. |
| XX | XX | 13-APR-2000; 2000US-196603P. |
| XX | XX | 24-APR-2000; 2000US-199417P. |
| XX | XX | (SMIK) SMITHKLINE BEECHAM CORP. |
| XX | XX | (SMIK) SMITHKLINE BEECHAM PLC. |
| XX | XX | Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z; |
| XX | XX | WP1: 2002-061975/08. |
| XX | XX | P-PSDB: AAU09871. |
| XX | XX | New secreted proteins or polypeptides, useful for treating e.g. cancer, |
| XX | XX | autoimmune diseases, wound healing disorder, infections, haematopoietic |
| XX | XX | disorders, inflammatory disorders, infertility, cancer |
| XX | XX | Claim 2; Page 44; 92pp; English. |
| XX | XX | The invention relates to an isolated novel secreted polypeptide (I) and |
| XX | XX | polynucleotide (II). (I) and (II) are useful for treating cancer, |
| XX | XX | autoimmune diseases, wound healing disorder, infections, haematopoietic |
| XX | XX | disorders, inflammatory disorders, infertility, neurological and |
| XX | XX | psychiatric diseases, cardiovascular disease, respiratory diseases, |
| XX | XX | renal diseases, or gastrointestinal disease. These may also be used to |
| XX | XX | treat diseases, abnormalities and disorders caused by abnormal |
| XX | XX | expression, production, function and/or metabolism of the genes, as |
| XX | XX | vaccines for inducing immunological response in a mammal, and in |
| XX | XX | screening methods for detecting the effect of added compounds on the |
| XX | XX | production of mRNA and polypeptide in cells. The polypeptides can be used |
| XX | XX | as immunogens to produce antibodies immunospecific for the polypeptides, |
| XX | XX | and to identify membrane-bound or soluble receptors. The polynucleotides |
| XX | XX | may be used as diagnostic reagents. In chromosome localisation studies, |
| XX | XX | and in tissue expression studies. The present sequence represents the |
| XX | XX | coding sequence of novel human secreted protein #12. |
| XX | XX | Sequence 387 BP; 101 A; 70 C; 106 G; 110 T; 0 other; |
| XX | XX | |
| XX | XX | Alignment Scores: |
| XX | XX | Prod. No.: 9,97e-70 Length: 387 |
| XX | XX | Score: 541.00 Matches: 98 |
| XX | XX | Percent Similarity: 95.45% Conservative: 7 |
| XX | XX | Best local Similarity: 89.09% Mismatch: 5 |
| XX | XX | Query Match: 91.54% Indels: 0 |
| XX | XX | DB: 24 Gaps: 0 |
| XX | XX | US-10-019-455A-49 (1-110) X AAS17583 (1-387) |
| XX | XX | |
| XX | XX | 1 HisG1WhepHeWetApLyIsLeuSeArLyIsLeuCySA1AAspCluGluCysVal 20 |
| XX | XX | 55 CATGAGATATTATGACGCTCTAGCTTCACAGAAAGCTCTGGCAGATGAGAGATGGTC 114 |

[illegible]

CC proteins. GRP polypeptides and polynucleotides of the invention
 CC can be used in the prophylaxis, treatment (including gene therapy)
 CC and diagnosis of disorders and diseases caused by, or involving,
 CC cartilage development and maintenance, inhibition of melanoma cell
 CC growth and tumors, including neuroectodermal tumors such as
 CC gliomas. The polynucleotides can also be used to design probes
 CC and primers, for chromosome and gene mapping, in the recombinant
 CC production of protein, in the generation of antisense, ribozyme, and
 CC peptide-nucleic acid molecules, and to produce transgenic animals.

XX Sequence 426 BP; 119 A; 73 G; 113 G; 120 T; 1 other;

Alignment Scores:

Pred. No.: 1,14e-69 Length: 426
 Score: 541.00 Matches: 98
 Percent Similarity: 95.45% Conservative: 7
 Best Local Similarity: 89.09% Mismatches: 5
 Query Match: 91.54% Indels: 0
 DB: 22 Gaps: 0

US-10-019-455A-49 (1-110) x AAH26341 (1-426)

QY 1 HisGlyMetPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysVal 20
 DB 73 CATGGAATATTATGACACCGCTAGCTTCCAGAGAGCTCTGCGAGATGATGATGCTC 132
 QY 21 TTTTThTleSerLeuAlaArgAlaGluGluAspTyrAsnAlaProAspCysArgPheLe 40
 DB 133 TATACATTATTCCTGGCTAGTGTCAAGAGATTATATATGCCCCGAGCTGATGATTCATT 192
 QY 41 AsnValLysLysGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 60
 DB 193 AACGTTAAAAAAGCGACGACGATCTATGTACTCAAACTGTTAAAAAATGAGAGCT 252
 QY 61 GlValAlaPheThrAlaGlySerValTyrGlyAspHisGluAspGluMetGlyLeuValGly 80
 DB 253 GCGAATTTTGGCTGGAGCTGTTTATGATGATGCGACGACGAGTGGAGTGGT 312
 QY 81 TyrPheProSerAsnLeuValArgGluGluArgValTyrGluGluAlaThrLysGluLe 100
 DB 313 TATTTCCCAAGAACTTGGTCAAGAAAGCGGTGTGTACAGAGAGCTACCAAGAGATT 372
 QY 101 ProThrThrAspLysAspPheCysGlu 110
 DB 373 CCCACCGAGATATGACTTCTTCTCGAG 402
 RESULT 10
 ABL95740
 ID ABL95740 standard; cDNA; 521 BP.
 XX
 AC ABL95740;
 XX
 DT 19-JUL-2002 (first entry)
 XX
 DE Human angiogenesis related cDNA PRO9873 SEQ ID NO: 359.
 XX
 KM Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
 KM atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
 KM cardiac; cytostatic; antiangiogenic; hypotensive; vulnertary;
 KM antitumoriscleotic; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200208284-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 09-JUL-2001; 2001WO-US21735.
 XX
 PR 20-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 25-JUL-2000; 2000US-220644P.
 PR 28-JUL-2000; 2000WO-US20710.

PR 02-AUG-2000; 2000US-222695P.
 PR 17-AUG-2000; 2000US-0643657.
 PR 23-AUG-2000; 2000WO-US23552.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 07-SEP-2000; 2000US-230978P.
 PR 15-SEP-2000; 2000US-000000P.
 PR 18-SEP-2000; 2000US-066450P.
 PR 18-SEP-2000; 2000US-0665350.
 PR 24-OCT-2000; 2000US-242922P.
 PR 08-NOV-2000; 2000US-0709238.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000US-074725P.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 22-JAN-2001; 2001US-0767609.
 PR 28-FEB-2001; 2001US-0796498.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 09-MAR-2001; 2001US-0802708.
 PR 14-MAR-2001; 2001US-0806889.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001US-086028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 30-MAY-2001; 2001US-0870574.
 PR 30-MAY-2001; 2001WO-US17443.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 28-JUN-2001; 2001WO-US00000.
 XX
 PA (GERTH) GENENTECH INC.
 PA (BAKE) BAKER K P.
 PA (FERR) FERRARA N.
 PA (GERB) GERBER H.
 PA (GERR) GERRTSEN M E.
 PA (GODD) GODDARD A.
 PA (GODO) GODDARD P. J.
 PA (GURN) GURNEY A L.
 PA (HILL) HILLAN K J.
 PA (MARS) MARSTERS S A.
 PA (PANU) PAN J.
 PA (PAON) PAONI N F.
 PA (STEP) STEPHAN J F.
 PA (WATA) WATANABE C K.
 PA (WILL) WILLIAMS P M.
 PA (WOOD) WOOD W I.
 XX
 PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 PI P-PSDB; ABB95602.
 DR WPI; 2002-171999/22.
 DR
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal -
 XX
 PS Claim 1; Fig 359; 567pp; English.
 XX
 CC The present invention provides the protein and coding sequences of human
 CC PRO proteins. These are useful for treating or diagnosing a
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac
 CC hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The present sequence is a coding sequence of the invention.

DB 152 TATACATTTCTCTGCTAGTCTCAAGAAATTATATATCCCGAGCTGTATCATTTATT 211
 QY 41 AenVallyslvsglynglnlnleTyValTySerlyseuValThrgluasnGlyala 60
 DB 212 AACGTTAAAGGCGAGCATCTATGTACTCAAGCTGTAAAGAAATGAGACT 271
 QY 61 GlyAlaPheTpaIagIseValTyrgIyAspHisGlnaaspGluMetGlyIleValGly 80
 DB 272 GGAGAAATTTGGGCTGGCAGTGTATTATGTGTATGCGAGACGAGATGGAGATCGTGGGT 331
 QY 81 TyPheProSerAsnLeuValArgGluGlnArgValTyrglnGlnAlaThrlyGluIle 100
 DB 332 TATTTCCCGAGAACTTGTCAGAGAACAGCGTGTACCGAGAACTACCAAGAAATT 391
 QY 101 ProThrThraPpIleaspPhePheCyseGlu 110
 DB 392 CCCACCGAGATATTGACTTCTTCTGCGAG 421
 RESULT 12
 ABRK3571 ID ABRK3571 standard; cDNA; 521 BP.
 AC ABRK3571;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE cDNA encoding human PRO protein, Seq ID No 71.
 XX
 KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
 KW breast cancer; prostate tumour; rectal tumour; liver tumour;
 KW pericyte cell proliferation; chondrocyte cell proliferation;
 KW tumour necrosis factor-alpha; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200208288-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 29-JUN-2001; 2001MO-US21066.
 XX
 PR 20-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220585P.
 PR 25-JUL-2000; 2000US-220605P.
 PR 25-JUL-2000; 2000US-220607P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 25-JUL-2000; 2000US-220638P.
 PR 25-JUL-2000; 2000US-220644P.
 PR 25-JUL-2000; 2000US-220666P.
 PR 25-JUL-2000; 2000US-220683P.
 PR 28-JUL-2000; 2000MO-US20710.
 PR 23-AUG-2000; 2000MO-US23522.
 PR 24-AUG-2000; 2000MO-US23328.
 PR 15-SEP-2000; 2000US-00000P.
 PR 10-NOV-2000; 2000MO-US30873.
 PR 28-NOV-2000; 2000US-253646P.
 PR 01-DEC-2000; 2000MO-US32678.
 PR 20-DEC-2000; 2000US-0747259.
 PR 20-DEC-2000; 2000MO-US34956.
 PR 28-FEB-2001; 2001MO-US06520.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001MO-US17092.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WT;
 DR WPI; 2002-172001/22.
 DR P-PSDB; AAU83627.
 XX
 PT One hundred and twenty two nucleic acids encoding PRO polypeptides,

PT useful for treating a PRO related disorder and for diagnosing tumours
 PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
 PT tumour or liver tumour.
 XX
 XX Claim 2; Figure 71; 359pp; English.
 CC The invention relates to one hundred and twenty two nucleic acids
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
 CC agonists and antagonists are useful for treating a PRO related disorder.
 CC The PRO polypeptides are useful for diagnosing tumours, especially lung
 CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. The PRO polypeptides are useful for stimulating the
 CC proliferation of, or gene expression, in pericyte cells, for stimulating
 CC the proliferation or differentiation of chondrocyte cells, for
 CC stimulating the release of tumour necrosis factor-alpha from human blood,
 CC for stimulating or inhibiting the proliferation of normal human dermal
 CC fibroblast cells. The PRO polypeptide may also be used as molecular
 CC weight markers and for tissue typing. The PRO nucleic acids have
 CC applications in molecular biology, including use as hybridisation probes,
 CC and in chromosome and gene mapping. ABRK3536-ABRK3657 represent human
 CC PRO protein coding sequences of the invention.
 XX
 SQ Sequence 521 BP; 167 A; 86 C; 131 G; 137 T; 0 other;
 Alignment Scores:
 Pred. No.: 1,536-69 Length: 521
 Score: 541.00 Matches: 98
 Percent Similarity: 95.45% Conservative: 7
 Best Local Similarity: 89.09% Mismatches: 5
 Query Match: 91.54% Indels: 0
 DB: 24 Gaps: 0
 US-10-019-455a-49 (1-110) x ABRK3571 (1-521)
 QY 1 HisGlyMetPheMetAspLysLeuSerSerlyslsLeuCyAlaaspGluGlyCysVal 20
 DB 92 CATGGAATATTTATGAGACGCTAGCTTCCAGAGAGCTCTGTGAGATGAGAGTGTCTC 151
 QY 21 TyrThrIleSerLeuValArgAlaGlnGlnAspTyraAsnAlaProaspCyargPheIle 40
 DB 152 TATACATTTCTCTGCTAGTCTCAAGAAATTATATATCCCGAGCTGTATCATTTATT 211
 QY 41 AenVallyslvsglynglnlnleTyValTySerlyseuValThrgluasnGlyala 60
 DB 212 AACGTTAAAGGCGAGCATCTATGTACTCAAGCTGTAAAGAAATGAGACT 271
 QY 61 GlyAlaPheTpaIagIseValTyrgIyAspHisGlnaaspGluMetGlyIleValGly 80
 DB 272 GGAGAAATTTGGGCTGGCAGTGTATTATGTGTATGCGAGACGAGATGGAGATCGTGGGT 331
 QY 81 TyPheProSerAsnLeuValArgGluGlnArgValTyrglnGlnAlaThrlyGluIle 100
 DB 332 TATTTCCCGAGAACTTGTCAGAGAACAGCGTGTACCGAGAACTACCAAGAAATT 391
 QY 101 ProThrThraPpIleaspPhePheCyseGlu 110
 DB 392 CCCACCGAGATATTGACTTCTTCTGCGAG 421
 RESULT 13
 AAH98228 ID AAH98228 standard; cDNA; 891 BP.
 AC AAH98228;
 XX
 DT 12-OCT-2001 (first entry)
 XX
 DE Human EST-derived coding sequence SEQ ID NO: 85.
 XX
 KW Human; sheep; pig; cow; fruit fly; Yeast; hamster; macaque; horse;
 KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
 KW diagnostics; forensic test; gene mapping; genetic disorder;
 KW biodiversity; gene therapy; nutrition; ss.

```

XX Homo sapiens.
OS
XX MO200154477-A2.
XX
XX 02-AUG-2001.
XX
XX 25-JAN-2001; 2001W0-US02687.
XX
XX 25-JAN-2000; 2000US-0491404.
XX
XX 17-JUL-2000; 2000US-0617746.
XX
XX 03-AUG-2000; 2000US-0631451.
XX
XX 15-SEP-2000; 2000US-0663870.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
XX Cao Y, Drmanac RA, Zhang J, Werhman T;
XX
XX WPI; 2001-476164/51.
XX
XX P-PSDB; AAM23569.
XX
XX Isolated polypeptide for treatment of diseases, diagnostics, raising
XX antibodies and research use -
XX
XX Claim 1; Page 236; 1275pp; English.
XX
XX The present invention provides the protein and coding sequences of novel
XX proteins from a variety of organisms, including human, dog, cat, horse,
XX cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
XX urchin and tomato. These were derived from expressed sequence tags (ESTs)
XX from the organism of interest. They can be used in diagnostics,
XX forensics, gene mapping, identification of mutations, to assess
XX biodiversity and for nutritional purposes. The present sequence is a cDNA
XX of the invention.
XX
XX Sequence 891 BP; 272 A; 146 C; 214 G; 259 T; 0 other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 3,31e-69 Length: 891
XX Score: 541.00 Matches: 98
XX Percent Similarity: 95.45% Conservative: 7
XX Best Local Similarity: 89.09% Mismatches: 5
XX Query Match: 91.54% Indels: 0
XX DB: Gaps: 0
XX
XX US-10-019-455A-49 (1-110) x AAH98228 (1-891)
XX
XX 1 HisGlyMetPheMetAspLysLeuSerLysLysLeuCysAlaAspGluGluCysVal 20
XX 73 CATGAAATATTATGACCGCTGAGCTTCAAGAGCTCTGTGAGATGAGATGAGTGTGTC 132
XX 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
XX 133 TATATAATTTCTCTGGCTAGTGCCTCAAGAAATTTATATGCCCCGAGCTGAGTTTCAATT 192
XX
XX 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
XX 193 AACGTTAAAAAGGCGACAGATCTATGTACTCAAGCTGGTAAAGAAAGAAATGAGACT 252
XX
XX 61 GluAlaPheTTPAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
XX 253 GGAGAAATTTGGGCTGGCAGATGTTATGATGCGCCGAGCAGATGGGAGTGTGGGT 312
XX
XX TyrPheProSerAsnLeuValArgGluGlnArgValTyrGlnGluAlaThrLysGluIle 100
XX 313 TATTTCCCAAGAACTTGGTCAAGAACACAGCTGTGTACCGAAGACTACCAAGAACTT 372
XX
XX 101 ProThrThrAspIleAspPhePheCysGlu 110
XX
XX 373 CCCACACGAGATATTGACTTCTTCTGCGAG 402
XX
XX RESULT 14

```

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AAH26342
ID AAH26342 standard; cDNA; 891 BP.
XX
XX AAH26342;
XX
XX 02-OCT-2001 (first entry)
XX
XX Human growth regulatory-like polypeptide partial cDNA clone.
XX
XX Growth regulatory-like polypeptide; human; cartilage; melanoma;
XX neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;
XX ss.
XX
XX Homo sapiens.
XX
XX MO200155332-A2.
XX
XX 02-AUG-2001.
XX
XX 25-JAN-2001; 2001W0-US02455.
XX
XX 25-JAN-2000; 2000US-0491404.
XX
XX 02-MAY-2000; 2000US-0563786.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Mize NK, Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C;
XX Drmanac RT;
XX
XX WPI; 2001-48323/52.
XX
XX Isolated human growth regulatory-like polypeptide useful for treating
XX e.g. Alzheimer's disease, cancer, autoimmune disorders,
XX hyperproliferative disorders, coagulation disorders, and nervous system
XX disorders -
XX
XX Claim 1; Page 115; 119pp; English.
XX
XX The present sequence is that of a novel nucleic acid that was
XX assembled from human thymus cDNA library-derived Hyseq clone
XX identification number 16372272 (see AAH26341). A recursive
XX algorithm was used to extend the clone by pulling additional
XX sequences from different databases. A full-length sequence (see
XX AAH26343) encoding novel human growth regulatory-like polypeptide
XX (GRP, see AAH2671) was subsequently obtained. Human GRP
XX belongs to the same protein family as growth regulatory proteins,
XX growth factors, human melanoma derived growth regulatory protein
XX precursor (64% similarity and 45% identity over 111 amino acids)
XX or melanoma inhibitory activity, cattle cartilage-derived
XX retinoic acid sensitive protein (CD-RAP, 44% identity and 64%
XX similarity over 126 amino acids) and other retinoic acid-sensitive
XX proteins. GRP polypeptides and polynucleotides of the invention
XX can be used in the prophylaxis, treatment (including gene therapy)
XX and diagnosis of disorders and diseases caused by, or involving,
XX cartilage development and maintenance, inhibition of melanoma cell
XX growth and tumours, including neuroectodermal tumours such as
XX gliomas. The polynucleotides can also be used to design probes
XX and primers, for chromosome and gene mapping, in the recombinant
XX production of protein, in the generation of antisense, ribozyme and
XX peptide-nucleic acid molecules, and to produce transgenic animals.
XX
XX Sequence 891 BP; 272 A; 146 C; 214 G; 259 T; 0 other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 3,31e-69 Length: 891
XX Score: 541.00 Matches: 98
XX Percent Similarity: 95.45% Conservative: 7
XX Best Local Similarity: 89.09% Mismatches: 5
XX Query Match: 91.54% Indels: 0
XX DB: Gaps: 0
XX
XX US-10-019-455A-49 (1-110) x AAH26342 (1-891)

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QY 1 HisGlyMetPheMetAspLysLeuSerSerLysLysLeuCyAlaAspGluGluCysVal 20
 DB 73 CATGGAAATTTATGACCGCTCTAGCTTCCAGAAAGCTGTGCGAGATGATGAGTGTGC 132
 QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
 DB 133 TATACTATTCTCTGCTGCTAGTCTCAAGAAATTATTAAGCCCGAGCTGTGATTTCATT 192
 QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
 DB 193 AACGTTAAAAAGGCGACGATCTATGTGCTCAAGCTGTGTAAGAAATGAGCT 252
 QY 61 GlyAlaPheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
 DB 253 GGAGAAATTTGGCGCTGGCAGTGTATGCTGATGCCGAGACGAGATGGAGATCGTGGGT 312
 QY 81 TyrPheProSerAsnLeuValArgGluGlnArgValTyrGlnGluAlaThrLysGluIle 100
 DB 313 TATTTCCCGAGAACTTGCTCAAGAACGCTGTGTACAGAAAGCTACCAAGGAAGTT 372
 QY 101 ProThrThrAspIleAspPheCysGlu 110
 DB 373 CCCACCGAGATTTGACTTCTTCTGCGAG 402
 RESULT 15
 AAF59083
 ID AAF59083 standard; DNA; 923 BP.
 AC AAF59083;
 XX
 DT 23-APR-2001 (first entry)
 DE Human MLP nucleotide sequence SEQ ID NO:29.
 XX
 KM MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
 KM joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
 KM Cardiant; gene therapy; secretory cell function regulator; promoter;
 KM inhibitor; ds.
 XX
 OS Homo sapiens.
 XX
 PN MO200102564-A1.
 XX
 PD 11-JAN-2001.
 XX
 PF 29-JUN-2000; 2000WO-0P04278.
 XX
 PR 30-JUN-1999; 99JP-0186718.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Itoh Y, Nishi K, Ogi K, Okubo S, Mogi S, Noguchi Y, Yoshimura K;
 PI Tanaka H;
 XX
 DR WPI, 2001-159271/16.
 XX
 PT Safe, low-toxicity secretory cell function-regulatory protein and
 PT encoded DNA, applicable as drugs, in diagnosis and development of
 PT promoters and inhibitors for preventing or treating e.g. bone and joint
 PT diseases
 XX
 PS Example 1; Page 99-100; 11pp; Japanese.
 XX
 CC The present invention describes novel MLP proteins and their encoding
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
 CC activities, and can be used in gene therapy and as secretory cell
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in
 CC the diagnosis and development of promoters and inhibitors for preventing
 CC or treating bone and joint diseases as well as pathologic angiogenesis.
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
 CC in the exemplification of the present invention.
 XX
 SQ Sequence 923 BP; 303 A; 147 C; 213 G; 260 T; 0 other;

Alignment Scores:
 Pred. No.: 3,48e-69 Length: 923
 Score: 541.00 Matches: 98
 Percent Similarity: 95.45% Conservative: 7
 Best Local Similarity: 89.09% Mismatches: 5
 Query Match: 91.54% Indels: 0
 DB: 22 Gaps: 0
 US-10-019-455a-49 (1-110) x AAF59083 (1-923)
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 DB 88 CATGGAAATTTATGACCGCTCTAGCTTCCAGAAAGCTGTGCGAGATGATGAGTGTGC 147
 QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
 DB 148 TATACTATTCTCTGCTGCTAGTCTCAAGAAATTATATGCCCGAGCTGTGATTTCATT 207
 QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
 DB 208 AACGTTAAAAAGGCGACGATCTATGTGCTCAAGCTGTGTAAGAAATGAGCT 267
 QY 61 GlyAlaPheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
 DB 268 GGAGAAATTTGGCGCTGGCAGTGTATGCTGATGCCGAGACGAGATGGAGATCGTGGGT 327
 QY 81 TyrPheProSerAsnLeuValArgGluGlnArgValTyrGlnGluAlaThrLysGluIle 100
 DB 328 TATTTCCCGAGAACTTGCTCAAGAACGCTGTGTACAGAAAGCTACCAAGGAAGTT 387
 QY 101 ProThrThrAspIleAspPheCysGlu 110
 DB 388 CCCACCGAGATTTGACTTCTTCTGCGAG 417

Search completed: December 29, 2003, 16:41:16
 Job time : 134.647 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 29, 2003, 19:57:30 ; Search time 246.807 Seconds
(without alignments)
1527.048 Million cell updates/sec

Title: US-10-019-455A-49
Perfect score: 591
Sequence: 1 HGMFMKUSKKLCADEECV.....RYVQATEIPPTIDPFCE 110

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Ygapop 10.0 , Ygapext 0.5
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Searched: 2244575 seqs, 173117285 residues

Total number of hits satisfying chosen parameters: 4489150

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-TRANS-human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
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Database : Published Applications NA:

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11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
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15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
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18: /cgn2_6/ptodata/2/pubpna/US00_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
|------------|-------|-------------|--------|----|-------------|

| Result No. | Score | Query Match | Length | ID | Description |
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| 2 | 541 | 91.5 | 521 | 13 | US-10-216-163-71 |
| 3 | 541 | 91.5 | 521 | 13 | US-10-218-765-71 |
| 4 | 541 | 91.5 | 521 | 13 | US-10-219-063-71 |
| 5 | 541 | 91.5 | 521 | 13 | US-10-219-066-71 |
| 6 | 541 | 91.5 | 521 | 13 | US-10-219-067-71 |
| 7 | 541 | 91.5 | 521 | 13 | US-10-219-068-71 |
| 8 | 541 | 91.5 | 521 | 13 | US-10-219-069-71 |
| 9 | 541 | 91.5 | 521 | 13 | US-10-219-073-71 |
| 10 | 541 | 91.5 | 521 | 13 | US-10-219-475-71 |
| 11 | 541 | 91.5 | 521 | 13 | US-10-219-480-71 |
| 12 | 541 | 91.5 | 521 | 13 | US-10-219-483-71 |
| 13 | 541 | 91.5 | 521 | 13 | US-10-219-525-71 |
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| 20 | 541 | 91.5 | 521 | 13 | US-10-219-536-71 |
| 21 | 541 | 91.5 | 521 | 13 | US-10-219-537-71 |
| 22 | 541 | 91.5 | 521 | 13 | US-10-219-538-71 |
| 23 | 541 | 91.5 | 521 | 13 | US-10-219-539-71 |
| 24 | 541 | 91.5 | 521 | 13 | US-10-219-540-71 |
| 25 | 541 | 91.5 | 521 | 13 | US-10-219-541-71 |
| 26 | 541 | 91.5 | 521 | 13 | US-10-219-542-71 |
| 27 | 541 | 91.5 | 521 | 13 | US-10-219-543-71 |
| 28 | 541 | 91.5 | 521 | 13 | US-10-219-544-71 |
| 29 | 541 | 91.5 | 521 | 13 | US-10-219-545-71 |
| 30 | 541 | 91.5 | 521 | 13 | US-10-219-546-71 |
| 31 | 541 | 91.5 | 521 | 13 | US-10-219-547-71 |
| 32 | 541 | 91.5 | 521 | 13 | US-10-219-548-71 |
| 33 | 541 | 91.5 | 521 | 13 | US-10-219-549-71 |
| 34 | 541 | 91.5 | 521 | 13 | US-10-219-550-71 |
| 35 | 541 | 91.5 | 521 | 13 | US-10-219-551-71 |
| 36 | 541 | 91.5 | 521 | 13 | US-10-219-552-71 |
| 37 | 541 | 91.5 | 521 | 13 | US-10-219-553-71 |
| 38 | 541 | 91.5 | 521 | 13 | US-10-219-554-71 |
| 39 | 541 | 91.5 | 521 | 13 | US-10-219-555-71 |
| 40 | 541 | 91.5 | 521 | 13 | US-10-219-556-71 |
| 41 | 541 | 91.5 | 521 | 13 | US-10-219-557-71 |
| 42 | 541 | 91.5 | 521 | 13 | US-10-219-558-71 |
| 43 | 541 | 91.5 | 521 | 13 | US-10-219-559-71 |
| 44 | 541 | 91.5 | 521 | 13 | US-10-219-560-71 |
| 45 | 541 | 91.5 | 521 | 13 | US-10-219-561-71 |

ALIGNMENTS

RESULT 1
US-10-216-038-1
Sequence 1, Application US/10216038
Publication No. US20030124573A1
GENERAL INFORMATION:
APPLICANT: Mize, Nancy K
APPLICANT: Boyle, Bryan J
APPLICANT: Ford, John E
APPLICANT: Atterburn, Matthew C
APPLICANT: Tang, Y Tom
APPLICANT: Liu, Chenghua
APPLICANT: Demanc, Radoje T
APPLICANT: Song, Yong
TITLE OF INVENTION: Methods and Materials Relating to No. US20030124573A1 Growth R
FILE REFERENCE: HVS-7CIP
CURRENT FILING DATE: 2002-08-08
PRIORITY FILING DATE: 2000-05-02
PRIORITY FILING DATE: 2000-01-25
PRIORITY FILING DATE: 2000-01-25
NUMBER OF SEQ ID NOS: 8

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 426
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (426) (426)
; OTHER INFORMATION: n = A, T, G, or C
US-10-216-038-1

Alignment Scores:
Pred. No.: 4,08e-75 Length: 426
Score: 541.00 Matches: 98
Percent Similarity: 95.45% Conservative: 7
Best Local Similarity: 89.09% Mismatches: 5
Query Match: 91.54% Indels: 0
DB: 15 Gaps: 0

US-10-019-455a-49 (1-110) x US-10-216-038-1 (1-426)

QY 1 HisGlyMetPheMetAspLysLeuSerSerLysLysLeuCyAlaAspGluGluCysVal 20
Db CATGGAATATTATTATGACCGCTGCTAGCTCCAGAGAGCTGTGACAGTATGAGTGTGTC 132
QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrTrsAlaProAspCysArgPheIle 40
Db TATACGATTTCTCTGGCTAGTCTCAAGAGATTATATATCCCCGAGCTGTAGATTCAATT 192
QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
Db 193 AACCTTAAAAAAGGCGACAGCATCTATCTACTCAAGCTGTAAAGAAAATGAGACT 252
QY 61 GlyAlaPheTyrPalaglySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
Db 253 GGAAGATTTTGGGCTGGCAGGTATTATGTATGTATGATGGCAGACAGATGGAGCTGTGGGT 312
QY 81 TyrPheProSerAsnLeuValArgGlnGlnIleTyrValTyrGlnGlnIleTyrLysGluIle 100
Db 313 TATTTCCTCCAGGAAGCTGTGCAAGAACAGCTGTGTATACAGAGACTACCAAGAGATT 372
QY 101 ProThrThrAspIleAspPheCysGlu 110
Db 373 CCCACCAAGATATTGACTTCTTCTGCGAG 402

RESULT 2
US-10-216-163-71
; Sequence 71, Application US/10216163
; Publication No. US20030149239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Matanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P350P1G3
; CURRENT APPLICATION NUMBER: US/10/216,163
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549

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; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining prior application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-216-163-71

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Pred. No.: 5.47e-75 Length: 521
Score: 541.00 Matches: 98
Percent Similarity: 95.45% Conservative: 7
Best Local Similarity: 89.09% Mismatches: 5
Query Match: 91.54% Indels: 0
DB: 13 Gaps: 0

US-10-019-455a-49 (1-110) x US-10-216-163-71 (1-521)

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Db 152 TATACGATTTCTCTGGCTAGTCTCAAGAGATTATATATCCCCGAGCTGTAGATTCAATT 211
QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
Db 212 AACCTTAAAAAAGGCGACAGCATCTATCTACTCAAGCTGTAAAGAAAATGAGACT 271
QY 61 GlyAlaPheTyrPalaglySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
Db 272 GGAAGATTTTGGGCTGGCAGGTATTATGTATGTATGATGGCAGACAGATGGAGCTGTGGGT 331
QY 81 TyrPheProSerAsnLeuValArgGlnGlnIleTyrValTyrGlnGlnIleTyrLysGluIle 100
Db 332 TATTTCCTCCAGGAAGCTGTGCAAGAACAGCTGTGTATACAGAGACTACCAAGAGATT 391
QY 101 ProThrThrAspIleAspPheCysGlu 110
Db 392 CCCACCAAGATATTGACTTCTTCTGCGAG 421

RESULT 3
US-10-218-765-71
; Sequence 71, Application US/10218765
; Publication No. US20030187201A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Matanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P350P1G3
; CURRENT APPLICATION NUMBER: US/10/218,765
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549

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FILE REFERENCE: P3530P1C19
CURRENT APPLICATION NUMBER: US/10/218,765
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/086392
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089905
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090691
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/095302
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/095318
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/095916
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/096146
PRIOR FILING DATE: 1998-08-11
PRIOR APPLICATION NUMBER: 60/096791
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 60/097986
PRIOR FILING DATE: 1998-08-26
PRIOR APPLICATION NUMBER: 60/098544
PRIOR FILING DATE: 1998-08-31
PRIOR APPLICATION NUMBER: 60/099596
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099598
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099803
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099811
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099812
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099816
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/100038
PRIOR FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: 60/100385
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100390
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100627
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100848
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/100919
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/101477
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101738
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101741
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101786
PRIOR FILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: 60/101916
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101922
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/106178
PRIOR FILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: 60/106248
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 60/106464
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 60/106905
PRIOR FILING DATE: 1998-11-03
PRIOR APPLICATION NUMBER: 60/108787
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/108801
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/108849
PRIOR FILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: 60/112422
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/113296
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/113605
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113621
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/115558
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115565
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115733
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/119549
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/123618
PRIOR FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: 60/125259
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 60/125775
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 60/126773
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: 60/127887
PRIOR FILING DATE: 1999-04-05
PRIOR APPLICATION NUMBER: 60/130232
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/131022

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; PRIOR FILING DATE: 1999-04-26
; PRIOR APPLICATION NUMBER: 60/131270
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131291
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131445
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 60/134287
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/140650
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/140723
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/141037
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/144758
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/145698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 60/146222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 60/146963
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/149320
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/149638
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/151733
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/164418
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: 60/166361
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/169445
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835

```

```

Alignment Scores:
Pred. No.: 5,47e-75 Length: 521
Score: 541.00 Matches: 98
Percent Similarity: 95.45% Conservative: 7
Best Local Similarity: 89.09% Mismatches: 5
Query Match: 91.54% Indels: 0
DB: 13 Gaps: 0

```

US-10-019-455a-49 (1-110) x US-10-219-765-71 (1-521)

```

QY 1 HisGlyMetPheMetAspLysLeuSerLysLeuCySAIAspGluGluCysVal 20
DB 92 CATGGAATATTATGACCGCTCTAGCTCCAGAACTGCTGTGCAATGATGATGTC 151
QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
DB 152 TATACTATTCTCTGCGCTAGTGTCTCAAGAAATTATTAATGCCCCGAGCTGTAGATTCAAT 211
QY 41 AsnValLysLysGlnGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
DB 212 AACGTTAAAAAGGCGCAGCATCTATGTCTCAAGCTGTTAAAAAGAAATGGAGCT 271
QY 61 GlValAphetPrlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
DB 272 GGAAGATTTTGGCTGGCAGTGTATTATGTGATGCGCAGACAGATGGAGTGGT 331
QY 81 TyrPheProSerAsnLeuValArgGluGlnArgValTyrGlnGluAlaThrLysGluIle 100
DB 332 TATTTCCCGAAGAACTGTCAAGAAACAGCGTGTGTACAGAAAGCTCAAGAAAGTT 391
QY 101 ProThrThrAspIleAspPhePheCysGlu 110
DB 392 CCCACGACGAGATATGACTTCTTCTGCGAG 421

```

RESULT 4

```

US-10-219-063-71
; Sequence 71, Application US/10219063
; Publication No. US20030187202A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gettitsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C24
; CURRENT APPLICATION NUMBER: US/10/219,063
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien

```

US-10-219-063-71

```

Alignment Scores:
Pred. No.: 5,47e-75 Length: 521
Score: 541.00 Matches: 98
Percent Similarity: 95.45% Conservative: 7
Best Local Similarity: 89.09% Mismatches: 5
Query Match: 91.54% Indels: 0
DB: 13 Gaps: 0

```

US-10-019-455a-49 (1-110) x US-10-219-063-71 (1-521)

```

QY 1 HisGlyMetPheMetAspLysLeuSerLysLeuCySAIAspGluGluCysVal 20
DB 92 CATGGAATATTATGACCGCTCTAGCTCCAGAACTGCTGTGCAATGATGATGTC 151
QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
DB 152 TATACTATTCTCTGCGCTAGTGTCTCAAGAAATTATTAATGCCCCGAGCTGTAGATTCAAT 211
QY 41 AsnValLysLysGlnGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
DB 212 AACGTTAAAAAGGCGCAGCATCTATGTCTCAAGCTGTTAAAAAGAAATGGAGCT 271
QY 61 GlValAphetPrlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80

```

Db 272 GGAGATTGGCTGGAGTCTTTATGATGACGACGAGATGGAGTCTGGCT 331
 Qy 81 TyrPheProSerAsnLeuValArgGlnGlnArgValTyrGlnGlnAlaThrLysGluIle 100
 Db 332 TATTTCCCGAGAACTTGTGTCAAGAACAGCGTGTGTACCAAGAGCTTACCAAGAGATT 391
 Qy 101 ProThrThrAspIleAspPhePheCysGlu 110
 Db 392 CCCACCGAGATATTGACTTCTTCTGCGAG 421

RESULT 5

US-10-219-066-71
 ; Sequence 71, Application US/10219066
 ; Publication No. US20030187203A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3530P1C37
 ; CURRENT FILING DATE: US/10/219,066
 ; PRIOR FILING DATE: 2002-08-13
 ; PRIOR APPLICATION NUMBER: 10/119,480
 ; PRIOR FILING DATE: 2002-04-09
 ; PRIOR APPLICATION NUMBER: 60/059113
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/062287
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/063549
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/064103
 ; PRIOR FILING DATE: 1997-10-31
 ; PRIOR APPLICATION NUMBER: 60/069873
 ; PRIOR FILING DATE: 1997-12-17
 ; PRIOR APPLICATION NUMBER: 60/078910
 ; PRIOR FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: 60/079294
 ; PRIOR FILING DATE: 1998-03-25
 ; PRIOR APPLICATION NUMBER: 60/079656
 ; PRIOR FILING DATE: 1998-03-26
 ; PRIOR APPLICATION NUMBER: 60/079728
 ; PRIOR FILING DATE: 1998-03-27
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 246
 ; SEQ ID NO 71
 ; LENGTH: 521
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 ; US-10-219-066-71

Alignment Scores:

Pred. No.: 5,47e-75 Length: 521
 Score: 541.00 Matches: 98
 Percent Similarity: 95.45% Conservative: 7
 Best Local Similarity: 89.09% Mismatches: 5
 Query Match: 91.54% Indels: 0
 DB: 13 Gaps: 0

US-10-019-455a-49 (1-110) x US-10-219-066-71 (1-521)

Qy 1 HisGlyMetPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGlnGlnCysVal 20
 Db 92 CATGGAATATTATGACCGTCTAGCTTCCAGAAAGCTGTGTCCAGATGATGATGTGTTC 151

Qy 21 TyrThrIleSerIleuAlaArgAlaGlnGlnuAspTyrAsnAlaProAspCysArgPheIle 40
 Db 152 TATATCAATTTCTTGTGCTAGTGTCTCAAGAAAGATTATTAAGCCCCGAGCTGTGATTCAATT 211
 Qy 41 AsnValLysLysGlnGlnGlnIleTyrValTyrSerLysLeuValThrGlnuAsnGlyAla 60
 Db 212 AACGTTAAATAAAGGCGACGAGATCTATGTGTACTCAAAAGCTGTAAAGAAATGGAGCT 271
 Qy 61 GlyAlaPheTPrAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
 Db 272 GGAGATTGGCTGGAGTCTTTATGATGACGACGACGACGACGATGGAGTCTGGCT 331
 Qy 81 TyrPheProSerAsnLeuValArgGlnGlnArgValTyrGlnGlnAlaThrLysGluIle 100
 Db 332 TATTTCCCGAGAACTTGTGTCAAGAACAGCGTGTGTACCAAGAGCTTACCAAGAGATT 391
 Qy 101 ProThrThrAspIleAspPhePheCysGlu 110
 Db 392 CCCACCGAGATATTGACTTCTTCTGCGAG 421

RESULT 6

US-10-219-067-71
 ; Sequence 71, Application US/10219067
 ; Publication No. US20030187204A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3530P1C51
 ; CURRENT FILING DATE: US/10/219,067
 ; PRIOR FILING DATE: 2002-08-14
 ; PRIOR APPLICATION NUMBER: 10/119,480
 ; PRIOR FILING DATE: 2002-04-09
 ; PRIOR APPLICATION NUMBER: 60/059113
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/062287
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/063549
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/064103
 ; PRIOR FILING DATE: 1997-10-31
 ; PRIOR APPLICATION NUMBER: 60/069873
 ; PRIOR FILING DATE: 1997-12-17
 ; PRIOR APPLICATION NUMBER: 60/078910
 ; PRIOR FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: 60/079294
 ; PRIOR FILING DATE: 1998-03-25
 ; PRIOR APPLICATION NUMBER: 60/079656
 ; PRIOR FILING DATE: 1998-03-26
 ; PRIOR APPLICATION NUMBER: 60/079728
 ; PRIOR FILING DATE: 1998-03-27
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 246
 ; SEQ ID NO 71
 ; LENGTH: 521
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 ; US-10-219-067-71

Alignment Scores:

Pred. No.: 5,47e-75 Length: 521
 Score: 541.00 Matches: 98
 Percent Similarity: 95.45% Conservative: 7

Best Local Similarity: 89.09% Mismatches: 5
 Query Match: 91.54% Indels: 0
 DB: 13 Gaps: 0

US-10-019-455a-49 (1-110) x US-10-219-067-71 (1-521)

QY 1 HisGlyMetPheMetAspLysSerLysSerLysLysLeuCYsaAlaAspGluGluCYsaVal 20
 DB 92 CATGGAATTTTATGACCGCTCTAGCTTCCAGAAAGCTCTGTGCGAGATGATGATGCTC 151
 QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnaAlaProAspCysArgPheIle 40
 DB 152 TATACATTTCTCTGCTGCTGCTCAAGATTAATATGCCCCGAGCTGTGATTCATT 211
 QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
 DB 212 AACGTTAAAAAGGCGACGACATCTATGTACTCAAAAGCTGTAAAAAATGAGACT 271
 QY 61 GlyAlaPheTPrAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyTLeValGly 80
 DB 272 GAGGAATTTTGCGCTGCGAGCTTTTATGCTGATGCGCCAGACGAGATGGAGCTCGTGGT 331
 QY 81 TyrPheProSerAsnLeuValArgGluGlnArgValTyrGlnGluAlaThrLysGluIle 100
 DB 332 TATTTCCCGAGAACTGTGTCAGAAAGACGCGTGTGTACAGAAAGCTACCAAGAGATT 391
 QY 101 ProThrThrAspLysPhePheCysGlu 110
 DB 392 CCCACACGAGATTTGACTTCTTCTGCGAG 421

RESULT 7

US-10-219-068-71
 ; Sequence 71, Application US/10219068
 ; Publication No. US20030187205A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gueney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3530P1C31
 ; CURRENT APPLICATION NUMBER: US/10/219,068
 ; PRIOR FILING DATE: 2002-08-13
 ; PRIOR APPLICATION NUMBER: 10/119,480
 ; PRIOR FILING DATE: 2002-04-09
 ; PRIOR APPLICATION NUMBER: 60/059113
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/062287
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/063549
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/064103
 ; PRIOR FILING DATE: 1997-10-31
 ; PRIOR APPLICATION NUMBER: 60/069873
 ; PRIOR FILING DATE: 1997-12-17
 ; PRIOR APPLICATION NUMBER: 60/078910
 ; PRIOR FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: 60/079294
 ; PRIOR FILING DATE: 1998-03-25
 ; PRIOR APPLICATION NUMBER: 60/079656
 ; PRIOR FILING DATE: 1998-03-26
 ; PRIOR APPLICATION NUMBER: 60/079728
 ; PRIOR FILING DATE: 1998-03-27
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 246

; SEQ ID NO 71
 ; LENGTH: 521
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 US-10-219-068-71

Alignment Scores:

Pred. No.: 5,47e-75 Length: 521
 Score: 541.00 Matches: 98
 Percent Similarity: 95.45% Conservative: 7
 Best Local Similarity: 89.09% Mismatches: 5
 Query Match: 91.54% Indels: 0
 DB: 13 Gaps: 0

US-10-019-455a-49 (1-110) x US-10-219-068-71 (1-521)

QY 1 HisGlyMetPheMetAspLysSerLysSerLysLysLeuCYsaAlaAspGluGluCYsaVal 20
 DB 92 CATGGAATTTTATGACCGCTCTAGCTTCCAGAAAGCTCTGTGCGAGATGATGATGCTC 151
 QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnaAlaProAspCysArgPheIle 40
 DB 152 TATACATTTCTCTGCTGCTGCTCAAGATTAATATGCCCCGAGCTGTGATTCATT 211
 QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
 DB 212 AACGTTAAAAAGGCGACGACATCTATGTACTCAAAAGCTGTAAAAAATGAGACT 271
 QY 61 GlyAlaPheTPrAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyTLeValGly 80
 DB 272 GAGGAATTTTGCGCTGCGAGCTTTTATGCTGATGCGCCAGACGAGATGGAGCTCGTGGT 331
 QY 81 TyrPheProSerAsnLeuValArgGluGlnArgValTyrGlnGluAlaThrLysGluIle 100
 DB 332 TATTTCCCGAGAACTGTGTCAGAAAGACGCGTGTGTACAGAAAGCTACCAAGAGATT 391
 QY 101 ProThrThrAspLysPhePheCysGlu 110
 DB 392 CCCACACGAGATTTGACTTCTTCTGCGAG 421

RESULT 8

US-10-219-069-71
 ; Sequence 71, Application US/10219069
 ; Publication No. US20030187206A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gueney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3530P1C40
 ; CURRENT APPLICATION NUMBER: US/10/219,069
 ; PRIOR FILING DATE: 2002-08-13
 ; PRIOR APPLICATION NUMBER: 10/119,480
 ; PRIOR FILING DATE: 2002-04-09
 ; PRIOR APPLICATION NUMBER: 60/059113
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/062287
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/063549
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/064103
 ; PRIOR FILING DATE: 1997-10-31
 ; PRIOR APPLICATION NUMBER: 60/069873
 ; PRIOR FILING DATE: 1997-12-17

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; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-069-71

Alignment Scores:
Pred. No.: 5,47e-75 Length: 521
Score: 541.00 Matches: 98
Percent Similarity: 95.45% Conservative: 7
Best Local Similarity: 89.09% Mismatches: 5
Query Match: 91.54% Indels: 0
DB: 13 Gaps: 0

US-10-019-455a-49 (1-110) x US-10-219-069-71 (1-521)

QY 1 HisGlyMetPheMetAspIleuSerLeuGlyLeuGlyAlaAspGluGluCysVal 20
DB 92 CATGGAATATTATGACCGCTGCTACCTCCAGAAAGCTCTGCGAGATGAGTGTGTC 151
QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
DB 152 TATACTATTCTCTGCGCTAGTGTCTCAAGAGATTATATGCCCGGACTGTAGATTATT 211
QY 41 AsnValIleLysGlyGlnGlnIleTyrValIleTyrSerLysLeuValThrGluAsnGlyAla 60
DB 212 AACGTTAAAAAGGCGACAGATCTATGTACTCAAAAGCTGTAAAAAGAAATGAGAGCT 271
QY 61 GlyAlaPheTyrPalaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
DB 272 GGAGAAATTTGGCGTGGCAGTGTATTATGTTATGTCGCGCAGGAGATGGGAGTGTGGGT 331
QY 81 TyrPheProSerAsnLeuValArgGlnArgValTyrGlnGluAlaThrLysGluIle 100
DB 332 TATTTCCCGAGAACTTGTCACAGAAACGCTGTGTACCGAGAACTTCCAGAAAGTT 391
QY 101 ProThrThrAspIleAspPhePheCysGlu 110
DB 392 CCCACACGAGATATTGACTTCTTCTGCGAG 421

RESULT 9
US-10-219-073-71
; Sequence 71, Application US/10219073
; Publication No. US20030187207A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1G2
; CURRENT APPLICATION NUMBER: US/10/219,073
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09

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; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-073-71

Alignment Scores:
Pred. No.: 5,47e-75 Length: 521
Score: 541.00 Matches: 98
Percent Similarity: 95.45% Conservative: 7
Best Local Similarity: 89.09% Mismatches: 5
Query Match: 91.54% Indels: 0
DB: 13 Gaps: 0

US-10-019-455a-49 (1-110) x US-10-219-073-71 (1-521)

QY 1 HisGlyMetPheMetAspIleuSerLeuGlyLeuGlyAlaAspGluGluCysVal 20
DB 92 CATGGAATATTATGACCGCTGCTACCTCCAGAAAGCTCTGCGAGATGAGTGTGTC 151
QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
DB 152 TATACTATTCTCTGCGCTAGTGTCTCAAGAGATTATATGCCCGGACTGTAGATTATT 211
QY 41 AsnValIleLysGlyGlnGlnIleTyrValIleTyrSerLysLeuValThrGluAsnGlyAla 60
DB 212 AACGTTAAAAAGGCGACAGATCTATGTACTCAAAAGCTGTAAAAAGAAATGAGAGCT 271
QY 61 GlyAlaPheTyrPalaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
DB 272 GGAGAAATTTGGCGTGGCAGTGTATTATGTTATGTCGCGCAGGAGATGGGAGTGTGGGT 331
QY 81 TyrPheProSerAsnLeuValArgGlnArgValTyrGlnGluAlaThrLysGluIle 100
DB 332 TATTTCCCGAGAACTTGTCACAGAAACGCTGTGTACCGAGAACTTCCAGAAAGTT 391
QY 101 ProThrThrAspIleAspPhePheCysGlu 110
DB 392 CCCACACGAGATATTGACTTCTTCTGCGAG 421

RESULT 10
US-10-219-475-71
; Sequence 71, Application US/10219475
; Publication No. US20030187208A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria

```

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APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C49
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 71
LENGTH: 521
TYPE: DNA
ORGANISM: Homo Sapien
US-10-019-475-71

Alignment Scores:
Pred. No.: 5,47e-75 Length: 521
Score: 541.00 Matches: 98
Percent Similarity: 95.45% Conservative: 7
Best Local Similarity: 89.09% Mismatches: 5
Query Match: 91.54% Indels: 0
DB: 13 Gaps: 0

US-10-019-455a-49 (1-110) x US-10-219-475-71 (1-521)
QY 1 HisGlyMetPheMetAspLysLeuSerSerLysLysLeuCyaaLaAspGluGluCysVal 20
Db 92 CATGGAATATTATGACCGCTAGCTCCAGAGAGCTCTGTGCAGATGATGAGTGTCTC 151
QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
Db 152 TATACTATTCTCTGGCTAGTGTCTCAAGAGATTATTAATGCCCCGAGCTGATGATTCATT 211
QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
Db 212 AACGTTAAAAAGGCGACAGATCTATGTGTACTCAAAGCTGTGTAAGAAAAATGAGACT 271
QY 61 GlyAlaPheTyrAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
Db 272 GGAGAAATTTGGCTGGCGAGTGTATGTATGTATGCGCCAGACGAGATGCGAGTGTGGCT 331
QY 81 TyrPheProSerAsnLeuValArgGluGlnArgValTyrGlnGlnAlaThrLysGluIle 100
Db 332 TATTTCCCGAGAACCTTGTCTCAAGACGCTGTGTACCGAGAGCTTACCAAGAGAGTT 391
QY 101 ProThrThrAspIleAspPhePheCysGlu 110
Db 392 CCCACCACGAGATATGACTTCTTCTGCGAG 421
RESULT 11
US-10-219-480-71
; Sequence 71, Application US/10219480

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Publication No. US20030187209A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C48
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 71
LENGTH: 521
TYPE: DNA
ORGANISM: Homo Sapien
US-10-219-480-71

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Alignment Scores:
Pred. No.: 5,47e-75 Length: 521
Score: 541.00 Matches: 98
Percent Similarity: 95.45% Conservative: 7
Best Local Similarity: 89.09% Mismatches: 5
Query Match: 91.54% Indels: 0
DB: 13 Gaps: 0

US-10-019-455a-49 (1-110) x US-10-219-480-71 (1-521)
QY 1 HisGlyMetPheMetAspLysLeuSerSerLysLysLeuCyaaLaAspGluGluCysVal 20
Db 92 CATGGAATATTATGACCGCTAGCTCCAGAGAGCTCTGTGCAGATGATGAGTGTCTC 151
QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
Db 152 TATACTATTCTCTGGCTAGTGTCTCAAGAGATTATTAATGCCCCGAGCTGATGATTCATT 211
QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
Db 212 AACGTTAAAAAGGCGACAGATCTATGTGTACTCAAAGCTGTGTAAGAAAAATGAGACT 271
QY 61 GlyAlaPheTyrAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
Db 272 GGAGAAATTTGGCTGGCGAGTGTATGTATGTATGCGCCAGACGAGATGCGAGTGTGGCT 331
QY 81 TyrPheProSerAsnLeuValArgGluGlnArgValTyrGlnGlnAlaThrLysGluIle 100

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DB 332 TATTTCCCGAGAACTTGTGTCACAGAACGCTGTGTCACGAGACTTCCAGAGAACTT 391
QY 101 ProThrThrAspIleaspPhePheCysGlu 110
DB 392 CCCACACGAGATATTGACTTCTTCTGCGAG 421

RESULT 12
US-10-219-483-71
Sequence 71, Application US/10219483
Publication No. US20030187210A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530PIC43
CURRENT APPLICATION NUMBER: US/10/219,483
PRIOR FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 71
LENGTH: 521
TYPE: DNA
ORGANISM: Homo Sapien
US-10-219-483-71

Alignment Scores:
Pred. No.: 5,47e-75 Length: 521
Score: 541.00 Matches: 98
Percent Similarity: 95.45% Conservative: 7
Best Local Similarity: 89.09% Mismatches: 5
Query Match: 91.54% Indels: 0
Gaps: 13
DB: 13

US-10-019-455A-49 (1-110) x US-10-219-483-71 (1-521)

QY 1 HisGlyMetPheMetAspLysLeuSerLysLeuCysAlaAspGluGluCysVal 20
DB 92 CARGAATATTATGACCGCTTACGCTTCCAGAAAGCTTGTGCGAGATGATAGTGTGC 151
QY 21 TTTTThiIleSerLeuAlaArgAlaGluGluAspTyrAsnAlaProAspCysArgPheIle 40
DB 152 TATACTATTCTCTGCTAGTGTCTCAAGAAATTAATTAATGCCCGAGACTGATTCATT 211

QY 41 AsnValIleYsgIYgInGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
DB 212 AACGTTAAAAAGGCGACAGACTTATGTACTCAAACTGGTAAAGAAATGAGACT 271
QY 61 GlyAlaPheTAlaIleGlySerValTyrGlyAspPheGlnAspGluMetCylIleValGly 80
DB 272 GGAGAAATTTGGCTGGCAGTGTATTATGTGTGATGGCCAGACGAGATGGAGTGGTGGCT 331
QY 81 TyrPheProSerAsnLeuValArgGluGluArgValTyrGlnGluAlaThrLysGluIle 100
DB 332 TATTTCCCGAGAACTTGTGTCACAGAACGCTGTGTCACGAGACTTCCAGAGAACTT 391
QY 101 ProThrThrAspIleaspPhePheCysGlu 110
DB 392 CCCACACGAGATATTGACTTCTTCTGCGAG 421

RESULT 13
US-10-219-525-71
Sequence 71, Application US/10219525
Publication No. US20030187211A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530PIC29
CURRENT APPLICATION NUMBER: US/10/219,525
PRIOR FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 71
LENGTH: 521
TYPE: DNA
ORGANISM: Homo Sapien
US-10-219-525-71

Alignment Scores:
Pred. No.: 5,47e-75 Length: 521
Score: 541.00 Matches: 98
Percent Similarity: 95.45% Conservative: 7
Best Local Similarity: 89.09% Mismatches: 5
Query Match: 91.54% Indels: 0
Gaps: 13
DB: 13

US-10-019-455a-49 (1-110) x US-10-219-526-71 (1-521)

```
QY 1 HisGlyMetPheMetAspLysLeuSerSerLysLysLeuCyAlaAspGluGluCyVal 20
   92 CATGAAATATTATGACCGCTGCTAGCTTCAAGAAAGCTCTGCGAGATGATGATGCTC 151
QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
   152 TATACTATTCTCTGCTAGTCTCTCAAGAAATATTAATGCCCCGAGCTGTAGATTCTT 211
QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
   212 AACGTTAAAAAGGCGACAGATCTATGCTCTCAAGCTGTAAAAAGAAATGAGACT 271
QY 61 GlyAlaPheTyrAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
   272 GGAAGATTTTGGCTGCGCTGCTTATGCTGATGCGCCAGACGAGATGAGAGTCTGCTG 331
QY 81 TyrPheProSerAsnLeuValArgGluGlnArgValTyrGlnGluAlaThrLysGluIle 100
   332 TATTTCCCGAGAACTGTGTCAAGAACGCGTGTGTACCAAGAACTTACCAAGAAAGTT 391
QY 101 ProThrThrAspIleAspPhePheCysGlu 110
   392 CCCACCGAGATATTGACTTCTTCTGCGAG 421
Db
```

RESULT 14

```
US-10-219-526-71
; Sequence 71, Application US/10219526
; Publication No. US20030187212A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerltsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCES: P3530P1C41
; CURRENT APPLICATION NUMBER: US/10/219,526
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
```

; ORGANISM: Homo Sapien
US-10-219-526-71

| Alignment Scores: | |
|------------------------|----------|
| Pred. No.: | 5,47e-75 |
| Score: | 541.00 |
| Percent Similarity: | 95.45% |
| Best Local Similarity: | 89.09% |
| Query Match: | 91.54% |
| DB: | 13 |
| Length: | 521 |
| Matches: | 98 |
| Conservative: | 7 |
| Mismatches: | 5 |
| Indels: | 0 |
| Gaps: | 0 |

US-10-019-455a-49 (1-110) x US-10-219-526-71 (1-521)

```
QY 1 HisGlyMetPheMetAspLysLeuSerSerLysLysLeuCyAlaAspGluGluCyVal 20
   92 CATGAAATATTATGACCGCTGCTAGCTTCAAGAAAGCTCTGCGAGATGATGATGCTC 151
QY 21 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
   152 TATACTATTCTCTGCTAGTCTCTCAAGAAATATTAATGCCCCGAGCTGTAGATTCTT 211
QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 60
   212 AACGTTAAAAAGGCGACAGATCTATGCTCTCAAGCTGTAAAAAGAAATGAGACT 271
QY 61 GlyAlaPheTyrAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 80
   272 GGAAGATTTTGGCTGCGCTGCTTATGCTGATGCGCCAGACGAGATGAGAGTCTGCTG 331
QY 81 TyrPheProSerAsnLeuValArgGluGlnArgValTyrGlnGluAlaThrLysGluIle 100
   332 TATTTCCCGAGAACTGTGTCAAGAACGCGTGTGTACCAAGAACTTACCAAGAAAGTT 391
QY 101 ProThrThrAspIleAspPhePheCysGlu 110
   392 CCCACCGAGATATTGACTTCTTCTGCGAG 421
Db
```

RESULT 15

```
US-10-219-530-71
; Sequence 71, Application US/10219530
; Publication No. US20030187213A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerltsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCES: P3530P1C54
; CURRENT APPLICATION NUMBER: US/10/219,530
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
```

PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO: 71
LENGTH: 521
TYPE: DNA
ORGANISM: Homo Sapien
US-10-219-530-71

Alignment Scores:
Pred. No.: 5,47e-75 Length: 521
Score: 541.00 Matches: 98
Percent Similarity: 95.45% Conservative: 7
Best Local Similarity: 89.09% Mismatches: 5
Query Match: 91.54% Indels: 0
DB: 13 Gaps: 0

US-10-019-455a-49 (1-110) x US-10-219-530-71 (1-521)

QY 1 HIGLWEPHEWETAPLYSLEUSERLYSLYSLYCYSAIAAPGUNGICYSVAL 20
DB 92 CATGGAATATTATGACCGCTTAGCTTCCAGAGCTGTGCAGATGATGATGCTGC 151
QY 21 TYTHRIESESERLEUALARGAAGINGLUASPTYRASNLAAPROAEPCYSAARGPHEILE 40
DB 152 TATCTATTCTCTCGCTAGAGCTCAAGAGATTATATGCCCCGGACTGTAGATTCAAT 211
QY 41 ASNVALYSLYSGLYGINGINILETYRVALTYRSELYSLEUVALTHRGUAENGLYALA 60
DB 212 AACGTTAAAAAGCGCAGCATCTATGTACTCAAGCTGGTAAAGAAATGGAGCT 271
QY 61 GLVALAHERTPALAGLYSERVALTYRGLYASPHISGINASPGIUMETGLYLEVALGLY 80
DB 272 GGAGAAATTTGGCTGGCGAGGTATTATGATGATGCGCAGACGAGATGGAGTGTGGT 331
QY 81 TYRHEPPOSEASNLEUVALARGGLUGLARGVALTYRGINGLUALATHRLYSGLUILE 100
DB 332 TATTTCCTCCAGCACTTGTGTAAGGAACAGCGTGTGTACCGAAGCTACCAAGAAAGTT 391
QY 101 PROTHRTHASPILEASPHEPHECYSGLU 110
DB 392 CCCACACGAGATATGACTCTCTGCGAG 421

Search completed: December 30, 2003, 02:01:10
Job time : 248.807 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 29, 2003, 16:24:24 ; Search time 34.972 Seconds
(without alignments)
1388.315 Million cell updates/sec

Title: US-10-019-455A-49

Perfect score: 591
Sequence: 1 HGMFMXLSKKLCADCECV.....RVQEAATKEIPTTIDPFCE 110

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delcp 6.0, Delcxt 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -STRAT=1 -END=1 -MATRIX=bl0sum62 -TRANS=human40.cdi
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Issued Patents NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 264.5 | 44.8 | 330 | 1 | US-08-578-649-18 |
| 2 | 264.5 | 44.8 | 459 | 1 | US-08-578-649-1 |
| 3 | 244.5 | 41.4 | 581 | 1 | US-08-578-649-4 |
| 4 | 222.5 | 37.6 | 305 | 1 | US-08-578-649-8 |
| 5 | 197 | 33.3 | 596 | 1 | US-08-578-649-24 |
| 6 | 160.5 | 27.2 | 3565 | 1 | US-08-578-649-3 |
| 7 | 93.5 | 15.8 | 2793 | 1 | US-07-646-537B-1 |
| 8 | 91.5 | 15.5 | 2757 | 1 | US-08-306-691B-48 |
| 9 | 91.5 | 15.5 | 2757 | 5 | PCT-US93-06251-79 |
| 10 | 91.5 | 15.5 | 4762 | 4 | US-09-300-958A-30 |
| 11 | 85 | 14.4 | 467 | 4 | US-09-300-958A-28 |
| 12 | 82.5 | 14.0 | 5398 | 3 | US-09-356-952-11 |

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| 13 | 74 | 12.5 | 2085 | 1 | US-08-164-839-3 | Sequence 3, Appl1 |
| 14 | 74 | 12.5 | 2085 | 1 | US-08-583-799-3 | Sequence 3, Appl1 |
| 15 | 74 | 12.5 | 2520 | 1 | US-08-164-839-5 | Sequence 5, Appl1 |
| 16 | 74 | 12.5 | 2520 | 1 | US-08-583-799-5 | Sequence 5, Appl1 |
| 17 | 69 | 11.7 | 971 | 4 | US-08-630-915A-197 | Sequence 197, App |
| 18 | 69 | 11.7 | 1457 | 3 | US-09-444-053-3 | Sequence 3, Appl1 |
| 19 | 67 | 11.3 | 1664976 | 4 | US-08-916-421B-1 | Sequence 1, Appl1 |
| 20 | 67 | 11.3 | 1664976 | 4 | US-08-916-421B-1 | Sequence 1, Appl1 |
| 21 | 66.5 | 11.3 | 2064 | 1 | US-08-164-839-30 | Sequence 30, Appl1 |
| 22 | 66.5 | 11.3 | 2064 | 1 | US-08-164-839-32 | Sequence 32, Appl1 |
| 23 | 66.5 | 11.3 | 2064 | 1 | US-08-583-799-30 | Sequence 30, Appl1 |
| 24 | 66.5 | 11.3 | 2064 | 1 | US-08-583-799-32 | Sequence 32, Appl1 |
| 25 | 66.5 | 11.3 | 2148 | 1 | US-08-164-839-69 | Sequence 69, Appl1 |
| 26 | 66.5 | 11.3 | 2148 | 1 | US-08-164-839-71 | Sequence 71, Appl1 |
| 27 | 66.5 | 11.3 | 2148 | 1 | US-08-583-799-69 | Sequence 69, Appl1 |
| 28 | 66.5 | 11.3 | 2148 | 1 | US-08-583-799-71 | Sequence 71, Appl1 |
| 29 | 66 | 11.2 | 840 | 1 | US-08-434-255-7 | Sequence 7, Appl1 |
| 30 | 66 | 11.2 | 840 | 1 | US-08-459-967-7 | Sequence 7, Appl1 |
| 31 | 66 | 11.2 | 840 | 1 | US-08-460-327-7 | Sequence 7, Appl1 |
| 32 | 66 | 11.2 | 840 | 1 | US-08-459-967-1 | Sequence 7, Appl1 |
| 33 | 66 | 11.2 | 840 | 3 | US-09-024-532-1 | Sequence 1, Appl1 |
| 34 | 66 | 11.2 | 840 | 4 | US-09-104-623A-1 | Sequence 1, Appl1 |
| 35 | 66 | 11.2 | 840 | 4 | US-09-019-532-1 | Sequence 1, Appl1 |
| 36 | 66 | 11.2 | 840 | 1 | US-09-417-359A-1 | Sequence 1, Appl1 |
| 37 | 66 | 11.2 | 1110 | 1 | US-08-434-255-5 | Sequence 5, Appl1 |
| 38 | 66 | 11.2 | 1110 | 1 | US-08-459-967-5 | Sequence 5, Appl1 |
| 39 | 66 | 11.2 | 1110 | 1 | US-08-460-327-5 | Sequence 5, Appl1 |
| 40 | 66 | 11.2 | 1110 | 1 | US-08-459-871-5 | Sequence 5, Appl1 |
| 41 | 66 | 11.2 | 1191 | 1 | US-08-434-255-3 | Sequence 3, Appl1 |
| 42 | 66 | 11.2 | 1191 | 1 | US-08-459-967-3 | Sequence 3, Appl1 |
| 43 | 66 | 11.2 | 1191 | 1 | US-08-460-327-3 | Sequence 3, Appl1 |
| 44 | 66 | 11.2 | 1191 | 1 | US-08-459-871-3 | Sequence 3, Appl1 |
| 45 | 66 | 11.2 | 2017 | 1 | US-08-434-255-27 | Sequence 27, Appl1 |

ALIGNMENTS

RESULT 1
US-08-578-649-18
; Sequence 18, Application US/08578649
; Patent No. 5770366
GENERAL INFORMATION:
APPLICANT: Ulrich Bogdan
APPLICANT: Reinhard Butner
APPLICANT: Brigitte Kaluza
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-July-1993
ATTORNEY/AGENT INFORMATION:
NAME: Andrew L. Tiajoloie
REGISTRATION NUMBER: 31,575
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 330 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 7..327
NAME/KEY: misc_RNA
LOCATION: 4..6
OTHER INFORMATION: /function= "Startcodon Met"
US-08-578-649-18
Alignment Scores:
Pred. No.: 1.08e-29 Length: 330
Score: 264.50 Matches: 50
Percent Similarity: 67.59% Conservative: 23
Best Local Similarity: 46.30% Mismatches: 30
Query Match: 44.75% Indels: 5
DB: 1 Gaps: 3
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QY MetAspLysLeuSerSerLysLeuCyAlaAspGluGluCyValTyrThrIleSer 24
13 ATGCCAAATTAGAGATCGTAATTATGTGCAGATCAGAGATGCCACCACTATCTCC 72
DB 25 LeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnValLys 44
73 ATGGCTGTGGCCCTTCAGACTACATGGCCCCGACCTGCAGATTCTGCACCATTCACCG 132
QY 45 GlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaPhe 63
133 GGGCAATGTGTATGATCTTCTCCAAAGCTG-----AAGGCCGTGGCGGCTCTTC 183
DB 64 TrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyLeu---ValGlyTyrPhe 82
184 TGGGAGGACGACCTTCAGGAGATTTACTATGAGATCTGCTGCTGCGCTATTTTC 243
QY 83 ProSerAsnLeuValArgGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 102
244 CCCAGTAGCATTTGCCAGAGACCAACCTGAAACCTGGCAAAATGCATGTGAAGACA 303
DB 103 ThrAspIleAspPhePheCysGlu 110
304 GACCAATGGATTTCTACTGCCAG 327
RESULT 2
US-08-578-649-1
Sequence 1, Application US/08578649
Patent No. 5770366
GENERAL INFORMATION:
APPLICANT: Ulrich Bogdan
APPLICANT: Reinhard Buttner
APPLICANT: Brigitte Kaluza
TITLE OF INVENTION: MELANOMA-INHIBITTING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felle & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-July-1993
ATTORNEY/AGENT INFORMATION:
NAME: Andrew L. Tiajoloft
REGISTRATION NUMBER: 31,575
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 459 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 40..432
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 40..111
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 112..432
US-08-578-649-1
Alignment Scores:
Pred. No.: 1.73e-29 Length: 459
Score: 264.50 Matches: 50
Percent Similarity: 67.59% Conservative: 23
Best Local Similarity: 46.30% Mismatches: 30
Query Match: 44.75% Indels: 5
DB: 1 Gaps: 3
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DB 25 LeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnValLys 44
178 ATGGCTGTGGCCCTTCAGACTACATGAGCCCCCGACCTGCAGATTCTGCACCATTCACCG 237
QY 45 GlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaPhe 63
238 GGGCAAGTGTATGATCTTCTCCAAAGCTG-----AAGGCCGTGGCGGCTCTTC 288
DB 64 TrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyLeu---ValGlyTyrPhe 82
289 TGGGAGGACGACCTTCAGGAGATTTACTATGAGATCTGCTGCTGCGCTATTTTC 348
QY 83 ProSerAsnLeuValArgGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 102
349 CCCAGTAGCATTTGCCAGAGACCAACCTGAAACCTGGCAAAATGCATGTGAAGACA 408
DB 103 ThrAspIleAspPhePheCysGlu 110
409 GACCAATGGATTTCTACTGCCAG 432
RESULT 3
US-08-578-649-4
Sequence 4, Application US/08578649
Patent No. 5770366
GENERAL INFORMATION:
APPLICANT: Ulrich Bogdan
APPLICANT: Reinhard Buttner
APPLICANT: Brigitte Kaluza

TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-July-1993
ATTORNEY/AGENT INFORMATION:
NAME: Andrew L. Tiajolo
REGISTRATION NUMBER: 31,575
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 581 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 110..499
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 110..178
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 179..499
US-08-578-649-4
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Pred. No.: 1,976-26 Length: 581
Score: 244.50 Matches: 50
Percent Similarity: 64.81% Conservative: 20
Best Local Similarity: 46.30% Mismatches: 33
Query Match: 41.37% Indels: 5
Gaps: 3
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QY 25 LeuAlaArgAlaGlnGluAspTYrAsnAlaProAspCySAAspPheIleAsnValLys 44
DB 245 ATGCTGTGGCCCTCCAGAGCTACCTGCGCCCTTATTCCTTGACTATATATAGG 304
QY 45 GlyGlnGlnIleTYrValTYrSerLysLeuValThrGluSncjYalagly---AlaPhe 63
DB 305 GGCCCAAGTGGCTGACTGAGAGCTGTGCGAGCAGAGATCAACCACTTATCTCC 355
QY 64 ThrAlaGlySerValTYrGlyAspHisGlnAspGluMetGlyIle---ValGlyTYrPhe 82
DB 356 TGGGAGGAGCAGTGTTCAGGAGGAGTTACTATGAGACCTGAGCCCGCTGGGCTATTTTC 415
QY 83 ProSerAsnLeuValArgGluGlnArgValTYrGlnGlnIleThrLysGluIleProThr 102

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QY 103 ThrAspIleAspPhePheCyGlu 110
DB 476 GATCATGGAGTTTCTACTGCGAG 499
RESULT 4
US-08-578-649-8
Sequence 8, Application US/08578649
Patent No. 5770366
GENERAL INFORMATION:
APPLICANT: Ulrich Bogdan
APPLICANT: Reinhard Buttner
APPLICANT: Brigitte Kaluza
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-July-1993
ATTORNEY/AGENT INFORMATION:
NAME: Andrew L. Tiajolo
REGISTRATION NUMBER: 31,575
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 305 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: misc RNA
LOCATION: join(1..29, 277..305)
OTHER INFORMATION: /function="Primer"
US-08-578-649-8
Alignment Scores:
Pred. No.: 1,256-23 Length: 305
Score: 222.50 Matches: 45
Percent Similarity: 64.65% Conservative: 15
Best Local Similarity: 45.45% Mismatches: 30
Query Match: 37.65% Indels: 5
Gaps: 3
US-10-019-455a-49 (1-110) x US-08-578-649-8 (1-305)
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DB 7 AAGTTTGGCGGAGTACGAGAGTGCAGCACCTATCTCATGCGTGTGCGCTTCAGAGAC 66
QY 32 TyrAsnAlaProAspCySAAspPheIleAsnValLysGlyGlnGlnIleTYrValTYr 51
DB 67 TACATGGCCCGCTGCGATCTCTGACCACTTACCGGAGGCGCAAGTGTGTATCTCTTC 126

QY 52 SerLysLeuValThrGluAsnGlyAlaGly---AlaPheTrpAlaGlySerValTyrGly 70
 Db 127 TCCAGCTG-----AAGGCCCGTGGCGGCTCTTCTGGGAGGAGCGGTTCAAGGA 177
 QY 71 AsnHisGln---AspGluMetGlyIleValGlyTyrPheProSerAsnLeuValArgGlu 89
 Db 178 GATTACTATGAGATCTGTGCTCGCTGCGCTGAGCTATTTCCCGCTGACATTGTCCGAGAG 237
 QY 90 GluArgValTyrGlnGluAlaThrLysGluIleProThrThrAspIleAspPhePhe 108
 Db 238 GACCAGACCTGTAACCTGGCAAGTCGATGTAAGACGATTAATGGATTCTTAC 294
 RESULT 5
 ; Sequence 24, Application US/08578649
 ; Patent No. 5770366
 ; GENERAL INFORMATION:
 ; APPLICANT: Ulrich Bogdan
 ; APPLICANT: Reinhard Butner
 ; APPLICANT: Brigitte Kaluza
 ; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Felfe & Lynch
 ; STREET: 805 Third Avenue
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10022
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
 ; COMPUTER: IBM PS/2
 ; OPERATING SYSTEM: PC-DOS
 ; SOFTWARE: Wordperfect
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/578,649
 ; FILING DATE: 29-July-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: DE P 43 24 247.2
 ; FILING DATE: 20-July-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Andrew L. Tiajoleff
 ; REGISTRATION NUMBER: 31,575
 ; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 688-9200
 ; TELEFAX: (212) 838-3864
 ; INFORMATION FOR SEQ. ID NO: 24:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 596 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: join(40..111, 40..166, 214..347, 393..503, 549
 ; LOCATION: ..569)
 ; FEATURE:
 ; NAME/KEY: sig_peptide
 ; LOCATION: 40..111
 ; FEATURE:
 ; NAME/KEY: exon
 ; LOCATION: 40..166
 ; FEATURE:
 ; NAME/KEY: exon
 ; LOCATION: 214..347
 ; FEATURE:
 ; NAME/KEY: exon
 ; LOCATION: 393..503
 ; FEATURE:

NAME/KEY: exon
 LOCATION: 549..569
 FEATURE:
 NAME/KEY:
 LOCATION: one-of(194, 369, 527)
 OTHER INFORMATION: /note= "N in positions 194, 369
 OTHER INFORMATION: and 527 denotes an indefinite number and sequence
 OTHER INFORMATION: of nucleotides "
 US-08-578-649-24
 Alignment Scores:
 Pred. No.: 1.67e-19 Length: 596
 Score: 197.00 Matches: 51
 Percent Similarity: 47.74% Conservative: 23
 Best Local Similarity: 32.90% Mismatches: 28
 Query Match: 33.33% Indels: 54
 DB: 1 Gaps: 7
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 Db 118 ATGCCAAGCTGCTGACCGAGAGCTGTGCGACCGAGAGTCAAGCC-TAAGAAATCG 176
 QY 22 -----ThrlSerLeuAlaArgAla 28
 Db 177 GAGGCTAGATTGGAGCCCTTATTCTTCTCCCTAGACCTATCTCATGCTGTGGCC 236
 QY 29 GlnGluAspTyrAsnAlaProAspCysArgPheIleAsnValLysGlyGlnIle 48
 Db 237 CTTCAGAGCTACATGCGCCCGGACTGCGGATTCCTGACCAATTCACCGGCGCAAGTGTG 296
 QY 49 TyrValTyrSerLysLeuValThrGluAsnGlyAlaGly---AlaPheTrpAlaGlySer 67
 Db 297 TATGCTTCTTCAAGCTG-----AAGGCCGTGGCGGCTCTTCTGTGGAGGAGCG 347
 QY 68 -----ValTyrGlyAspHis 72
 Db 348 GTGGCTCTGGAGAGTGAAGAAAGCTTTTAATCTCTCTCCCGGAGTTCAAGGAGATTAC 407
 QY 73 GlnAspGluMetGlyIle---ValGlyTyrPheProSerAsnLeuValArgGluGlnArg 91
 Db 408 TATGAGATCTGGCTGCTGCGCTCGGCTATTTCCCGAGTACATGTCGAGAGGACAG 467
 QY 92 ValTyrGlnGluAlaThrLysGluIleProThrThrAspIle----- 105
 Db 468 ACCCTGAACCTGGCAAGTCGATGTG---AAGACAGACGTGAGTGTATGAGGGGCTCG 524
 QY 106 -----AspPheCysGlu 110
 Db 525 CANTTCCCTTTCTCTTTTCAAGAAATGGGATTCTTACGTCCAG 569
 RESULT 6
 ; Sequence 3, Application US/08578649
 ; Patent No. 5770366
 ; GENERAL INFORMATION:
 ; APPLICANT: Ulrich Bogdan
 ; APPLICANT: Reinhard Butner
 ; APPLICANT: Brigitte Kaluza
 ; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Felfe & Lynch
 ; STREET: 805 Third Avenue
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10022
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
 ; COMPUTER: IBM PS/2
 ; OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-July-1993
ATTORNEY/AGENT INFORMATION:
NAME: Andrew L. TiaJolofe
REGISTRATION NUMBER: 31,575
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3565 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 1378..1449
FEATURE:
NAME/KEY: exon
LOCATION: 1378..1504
FEATURE:
NAME/KEY: exon
LOCATION: 1586..1719
FEATURE:
NAME/KEY: exon
LOCATION: 2804..2914
FEATURE:
NAME/KEY: exon
LOCATION: 3232..3252
FEATURE:
NAME/KEY:
LOCATION: one-of(2216)
OTHER INFORMATION: /note= "N in position 2216
OTHER INFORMATION: denotes an indefinite number ans sequence of
US-08-578-649-3
Alignment Scores:
Pred. No.: 4,38e-13 Length: 3565
Score: 160.50 Matches: 36
Percent Similarity: 51.09% Conservative: 11
Best Local Similarity: 39.13% Mismatches: 14
Query Match: 27.16% Indels: 31
Gaps: 3
US-10-019-455A-49 (1-110) x US-08-578-649-3 (1-3565)
QY 5 MetAspLysLeuSerLysLeuCyAlaAspGluGlyCys----- 19
Db 1456 ATGCCAAGCTGCGTGCAGCCGAGAGCTGTGTGCGACCGAGAGTGCAGCCCGTAAGAGATGGG 1515
QY 19 ----- 19
Db 1516 GAGGGGTAGATGGCTTGGGTGTAGCTGTGTGATGCTGATTCCTTCATT 1575
QY 20 -----ValTyrTrpLysSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCys 37
Db 1576 CTTTCCCTAGACCTTATCTCCATGCTGCTGTGCTTCAGAGCTTCATGCGCCCGACTGC 1635
QY 38 ArgPheIleAsnValLysLysGlnGlnIleTyrValTyrSerLysLeuValThrGlu 57
Db 1636 CGATTCTGACCATTCACCGGGCCCAAGTGTGTATGTTCTTCCAGAGCTG----- 1686
QY 58 AsnGlyAlaGly---AlaPheTrpAlaGlySerVal 68

Db 1687 AAGGCGCTGGAGCGCTTCTTGGGAGGACGCGTG 1722
RESULT 7
US-07-646-537B-1
Sequence 1, Application US/07646537B
Patent No. 5348864
GENERAL INFORMATION:
APPLICANT: Barbacid, Mariano
TITLE OF INVENTION: Vav Proto-Oncogene Protein
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: Bristol-Myers Squibb Company
STREET: P.O. Box 4000
CITY: Princeton
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 08543-4000
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/646,537B
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gault, Timothy J.
REGISTRATION NUMBER: 33,111
REFERENCE/DOCKET NUMBER: DC10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 921-5901
TELEFAX: (609) 921-4526
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2793 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
MOLECULE TYPE: linear
TOPOLOGY: linear
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 14..2545
US-07-646-537B-1
Alignment Scores:
Pred. No.: 0.00175 Length: 2793
Score: 93.50 Matches: 23
Percent Similarity: 52.86% Conservative: 14
Best Local Similarity: 32.86% Mismatches: 20
Query Match: 15.82% Indels: 13
Gaps: 3
US-10-019-455A-49 (1-110) x US-07-646-537B-1 (1-2793)
QY 26 AlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnValLysGly 45
Db 2369 GCCAAGCCCGCAGACCTTGTGTGCGGACAGTGCAGAACTGCTTAAAGAGGCT 2428
QY 46 GlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyAlaPheTrpAla 65
Db 2429 GATATCATC-----AAGATCCCTCATTAAGAGGACAGCAAGCGTGGTGGCT 2476
QY 66 GlySerValTyrGlyAspHisGlnAspGlnMetGlyIleValGlyTyrPheProSerAsn 85
Db 2477 GGGGAGATCTACGGCCGG-----ATCGGCTGTGTTCCCTTCTAC 2515
QY 86 LeuValArgGluGlnArgValTyrGlnGlu 95
Db 2516 TATGTGAGAGAGAC-----TATTCGAA 2539
RESULT 8


```

Db      565 CAACAAGGGGAAACCATTTATATCTTAACAAA-----AATCATCTGGG--- 609
Qy      63 PhetTPAlAGlYseerAlTYrGlYAspHISglAspGluMecGlylIeValGlYTYrPhe 82
Db      610 TGGTGGATGGATTAAGTATTATGACGACAGTAATGGAGAAATTAC---AGAGGCTGGTT 666
Qy      83 ProSerAsnLeuValArgGluGlnArg 91
Db      667 CTTCAAAACTTCGTGAGACCTTAAGA 693

RESULT 13
US-08-164-839-3
; Sequence 3, Application US/08164839
; Patent No. 5514573
; GENERAL INFORMATION:
; APPLICANT: YASUEDA, HISASHI
; APPLICANT: NAKANISHI, KAZUO
; APPLICANT: MOTOKI, MASAO
; APPLICANT: NAGASE, KAZUO
; APPLICANT: MATSUI, HIROSHI
; TITLE OF INVENTION: GENE ENCODING TRANSGLUTAMINASE DERIVED
; TITLE OF INVENTION: FROM FISH
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/164,839
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/004,729
; FILING DATE: 14-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5514573man F.
; REGISTRATION NUMBER: 24,618
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)412-3000
; TELEFAX: (703)413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2085 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE:
; ORGANISM: Pagrus major
; TISSUE TYPE: liver
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2082
; US-08-164-839-3

Alignment Scores:
Pred. No.: 0.796 Length: 2085
Score: 74.00 Matches: 21
Percent Similarity: 52.508 Conservative: 21
Best Local Similarity: 26.254 Mismatches: 28
Query Match: 12.524 Indels: 10

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DB:      1 Gaps:      3
US-10-019-455a-49 (1-110) x US-08-164-839-3 (1-2085)
Qy      31 AspTYrAsnAlaIProAspCyArgPheIlAsnValYelYsglYnglnlIetyVal 50
Db      1174 GAGGTGAACGGCTGACACCATTTACTGATGTCTCCAAAAGATGGCCAAACA----- 1224
Qy      51 TySerIYsLeuValThrGluAsnGlyAlaGlyAla-----PhetTPAlAGlYser 67
Db      1225 -----CGAAGATCACAAGAGGACCATCTAGTGTGGGAAAGAACATCAGACAAAAGC 1278
Qy      68 ValTYrGlYAspHISglAspGluMecGlylIeValGlYTYrPheProSerAsnLeuVal 87
Db      1279 GTTACGGCAACACACAGAGAAAGATGTCATCTGCACCTACAAATATCTGAAGCTCCAG 1338
Qy      88 ArgGluGlnArgValTYrGlnGlnAlaThrIYsGluIle-----ProThrThAspIle 105
Db      1339 AAGAGAGGGAAGTGTACAGAAAGCGGAGCGCGGTCAAGAGCCATCCACAGAGATC 1398

RESULT 14
US-08-583-799-3
; Sequence 3, Application US/08583799
; Patent No. 5607849
; GENERAL INFORMATION:
; APPLICANT: YASUEDA, HISASHI
; APPLICANT: NAKANISHI, KAZUO
; APPLICANT: MOTOKI, MASAO
; APPLICANT: NAGASE, KAZUO
; APPLICANT: MATSUI, HIROSHI
; TITLE OF INVENTION: GENE ENCODING TRANSGLUTAMINASE DERIVED
; TITLE OF INVENTION: FROM FISH
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,799
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/004,729
; FILING DATE: 14-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5607849man F.
; REGISTRATION NUMBER: 24,618
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)412-3000
; TELEFAX: (703)413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2085 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE:
; ORGANISM: Pagrus major
; TISSUE TYPE: liver
; FEATURE:
; NAME/KEY: CDS

```

LOCATION: 1.2082
US-08-583-799-3

Alignment Scores:

| Pred. No.: | Score: | Percent Similarity: | Best Local Similarity: | Query Match: | Length: | Matches: | Conservative: | Mismatches: | Indels: | Gaps: |
|------------|--------|---------------------|------------------------|--------------|---------|----------|---------------|-------------|---------|-------|
| 0.796 | 74.00 | 52.50% | 26.25% | 12.52% | 2085 | 21 | 28 | 10 | 3 | |

US-10-019-455a-49 (1-110) x US-08-583-799-3 (1-2085)

QY 31 AspTYrAsnAlaProAspCysArgPheIleAsnValIleValGlyTyrPheProSerAsnLeuVal 50
 Db 1174 GAGGTGAACCGCTGACACCATCTACTGATGCTCCAAAAGATGGCAAGA----- 1224
 QY 51 TySerIysLeuValThrGluAsnGlyAlaIle-----PheTrpAlaGlySer 67
 Db 1225 -----CGGAAGATCACAGAGGACCATCTAGTGTGGGAGAAACATCAGCAAAAAGC 1278
 QY 66 ValTYrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPheProSerAsnLeuVal 87
 Db 1279 GTTACGGCAACCAACAGAGATGCTGACTGCACTACCAATATCTGAAAGCTCCAG 1338
 QY 88 ArgGluGlnArgValTYrGlnGlnAlaThrIlysgluile-----ProThrThraspIle 105
 Db 1339 AAGGAGAGGAAGTGTACAGAAAGCGCGGAGCCGGGTACAGAGCCATCCACGAGATC 1398

RESULT 15

US-08-164-839-5
 Sequence 5, Application US/08164839
 Patent No. 5514573
 GENERAL INFORMATION:

APPLICANT: YASUEDA, HISASHI
 APPLICANT: NAKANISHI, KAZUO
 APPLICANT: MOTOKI, MASAO
 APPLICANT: NAGASE, KAZUO
 APPLICANT: MATSUI, HIROSHI
 TITLE OF INVENTION: GENE ENCODING TRANSGUTAMINASE DERIVED
 FROM FISH
 NUMBER OF SEQUENCES: 72
 CORRESPONDENCE ADDRESS:

ADDRESSER: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
 STREET: 1755 Jefferson Davis Highway, Fourth Floor
 CITY: Arlington
 STATE: Virginia
 COUNTRY: U.S.A.
 ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/164,839

FILING DATE:

CLASSIFICATION: 435
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/004,729

FILING DATE: 14-JAN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Olson, No. 5514573man F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 10-599-0

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)412-3000

TELEFAX: (703)412-2220

TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 2520 base pairs

TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 ORIGINAL SOURCE:

ORGANISM: Pagrus major

TISSUE TYPE: liver

FEATURE:

NAME/KEY: CDS

LOCATION: 34..2121

US-08-164-839-5

Alignment Scores:

| Pred. No.: | Score: | Percent Similarity: | Best Local Similarity: | Query Match: | Length: | Matches: | Conservative: | Mismatches: | Indels: | Gaps: |
|------------|--------|---------------------|------------------------|--------------|---------|----------|---------------|-------------|---------|-------|
| 1.04 | 74.00 | 52.50% | 26.25% | 12.52% | 2520 | 21 | 28 | 10 | 3 | |

US-10-019-455a-49 (1-110) x US-08-164-839-5 (1-2520)

QY 31 AspTYrAsnAlaProAspCysArgPheIleAsnValIleValGlyTyrPheProSerAsnLeuVal 50
 Db 1210 GAGGTGAACCGCTGACACCATCTACTGATGCTCCAAAAGATGGCAAGA----- 1260
 QY 51 TySerIysLeuValThrGluAsnGlyAlaIle-----PheTrpAlaGlySer 67
 Db 1261 -----CGGAAGATCACAGAGGACCATCTAGTGTGGGAGAAACATCAGCAAAAAGC 1314
 QY 66 ValTYrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPheProSerAsnLeuVal 87
 Db 1315 GTTACGGCAACCAACAGAGATGCTGACTGCACTACCAATATCTGAAAGCTCCAG 1374
 QY 88 ArgGluGlnArgValTYrGlnGlnAlaThrIlysgluile-----ProThrThraspIle 105
 Db 1375 AAGGAGAGGAAGTGTACAGAAAGCGCGGAGCCGGGTACAGAGCCATCCACGAGATC 1434

Search completed: December 29, 2003, 22:08:21
 Job time: 41.972 secs